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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 2944.03 Seconds

(without alignments)
16933.650 Million cell updates/sec

Title: US-09-776-910-1

Sequence: 1 atgaattcaacgttagttt.....aacatagagatttattttg 1713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBml: *
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
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13: gb.un:*
14: gb.vi:*
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16: em.fun:*
17: em.hum:*
18: em.in:*
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20: em.om:*
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40: em.htgo.mus:*
41: em.htgo.other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	100.0	1713	6	ARI53438
2	1711.4	99.9	1713	6	ARI53442
3	1709.8	99.8	1713	6	ARI53439
4	1706.6	99.6	1713	6	ARI53440
5	1701.8	99.3	1713	6	AR062837
6	1701.8	99.3	1713	6	ARI53441
7	1701.8	99.3	2240	3	LC056636
8	1676.6	97.9	1713	6	AR062838
9	987.2	57.6	2160	3	AF139341
10	959.4	56.0	2175	3	AF139082
11	956.6	55.8	1710	6	ARI53445
12	677.2	39.5	2017	3	AY051473
13	378.6	22.1	2660	3	AY121675
14	373.8	21.8	2820	3	DMU51050
15	369	21.5	5735	2	AC015272
16	369	21.5	188459	3	AC008312
17	369	21.5	197597	3	AC011253
18	369	21.5	309023	3	AE003671
19	365.4	21.3	1962	3	AY051497
20	323	18.9	2122	3	AY058637
21	303	17.7	1906	3	AY058345
22	300.4	17.5	13044	2	AC014297
23	300.4	17.5	117743	2	AC008098
24	300.4	17.5	173373	3	AC008349
25	300.4	17.5	307363	3	AE003457
26	286.6	16.7	2050	3	AF216210
27	278.4	16.3	1205	3	AF216215
28	269.6	15.7	1809	6	AX260182
29	242	14.1	3946	3	DMU51044
30	241.4	14.1	1630	3	COE57A2EA
31	239.8	14.0	10034	2	AC013139
32	239.8	14.0	188459	3	AC008312
33	239.8	14.0	197597	3	AC011253
34	239.8	14.0	309023	3	AE003671
35	229.6	13.4	1724	3	AY069743
36	227.6	13.3	2401	3	DMU51054
37	224.2	13.1	933	3	AF216216
38	224.2	13.1	1836	3	COSERE51
39	224	13.1	3447	3	DMU51052
40	219.2	12.8	1630	3	COSERE52
41	214	12.5	84252	2	AC009207
42	212	12.4	1401	3	CPU43544
43	207.4	12.1	6028	3	AF177382
44	204.8	12.0	1401	3	CPU43546
45	199.8	11.7	1401	3	CPU43545

ALIGNMENTS

RESULT 1
LOCUS ARI53438
DEFINITION Sequence 1 from patent US 6235515.
ACCESSION ARI53438
VERSION ARI53438.1 GI:15120970
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Roblin,G.Charlesde.,Quetteville.,Caudianos,C., Smyth,K.A.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
TITLE Malathion carboxylesterase

Pred. No. is the number of results predicted by chance to have a

JOURNAL	Patent: US 6235515-A 1 22-MAY-2001
FEATURES	Location/Qualifiers
SOURCE	1. 1713
BASE COUNT	/organism="unknown"
ORIGIN	515 a 304 c 370 g 524 t

Query Match	100.0%	Score 1713;	DB 6;	Length 1713;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1713; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0

[illegible]

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Qy	961	GCTGATGTGTCCTTAACCCAAACATCCTCGGGAATTGGTTAAACTGCTTGGGGTAATTCG	1020
Db	961	GCTGATGTGTCCTTAACCCAAACATCCTCGGGAATTGGTTAAACTGCTTGGGGTAATTCG	1020
Qy	1021	ATACCCACTATGATGGGTAAACACTTCATATAGAGGTCTATTTTCACCTCAATTCCTTAAG	1080
Db	1021	ATACCCACTATGATGGGTAAACACTTCATATAGAGGTCTATTTTCACCTCAATTCCTTAAG	1080
Qy	1081	CAAAATGCGCTATGCTTTGTTAAGGAATTGGAAACTGTGTCAATTTTGTGCCAAGTGAATG	1140
Db	1081	CAAAATGCGCTATGCTTTGTTAAGGAATTGGAAACTGTGTCAATTTTGTGCCAAGTGAATG	1140
Qy	1141	GCTGATGTGTTGAAGCAGCACC GCCCAGACACTTTGGAATAGGTGCTAAATTTAAAAAGGCT	1200
Db	1141	GCTGATGTGTTGAAGCAGCACC GCCCAGACACTTTGGAATAGGTGCTAAATTTAAAAAGGCT	1200
Qy	1201	CATGTATACAGAGGAACACACACACTCATATATTTATGATCTTGTGCTCAACATCAT	1260
Db	1201	CATGTATACAGAGGAACACACACACTCATATATTTATGATCTTGTGCTCAACATCAT	1260
Qy	1261	TTCTGTTGCCCATGCATCGTTTGTGCAATTAAGCTTTCAATCACACCTCCGGTACACC	1320
Db	1261	TTCTGTTGCCCATGCATCGTTTGTGCAATTAAGCTTTCAATCACACCTCCGGTACACC	1320
Qy	1321	GTCTACTTGTATCGCTTGCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGATTAATG	1380
Db	1321	GTCTACTTGTATCGCTTGCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGATTAATG	1380
Qy	1381	CGTATGAGCAGTGGTGTTAAGAGGTATTAAGTCATCGCTGATGAATTAACCTATTTCTTGG	1440
Db	1381	CGTATGAGCAGTGGTGTTAAGAGGTATTAAGTCATCGCTGATGAATTAACCTATTTCTTGG	1440
Qy	1441	AATCAATTTGGCCAAACGTAATGCTTAAAGATCGCTGAATACAAACATTTGAACGTATG	1500
Db	1441	AATCAATTTGGCCAAACGTAATGCTTAAAGATCGCTGAATACAAACATTTGAACGTATG	1500
Qy	1501	ACTGTGTAATATGATACAAATTTGGCCACACACTGTATATCCCTATAGCAATGAAATGAAAGT	1560
Db	1501	ACTGTGTAATATGATACAAATTTGGCCACACACTGTATATCCCTATAGCAATGAAATGAAAGT	1560
Qy	1561	ATGGAATAATGTTTCCCTGGGATCCAAATTAAGAAATCGATGAAGGTATACAAAGTGTGGAAT	1620
Db	1561	ATGGAATAATGTTTCCCTGGGATCCAAATTAAGAAATCGATGAAGGTATACAAAGTGTGGAAT	1620
Qy	1621	ATTAGTGAATGAATTGAATAATGATGATGTGCTGAAATGATTAAGATTAACAAATGGGAG	1680
Db	1621	ATTAGTGAATGAATTGAATAATGATGATGTGCTGAAATGATTAAGATTAACAAATGGGAG	1680
Qy	1681	TGCGATGTTGAAAAACATAGAGATTATTTTAAAG 1713	
Db	1681	TGCGATGTTGAAAAACATAGAGATTATTTTAAAG 1713	

RESULT 2	AR153442	1713 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR153442				
DEFINITION	Sequence	9 from patent US 6235515.			
ACCESSION	AR153442				
VERSION	AR153442.1	GI:15120974			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1713)				
	Russell, R., Joyce, Newcomb, R. David., Campbell, P. Malcolm.,				
	Robit, G., Charles, Quetteville., Claudianos, C., Smyth, K. A.,				
	Boyce, T. Mark., Oakeshott, J. Graham, and Brownlie, J. Colin.				
TITLE	Malachion carboxylesterase				
JOURNAL	Patent: US 6235515-A 9 22-MAY-2001;				
FEATURES	Location/Qualifiers				
source	1..1713				

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BASE COUNT      515 a      305 c      370 g      523 t
ORIGIN
Query Match      99.9% Score 1711.4; DB 6; Length 1713;
Best Local Similarly 99.9% Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATGAATTTTCAACGTTAGTGTGAGAGAAATTAATGAGAGATTAAATGATTTGAAAT 60
    |||||||
Db 1 ATGAATTTTCAACGTTAGTGTGAGAGAAATTAATGAGAGATTAAATGATTTGAAAT 60

OY 61 AAGTTTTTAACTATCGTTTAACTACCAATGAAGGAGGAGTGAAGTGAATATGAGC 120
    |||||||
Db 61 AAGTTTTTAACTATCGTTTAACTACCAATGAAGGAGGAGTGAAGTGAATATGAGC 120

OY 121 AAGTGAAGGCGTTAAACGTTTAACTAGTGTGAGAGATTCTTAACTAGAGGT 180
    |||||||
Db 121 AAGTGAAGGCGTTAAACGTTTAACTAGTGTGAGAGATTCTTAACTAGAGGT 180

OY 181 ATACCGAGCGCCCAACGCGGAGGAGGAGTGAATTAAGCAACCCGAGCAACA 240
    |||||||
Db 181 ATACCGAGCGCCCAACGCGGAGGAGGAGTGAATTAAGCAACCCGAGCAACA 240

OY 241 CCTGAGATGCTGCTGATTTGTCATCATTAAGATTAAGTCAAGTGAATTT 300
    |||||||
Db 241 CCTGAGATGCTGCTGATTTGTCATCATTAAGATTAAGTCAAGTGAATTT 300

OY 301 ATAAAGGCAAAAGTGTGCTGCTCAGAGAGATTGCTAATACCTAAGTGTCTATACGAATAT 360
    |||||||
Db 301 ATAAAGGCAAAAGTGTGCTGCTCAGAGAGATTGCTAATACCTAAGTGTCTATACGAATAT 360

OY 361 CTAAATCCCGAACTAAACGTCGCTTTTAACTATACATACATGCTGCTGCTTATTATTC 420
    |||||||
Db 361 CTAAATCCCGAACTAAACGTCGCTTTTAACTATACATACATGCTGCTGCTTATTATTC 420

OY 421 GGTGAATAATCATCGTATATGATGTCCTGATTTTCAATTAAGAGATGCTGTG 480
    |||||||
Db 421 GGTGAATAATCATCGTATATGATGTCCTGATTTTCAATTAAGAGATGCTGTG 480

OY 481 ATTAACATACATATTCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAAGCCTT 540
    |||||||
Db 481 ATTAACATACATATTCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAAGCCTT 540

OY 541 AATGCGCCGCTAATGCGGCTTAAGATCAATCAATGCGCTGCTGATTAATAAT 600
    |||||||
Db 541 AATGCGCCGCTAATGCGGCTTAAGATCAATCAATGCGCTGCTGATTAATAAT 600

OY 601 AATTGCGCAACTTGGTGGCAATCCGATATATTAACAGTCTTTGGTGAAGTCCGCT 660
    |||||||
Db 601 AATTGCGCAACTTGGTGGCAATCCGATATATTAACAGTCTTTGGTGAAGTCCGCT 660

OY 661 GCTGCTCTACCACTACATGATGTAAACGCAAACTCGCGGTCTTTCCATCGTGT 720
    |||||||
Db 661 GCTGCTCTACCACTACATGATGTAAACGCAAACTCGCGGTCTTTCCATCGTGT 720

OY 721 ATACTAATGTGGGTAATGCTATTTGTCATGCTTAATACCAATGCAATCGTCC 780
    |||||||
Db 721 ATACTAATGTGGGTAATGCTATTTGTCATGCTTAATACCAATGCAATCGTCC 780

OY 781 TTACACTTAGCCAAATTTGGCGGCTATTAAGGAGTAAATGATGATTTTGGAA 840
    |||||||
Db 781 TTACACTTAGCCAAATTTGGCGGCTATTAAGGAGTAAATGATGATTTTGGAA 840

OY 841 TTTCTTATGAAGCCAAAGCCAGAGATTTAATAAAGTGAAGAAAAAGTTTAACTCTA 900
    |||||||
Db 841 TTTCTTATGAAGCCAAAGCCAGAGATTTAATAAAGTGAAGAAAAAGTTTAACTCTA 900

OY 901 GAAGAGGTCATTAAGTATGTTTCTTCTTGTCCCACTGTTGAGCCATATCAGACC 960
    |||||||
Db 901 GAAGAGGTCATTAAGTATGTTTCTTCTTGTCCCACTGTTGAGCCATATCAGACC 960

OY 961 GCTGATGTGTCTTACCAAAACATCTCGGGAATGTTAAACTGCTTGGGTAAATTCG 1020
    |||||||

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Db 961 GCTGATGTGTCTTACCAAAACATCTCGGGAATGTTAAACTGCTTGGGTAAATTCG 1020

OY 1021 ATACCCATATGATGGGTAAACACTTTCATATGAGGCTCTATTTTCACTTCAATCTTAAG 1080
    |||||||
Db 1021 ATACCCATATGATGGGTAAACACTTTCATATGAGGCTCTATTTTCACTTCAATCTTAAG 1080

OY 1081 CAATGCTTATGCTTGTAAAGAAATGGAACCTGTGCAATTTTGTGCCAAGTGAATG 1140
    |||||||
Db 1081 CAATGCTTATGCTTGTAAAGAAATGGAACCTGTGCAATTTTGTGCCAAGTGAATG 1140

OY 1141 GCTGATGTGAAGCCACGCGCCGAGACCTTGAAGATGGGTGCTTAAATTAAGAGCT 1200
    |||||||
Db 1141 GCTGATGTGAAGCCACGCGCCGAGACCTTGAAGATGGGTGCTTAAATTAAGAGCT 1200

OY 1201 CATGTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTGCTCACATCTAT 1260
    |||||||
Db 1201 CATGTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTGCTCACATCTAT 1260

OY 1261 TTTGTTGCCCATGACATGTTGTTGCAATTAAGTTCATCAACCTCGGTACACCC 1320
    |||||||
Db 1261 TTTGTTGCCCATGACATGTTGTTGCAATTAAGTTCATCAACCTCGGTACACCC 1320

OY 1321 GTCTACTTGTATCGCTTGCATTCGATTCGGAAGATCTTATCAATCCTATGATATATG 1380
    |||||||
Db 1321 GTCTACTTGTATCGCTTGCATTCGATTCGGAAGATCTTATCAATCCTATGATATATG 1380

OY 1381 CGTAGTGACGTGTGTAAAGGTTGATGATGCTGATGATTAACCTATTTCTTCTG 1440
    |||||||
Db 1381 CGTAGTGACGTGTGTAAAGGTTGATGATGCTGATGATTAACCTATTTCTTCTG 1440

OY 1441 AATCAATGCGCAAAAGTATGCTTAAGAAATCGGTGATACCAAAAGCAATGAAGATG 1500
    |||||||
Db 1441 AATCAATGCGCAAAAGTATGCTTAAGAAATCGGTGATACCAAAAGCAATGAAGATG 1500

OY 1501 ACTGATATGATATACATTTGACACACCTGATATCCTTATAGCAATGAATGAAGT 1560
    |||||||
Db 1501 ACTGATATGATATACATTTGACACACCTGATATCCTTATAGCAATGAATGAAGT 1560

OY 1561 ATGGAATAATGTTCTCGTGAGTCAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
    |||||||
Db 1561 ATGGAATAATGTTCTCGTGAGTCAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620

OY 1621 ATTAGTATGATTAAGAAATGATGATGCTGCTGAAGTGAATGAATGAATGAATGAG 1680
    |||||||
Db 1621 ATTAGTATGATTAAGAAATGATGATGCTGCTGAAGTGAATGAATGAATGAATGAG 1680

OY 1681 TCATGTTTGAAGAAACATAGAGATTTATTTAG 1713
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Db 1681 TCATGTTTGAAGAAACATAGAGATTTATTTAG 1713

RESULT 3
ARI53439
LOCUS ARI53439 1713 bp DNA Linear PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6235515.
ACCESSION ARI53439
VERSION ARI53439.1 GI:15120971
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Roblin, G. Charlesde., Quetleville., Claudianos, C., Smyth, K. A.,
Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 3 22-MAY-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 515 a 306 c 370 g 522 t
ORIGIN

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Query Match	99.8%;	Score 1709.8;	DB 6;	Length 1713;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1711; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	ATGAAATTCAACCTTGTTGATGTGAGAAATTAAATGGAAGATTAAATGCAATTGAAAT	60
Db	1	ATGAAATTCAACCTTGTTGATGTGAGAAATTAAATGGAAGATTAAATGCAATTGAAAT	60
QY	61	AAGTTTAAACATATGTTTAACCTACCATGAAACGGGTGTAGCTGGAACATGCAATATGCG	120
Db	61	AAGTTTAAACATATGTTTAACTACCAATGAAACGGGTGTAGCTGGAACATGCAATATGCG	120
QY	121	AAATGGAAGGCGTTTAAACCTTTAACTGTGTACGATGATCTCTACTACAGTTTGAGGCT	180
Db	121	AAATGGAAGGCGTTTAAACCTTTAACTGTGTACGATGATCTCTACTACAGTTTGAGGCT	180
QY	181	ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCGACGACCAACA	240
Db	181	ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCGACGACCAACA	240
QY	241	CCCTGGAGTGGTGGCTGATTTGTTCCATTCATTAAGATAACTCACTGTCAGATGTGATTT	300
Db	241	CCCTGGAGTGGTGGCGGATGTTGTCATTCATTAAGATAACTCACTGTCAGATGTGATTT	300
QY	301	ATAACGGGCAAAAGTGTGGCTACAGAGATGCTATACCTTAAGTGTCTATAACGATAT	360
Db	301	ATAACGGGCAAAAGTGTGGCTACAGAGATGCTATACCTTAAGTGTCTATAACGATAT	360
QY	361	CTAATCCCGAAACATAACCTCCCGTTTGTAGTATACATACATGCTGGTGTATTATATC	420
Db	361	CTAATCCCGAAACATAACCTCCCGTTTGTAGTATACATACATGCTGGTGTATTATATC	420
QY	421	GCTGAATATCATGCTGATGTATGTAGTGGTCCGATATTTCATTAAGAGATGTGGTGTG	480
Db	421	GCTGAATATCATGCTGATGTATGTAGTGGTCCGATATTTCATTAAGAGATGTGGTGTG	480
QY	481	ATTAACTATACATATTCGTTTGGAGGCTCTAGTTTTCTAAGTTTAAATCAGAGACCTT	540
Db	481	ATTAACTATACATATTCGTTTGGAGGCTCTAGTTTTCTAAGTTTAAATCAGAGACCTT	540
QY	541	AATGGCCCGGTATGGCCGCCCTTAAAGATCAACATGACGCGTGGTGGATTAAAT	600
Db	541	AATGGCCCGGTATGGCCGCCCTTAAAGATCAACATGACGCGTGGTGGATTAAAT	600
QY	601	AATGGCCCACTTTGGTGGCAATCCCGATATATTACAGTCTTTGGTGAAGTCCGGT	660
Db	601	AATGGCCCACTTTGGTGGCAATCCCGATATATTACAGTCTTTGGTGAAGTCCGGT	660
QY	661	GCTGCTCTACCCACTACATGATGTTAACGGAACAACGCGGGCTTTCCATGCTGT	720
Db	661	GCTGCTCTACCCACTACATGATGTTAACGGAACAACGCGGGCTTTCCATGCTGT	720
QY	721	ATACTAATGTGGGTAAATGCTATTTGCTATTTGGCTAATACCAATGTCACATGCTGCC	780
Db	721	ATACTAATGTGGGTAAATGCTATTTGCTATTTGGCTAATACCAATGTCACATGCTGCC	780
QY	781	TTACACTTAGCCAAATTGGCCGGCTATTAAGGTCAGAGATATGATTAAGATTTTGGAA	840
Db	781	TTACACTTAGCCAAATTGGCCGGCTATTAAGGTCAGAGATATGATTAAGATTTTGGAA	840
QY	841	TTTCTTATGAAGCCAGGCCACAGATTATTAATAAATTGAGGAAAAAGTTTAACTCTA	900
Db	841	TTTCTTATGAAGCCAGGCCACAGATTATTAATAAATTGAGGAAAAAGTTTAACTCTA	900
QY	901	GAAGAGCGTACAATTAAGTTCATGTTTCTTTGGTCCACTGTGAGCCATATCAGAC	960
Db	901	GAAGAGCGTACAATTAAGTTCATGTTTCTTTGGTCCACTGTGAGCCATATCAGAC	960
QY	961	GCTGATTTGTCTTACCAAAACATCCCTGGGAAATGTTTAAACCTCTTGGGGTAAATCG	1020
Db	961	GCTGATTTGTCTTACCAAAACATCCCTGGGAAATGTTTAAACCTCTTGGGGTAAATCG	1020

QY	1021	ATACACTATGATGAGGGGATACACTTCATATGAGGGGTCATTTTTCACCTCAATTCCTTAAG	1080
Db	1021	ATACCACTATGATGAGGGGATACACTTCATATGAGGGGTCATTTTTCACCTCAATTCCTTAAG	1080
QY	1081	CAAAATGCGCTATGCTTGTTAAGGAATTGGAAACTGTGTCAATTTTGTGCCAAGTGAATTG	1140
Db	1081	CAAAATGCGCTATGCTTGTTAAGGAATTGGAAACTGTGTCAATTTTGTGCCAAGTGAATTG	1140
QY	1141	GCTGATGTTGAACGACCGCCCAAGACGCTTGGAAATGGGTCGTAATTAAGAAAGGCT	1200
Db	1141	GCTGATGCTGAACGACCGCCCAAGACGCTTGGAAATGGGTCGTAATTAAGAAAGGCT	1200
QY	1201	CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTGCTCACAATCTAT	1260
Db	1201	CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTGCTCACAATCTAT	1260
QY	1261	TTTCGTGTTCCCATCATGCTTTGTTGCAATTTACGTTTCATTCACACCTCCGGTACACC	1320
Db	1261	TTTCGTGTTCCCATCATGCTTTGTTGCAATTTACGTTTCATTCACACCTCCGGTACACC	1320
QY	1321	GTCCTAGTGTATGCGTTCGACTTGCATTCGGAAGATCTTATCAATCCCTATCGATTAATG	1380
Db	1321	GTCCTAGTGTATGCGTTCGACTTGCATTCGGAAGATCTTATCAATCCCTATCGATTAATG	1380
QY	1381	CCTAGTGCAGCTGTGTTTAAGGGTGTATGCTACTGCTGATGAATTAACCTATTTCTTGG	1440
Db	1381	CCTAGTGCAGCTGTGTTTAAGGGTGTATGCTACTGCTGATGAATTAACCTATTTCTTGG	1440
QY	1441	AATTCATTTGGCCAAACGATGCTCTAAAGATGCGCTGAATACAAAACAATTGAACGATATG	1500
Db	1441	AATTCATTTGGCCAAACGATGCTCTAAAGATGCGCTGAATACAAAACAATTGAACGATATG	1500
QY	1501	ACTGCTATATGATGATACATATTTGCCACACACTGCTATTCCTTATAGCAATGAATTAACGT	1560
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QY	1561	ATCGAATAATGTTTCCGCGGATCCAAATTAAGAATCCGATGAAGTATACAGTGTTCGAT	1620
Db	1561	ATCGAATAATGTTTCCGCGGATCCAAATTAAGAATCCGATGAAGTATACAGTGTTCGAT	1620
QY	1621	ATTAGTGAATGAAATGAAAATGATGTGCTGCTGAATGATGAATTAACATTAACATGGGAG	1680
Db	1621	ATTAGTGAATGAAATGAAAATGATGTGCTGCTGAATGATGAATTAACATTAACATGGGAG	1680
QY	1681	TCGATGTTGAAAACACATGAGACTTTATTTTAG	1713
Db	1681	TCGATGTTGAAAACACATGAGACTTTATTTTAG	1713
RESULT 4			
LOCUS	ARI53440	1713 bp	DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 5 from patent US 6235515.		
ACCESSION	ARI53440		
VERSION	ARI53440.1	GI:15120972	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1713)		
	Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,		
	Robln, G. Charlesde, Quetleville., Claudianos, C., Smyth, K. A.,		
	Boye, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Collin.		
TITLE	Malathion carboxylesterase		
JOURNAL	Patent: US 6235515-A 5 22-MAY-2001;		
FEATURES	Location/Qualifiers		
source	1..1713	/organism="unknown"	
BASE COUNT	516 a 305 c 369 g 523 t		
ORIGIN			
Query Match	99.6%;	Score 1706.6;	DB 6; Length 1713;
Best Local Similarity	99.8%;	Pred No. 0;	

Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 ATGAATTTCAACGTAGTTGATGAGAAATTAAGAGATTAAATGATGAATGAAT 60

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Db 61 AAGTTTTTAACTATCCTTAACACTACCAATGAAACGGTGTAGCTGAAGTGAATATGCG 120

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Db 1681 TCGATGTTTGAAMAAACATAGAGATTTATTTAG 1713

RESULT 5
AR062837 1713 bp DNA linear PAT 29-SEP-1999
LOCUS AR062837
DEFINITION Sequence 1 from patent US 5843758.
ACCESSION AR062837
VERSION AR062837.1 GI:5990528
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Robin,G.Charlesde.Quetteville.,
Boyce,T.Mark., Campbell,P.Malcolm.,
Oakeshott,J.Graham. and Smyth,K.-A.
TITLE Enzyme based bioremediation
JOURNAL Patent: US 5843758-A 1 01-DEC-1998;
FEATURES
source location/Qualifiers
1..1713
BASE COUNT 516 a 305 c 370 g 522 t
ORIGIN
Query Match 99.3%; Score 1701.8; DB 6; Length 1713;
Best Local Similarity 99.6%; Pred.No.0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 ATGAATTTCAACGTAGTTGATGAGAAATTAAGAGATTAAATGATGAATGAAT 60

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Db 361 CTAAATCCCGAAACTAAACGTCGCCCTTTAGTATACATACATACATACATACATACATAT 420
Oy 421 GGTGAATAATCATGCTGATATGATGCTGCTGATTTTCAATTAAGAGATGCTGTTATATC 480
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Db 1021 ATACCCATATGATGGGTAAACCTTCAATATGAGGCTATTTTTCACCTCAATTCCTAAG 1080
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RESULT 6
LOCUS AR153441 1713 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6235515.
ACCESSION AR153441
VERSION AR153441.1 GI:15120973
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Robin, G. Charlesde-Queleville., Claudiños, C., Smyth, K. -A.,
Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 7 22-MAY-2001;
FEATURES
source location/Qualifiers
1..1713
BASE COUNT 516 a 305 c 370 g 522 t
ORIGIN
Query Match 99.3% Score 1701.8; DB 6; Length 1713;
Best Local Similarity 99.6% Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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 LOCUS
 DEFINITION
 ACCESSION
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 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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 Oestroidea; Calliphoridae; Lucilia.
 1 (bases 1 to 2240)
 Newcomb,R.D., East,P.D., Russell,R.J. and Oakeshott,J.G.
 Isolation of alpha cluster esterase genes associated with
 organophosphate resistance in Lucilia cuprina
 Insect Mol. Biol. 5 (3), 211-216 (1996)
 JOURNAL
 MEDLINE
 PUBMED
 96392952
 8799740
 2 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Russell,R.J. and Oakeshott,J.G.
 cDNA cloning, baculovirus-expression and kinetic properties of the
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 cuprina
 Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
 JOURNAL
 MEDLINE
 PUBMED
 97215578
 9061925
 3 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Ollis,D.L., Cheah,E., Russell,R.J. and
 Oakeshott,J.G.
 A single amino acid substitution converts a carboxylesterase to an
 organophosphorus hydrolase and confers insecticide resistance on a

blowfly
Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
MEDLINE
97352821
PUBMED
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REFERENCE
TITLE
4 (bases 1 to 2240)
Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
Two different amino acid substitutions in the α -esterase, E3,
confer alternative types of organophosphorus insecticide resistance
in the sheep blowfly
Unpublished
5 (bases 1 to 2240)
Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
Direct Submission
Submitted (24-Apr-1996) Richard D. Newcomb, Molecular Genetics,
HortResearch, Private Bag 92 169, Auckland, New Zealand
FEATURES
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Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 241 CCCGTGATGATGCGGTATGTTGCATTCATTAAGATTAAGTCACTGCAAGTTATTT 300
|||||
Db 538 CCCGTGATGATGCGGTATGTTGCATTCATTAAGATTAAGTCACTGCAAGTTATTT 597
QY 301 ATACGGGCAAAAGTGTGAGCTGAGAGATGCTATACCTAAGTGTATACGAATAT 360
Db 598 ATACGGGCAAAAGTGTGAGCTGAGAGATGCTATACCTAAGTGTATACGAATAT 657
QY 361 CTAAATCCCGAAACTTAACGTCCTGTTTAACTACATACATGATGCTGTTTATATC 420
Db 658 CTAAATCCCGAAACTTAACGTCCTGTTTAACTACATACATGATGCTGTTTATATC 717
QY 421 GGTGAATATCATGATATGATATGATGCTGATATTTATTAATAAAGATGCTGTG 480
Db 718 GGTGAATATCATGATATGATATGATGCTGATATTTATTAATAAAGATGCTGTG 777
QY 481 ATTAACATATCATGATATGATGATGCTGATGCTGATGCTGATGCTGATGCTGAT 540
Db 778 ATTAACATATCATGATATGATGATGCTGATGCTGATGCTGATGCTGATGCTGAT 837
QY 541 AATGTCGCCGCTTAATGCGCGCTTAAGATCAATCAATGCTGCTGCTGCTGCTGCTG 600
Db 838 AATGTCGCCGCTTAATGCGCGCTTAAGATCAATCAATGCTGCTGCTGCTGCTGCTG 897
QY 601 AATGTCGCCGCTTAATGCGCGCTTAATGCGCGCTTAATGCGCGCTTAATGCGCGCT 660
Db 898 AATGTCGCCGCTTAATGCGCGCTTAATGCGCGCTTAATGCGCGCTTAATGCGCGCT 957
QY 661 GCTGCTGTACCACTACATGATGTTAAACCAACACGCGCTTTCATGCTGTGT 720
Db 958 GCTGCTGTACCACTACATGATGTTAAACCAACACGCGCTTTCATGCTGTGT 1017
QY 721 ATACATATGCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 780
Db 1018 ATACATATGCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1077
QY 781 TTACCTTACCAATATGCGCGCTTAAGAGTGAAGATTAAGATTAAGATTAAGATTA 840
Db 1078 TTACCTTACCAATATGCGCGCTTAAGAGTGAAGATTAAGATTAAGATTAAGATTA 1137
QY 841 TTCTTATGAAGCAACGACCAAGATTTATTAACCTGAGGAAAAAGTTTAACTCTA 900
Db 1138 TTCTTATGAAGCAACGACCAAGATTTATTAACCTGAGGAAAAAGTTTAACTCTA 1197
QY 901 GAAGAGGTATCAATATAGTCAATGCTTGTGCGCCAGTGTGAGGCAATATGAGACC 960
Db 1198 GAAGAGGTATCAATATAGTCAATGCTTGTGCGCCAGTGTGAGGCAATATGAGACC 1257
QY 961 GCTGATTTGTCTTACCAACATCTCTGCGGAAATGTTAAACGCTGGGATATTCG 1020
Db 1258 GCTGATTTGTCTTACCAACATCTCTGCGGAAATGTTAAACGCTGGGATATTCG 1317
QY 1021 ATACCACTATGATGCTATCACTTCAATATGAGGCTATTTTACTCTCAATTTAG 1080
Db 1318 ATACCACTATGATGCTATCACTTCAATATGAGGCTATTTTACTCTCAATTTAG 1377
QY 1081 CAATGCTATGCTTGAAGAAATGGAACCTGTGCAATTTGTGCTCAAGGAATG 1140
|||||

DB	1378	CAAAAGCCTATGCTTTGTTAAGGAANTTGGAAACTGTGTCAATTTTGGCCAAAGTAATG	1437
QY	1141	GCTGATGTTGAACGACCGCCCGCCAGAGACCTTGGAAATGGTGCTAAATTTAAAAAGCT	1200
DB	1438	GCTGATGCTGAACGACCGCCCGCCAGAGACCTTGGAAATGGTGCTAAATTTAAAAAGCT	1497
QY	1201	CATGTTACAGGAGAAACCAACAGCCTATATATTTATGATGATCTTGTCTCACATCAT	1260
DB	1498	CATGTTACAGGAGAAACCAACAGCCTATATATTTATGATGATCTTGTCTCACATCAT	1557
QY	1261	TTTCGTTCCCGATGCAATGTTTGTGCAATTTAGCTTTCATATCACACCTCCGGTACACC	1320
DB	1558	TTTCGTTCCCGATGCAATGTTTGTGCAATTTAGCTTTCATATCACACCTCCGGTACACC	1617
QY	1321	GCTGATGTTGAACGACCGCCCGCCAGAGACCTTGGAAATGGTGCTAAATTTAAAAAGCT	1380
DB	1618	GCTGATGTTGAACGACCGCCCGCCAGAGACCTTGGAAATGGTGCTAAATTTAAAAAGCT	1677
QY	1381	GCTGATGCAAGCGGTGTTAAGGTTTATGTCATGCTGATGATTAACCTATTTCTCTGG	1440
DB	1678	GCTGATGCAAGCGGTGTTAAGGTTTATGTCATGCTGATGATTAACCTATTTCTCTGG	1737
QY	1441	AATCAATTTGGCCAAACGATGCTTAAAGAAATCGCTGAATACAAAACAATTAAGCATATG	1500
DB	1738	AATCAATTTGGCCAAACGATGCTTAAAGAAATCGCTGAATACAAAACAATTAAGCATATG	1797
QY	1501	ACTGATATATGATATCAATTTTGGCCACCATGCTATATCTTATAGCAATGAATTAAGCT	1560
DB	1798	ACTGATATATGATATCAATTTTGGCCACCATGCTATATCTTATAGCAATGAATTAAGCT	1857
QY	1561	ATGCAAAATGTTTCCCTGGGATTCATTAATTAAGAAATCCGATGAAGTATACAGCTTGAAT	1620
DB	1858	ATGCAAAATGTTTCCCTGGGATTCATTAATTAAGAAATCCGATGAAGTATACAGCTTGAAT	1917
QY	1621	ATTAGTATATGATTAATTAAGAAATGATGATGCTGCTGAATATGATTAAGATTAAGATGAG	1680
DB	1918	ATTAGTATATGATTAATTAAGAAATGATGATGCTGCTGAATATGATTAAGATTAAGATGAG	1977
QY	1681	TGCGATGTTGAAAAACATAGAGATTTATTTTGG	1713
DB	1978	TGCGATGTTGAAAAACATAGAGATTTATTTTGG	2010
RESULT 8			
LOCUS	AR062838	1713 bp	DNA linear
DEFINITION	Sequence 2 from patent US 5843758.		
ACCESSION	AR062838		
VERSION	AR062838.1	GI:5990529	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1713)		
	Russell, R. Joyce., Newcomb, R. David., Robin, G. Charlesde, Quetteville.,		
	Boyce, T. Mark., Campbell, P. Malcolm., Parker, A. Gerard.,		
	Oakesholt, J. Graham. and Smyth, K. A.		
TITLE	Enzyme based bioremediation		
JOURNAL	Patent: US 5843758-A 2 01 -DEC-1998;		
FEATURES	Location/Qualifiers		
source	1..1713		
BASE COUNT	506 a 299 c 363 g	515 t	30 others
ORIGIN	/organism="unknown"		
Query Match	97.9%;	Score 1676.6;	DB 6; Length 1713;
Best Local Similarity	98.0%;	Pred. No. 0;	
Matches 1679;	Conservative 0;	Mismatches 34;	Indels 0; Gaps 0;
QY	1	ATGAATTTACAGCTTATGTTGATGAGAAATTTAAATGAGACATTAATGCAATTAAT	60
DB	1	ATGAATTTACAGCTTATGTTGATGAGAAATTTAAATGAGACATTAATGCAATTAAT	60

OY	61	AAATTTTAAACATGCTTTAACTACCAATGAAAGCGGTAGCTGGAACATGAAATGATGGC	120
Db	61	AAATTTTAAACATGCTTTAACTACCAATGAAAGCGGTAGCTGGAACATGAAATGATGGC	120
OY	121	AAATGTGAAGAGCGCTTAAACGTTTAACTGTGTACGATGATCTCTACATGTTTGAGGGT	180
Db	121	AAATGTGAAGAGCGCTTAAACGTTTAACTGTGTACGATGATCTCTACATGTTTGAGGGT	180
OY	121	AAATGTGAAGAGCGCTTAAACGTTTAACTGTGTACGATGATCTCTACATGTTTGAGGGT	180
Db	121	AAATGTGAAGAGCGCTTAAACGTTTAACTGTGTACGATGATCTCTACATGTTTGAGGGT	180
OY	181	ATACCGTAGCGCCACACCGCCAGTGGGTGAGCTGAGATTTTAAAGCACCCACGACACACA	240
Db	181	ATACCGTAGCGCCACACCGCCAGTGGGTGAGCTGAGATTTTAAAGCACCCACGACACACA	240
OY	241	CCCTGGGATGGTGGCTGATTTGTTCATTCATTTAAAGATTAAGTCAGTCCAGTGTGATTTT	300
Db	241	CCCTGGGATGGTGGCTGATTTGTTCATTCATTTAAAGATTAAGTCAGTCCAGTGTGATTTT	300
OY	301	ATAACGGGCAAAAGTGTGGCTCAGAGATTTGCTATACCTAAGTGTCTATACGAATAT	360
Db	301	ATAACGGGCAAAAGTGTGGCTCAGAGATTTGCTATACCTAAGTGTCTATACGAATAT	360
OY	361	CTAAATCCCGAAACTAAACGTCCTCCGTTTAAATATACATACATGATGGTGTTTATATATC	420
Db	361	CTAAATCCCGAAACTAAACGTCCTCCGTTTAAATATACATACATGATGGTGTTTATATATC	420
OY	421	GGTGAATATCATGCTGATATGATATGGTCCCTGATATTTTCATTTAAAGAGATGTGTGTG	480
Db	421	GGTGAATATCATGCTGATATGATATGGTCCCTGATATTTTCATTTAAAGAGATGTGTGTG	480
OY	481	ATTAACTATACATATTCCTTTGGGAGGCTTAGTTTTCTTAAGTTTAAATTCAGAAAGACCTT	540
Db	481	ATTAACTATACATATTCCTTTGGGAGGCTTAGTTTTCTTAAGTTTAAATTCAGAAAGACCTT	540
OY	541	AATGTGCCCGGTAAATGCGGCGCTTAAAGATCAAGTCATGCGCTTGCGTTGATTTAAATAT	600
Db	541	AATGTGCCCGGTAAATGCGGCGCTTAAAGATCAAGTCATGCGCTTGCGTTGATTTAAATAT	600
OY	601	AATGTGCCCGGTAAATGCGGCGCTTAAAGATCAAGTCATGCGCTTGCGTTGATTTAAATAT	600
Db	601	AATGTGCCCGGTAAATGCGGCGCTTAAAGATCAAGTCATGCGCTTGCGTTGATTTAAATAT	600
OY	661	GCTGCTCTACCCACTCATGATGATTTAACGGAACAACGCGGCTTTTCCATGCTGGT	720
Db	661	GCTGCTCTACCCACTCATGATGATTTAACGGAACAACGCGGCTTTTCCATGCTGGT	720
OY	721	ATACTAATGTGGGTAAATGCTATTTGTCCATTGGCTAATACCAATGTCAACATGTCGCC	780
Db	721	ATACTAATGTGGGTAAATGCTATTTGTCCATTGGCTAATACCAATGTCAACATGTCGCC	780
OY	781	TTACACTTTAGCCAAATTTGGCGGCTATTAAGGGTGAAGATTAATGATTAAGGATTTTGCAA	840
Db	781	TTACACTTTAGCCAAATTTGGCGGCTATTAAGGGTGAAGATTAATGATTAAGGATTTTGCAA	840
OY	841	TTTCTTTATGAAGCCAGCCACGAGATTTAATTAACCTGAGGAAAAAGTTTAACTCTTA	900
Db	841	TTTCTTTATGAAGCCAGCCACGAGATTTAATTAACCTGAGGAAAAAGTTTAACTCTTA	900
OY	901	GAAAGCGGTACAAATTAAGTCATGTTCCCTTTGGGCCACATGTTGAGCCATATACAGAC	960
Db	901	GAAAGCGGTACAAATTAAGTCATGTTCCCTTTGGGCCACATGTTGAGCCATATACAGAC	960
OY	961	GCTGATTTGTCTTACCCAAACATCTCTCGGGAAATGGTTTAAACCTGCTGGGGTAATTCG	1020
Db	961	GCTGATTTGTCTTACCCAAACATCTCTCGGGAAATGGTTTAAACCTGCTGGGGTAATTCG	1020
OY	1021	ATACCCACTATGATGGGTACACTTCATATGAGGGTCTATTTTCACTTCAATTCCTTAAG	1080
Db	1021	ATACCCACTATGATGGGTACACTTCATATGAGGGTCTATTTTCACTTCAATTCCTTAAG	1080
OY	1081	CAAAATGCTATGCTTTGTTAAGGAATTGGAACCTGTGCAATTTTGTGCAAGTAATTG	1140
Db	1081	CAAAATGCTATGCTTTGTTAAGGAATTGGAACCTGTGCAATTTTGTGCAAGTAATTG	1140
OY	1141	GCTGATTTGTGAAGCCACCGCCACGAGACCTTGGAATGGTGTCTAAATTTAAAGAGCT	1200

Db	1141	GCATGATNCTGAAGCAACGCCGCCAGAGACCTTGGAATAGGCTCTAAATTAAGAAGCT	1200
Qy	1201	CATGTTACAGGAGAAACACCAACAGCTGATTAATTTATGAGATCTTGGCTCACAATCAT	1260
Db	1201	CATGTTACAGGAGAAACACCAACACGCGATTAATTTATGAGATCTTGGCTCACAATCAT	1260
Qy	1261	TTCTGGTTCCTCCATGCATGCTTTGTTGGCAATTAACGTTCAATACACACGCCGTACACCC	1320
Db	1261	TTCTGGTTCCTCCATGCATGCTTTGTTGGCAATTAACGTTCAATACACACGCCGTACACCC	1320
Qy	1321	GTCCTACTGTTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTAG	1380
Db	1321	GTCCTACTGTTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTAG	1380
Qy	1381	GCTAGTGGACGTCGTCTTAAGGCTGTTACTCATGCTGATGAATTAACCTATTTCCTGTG	1440
Db	1381	GCTAGTGGACGTCGTCTTAAGGCTGTTACTCATGCTGATGAATTAACCTATTTCCTGTG	1440
Qy	1441	AATCAATTGGCCAAACGTAATGCCCTAAAGAAATGCCGTAATACAAACATTTGAAGCTAG	1500
Db	1441	AATCAATTGGCCAAACGTAATGCCCTAAAGAAATGCCGTAATACAAACATTTGAAGCTAG	1500
Qy	1501	ACTGCTATATGAGATACAAATTTGCCACACCTGCTAATCCTTATAGCAATGAATTTGAAGT	1560
Db	1501	ACTGCTATATGAGATACAAATTTGCCACACCTGCTAATCCTTATAGCAATGAATTTGAAGT	1560
Qy	1561	ATGGAANAATGCTTCCCTGGGATCCCATTTAGAAATCCGATGAAGTATACAAAGCTTTGAAT	1620
Db	1561	ATGGAANAATGCTTCCCTGGGATCCCATTTAGAAATCCGATGAAGTATACAAAGCTTTGAAT	1620
Qy	1621	ATTACTGATGAATTAAGAAATGATATGTCGCCCTGAANAATGATATAGATTAAACAATGGCAG	1680
Db	1621	ATTACTGATGAATTAAGAAATGATATGTCGCCCTGAANAATGATATAGATTAAACAATGGCAG	1680
Qy	1681	TGCGATGTTGAAAAACATAGACATTTATTTTNG	1713
Db	1681	TGCGATGTTGAAAAACATAGACATTTATTTTNG	1713

RESULT	9
AF133341	
LOCUS	
DEFINITION	2160 bp mRNA linear INV_17-AUG-2000
ACCESSION	Musca domestica carboxylesterase MdaE7 (MdaE7) mRNA, complete cds.
VERSION	AF133341
KEYWORDS	AF133341.1 GI:4768932
SOURCE	
ORGANISM	Musca domestica.
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
	Muscoidae; Muscidae; Musca.
REFERENCE	1 (bases 1 to 2160)
AUTHORS	Claudianos,C., Russell,I.R.J. and Oakeshott,J.G.
TITLE	The same amino acid substitution in orthologous esterases confers organophosphate resistance on the house fly and a blowfly
JOURNAL	organo phosphatase resistance on the house fly and a blowfly
PUBMED	Insect Biochem. Mol. Biol. 29 (8), 675-686 (1999)
MEDLINE	99381228
REFERENCE	10451921
AUTHORS	2 (bases 1 to 2160)
TITLE	Claudianos,C., Russell,I.R.J. and Oakeshott,J.G.
JOURNAL	Direct Submission
FEATURES	Submitted (07-MAR-1999) Entomology, CSIRO, Clunies Ross, Canberra,
source	ACT 2601, Australia
	Location/Qualifiers
	1..2160

gene 1.2160
/gene="MdaE7"

[illegible]

QY	661	GCTGCTCTTACCCACTATGATGTTTACCAGAAACAACCGCGGCTTTTCCATCGTGGT	720
Db	877	GGGGCCCTCAACCCATTACATGATGATACCGAACACCCCGGTGTTATTCATCTGTGT	936
QY	721	ATATCAATATGCGGGTATATGCTATTTGTCCATTGGGCTAATACCAATGTCAACATCGTCC	780
Db	937	ATCATGATGTCGGTATATTCATGCTCATGCGCCCTCTACAGAAATGCCAAAGTGTGCG	996
QY	781	TTTCACTTACCAAAATTTGGCCGGCTTAAAGGCTGAGGATTAATGATTAAGATGTTTGGAA	840
Db	997	CTCACCAATGGCCCAAAACGTGTGGCTTAAAGGAGAGACAAATGAAGAAAGATACCTGGAA	1056
QY	841	TTTTTATGAAAGCCAAAGCCAGATTTAATAAACTTGAGAAAGAAAGTTTAACTGTA	900
Db	1057	TTTCTATGAAAGCCAAATCCCTTATGATTTGATCAAAAGAGGCCAACAGTTTGTACACC	1116
QY	901	GAGAGCGGTCAAAATTAAGTCATGTTTCTTTTGTCCACTGTGTAGCCATATCAGACC	960
Db	1117	GAAACAAATGCAAAATTAAGTCATGTTTCTTTTGGACCCACTGTGAACATACAGACA	1176
QY	961	GCTATTTGTCTTACCCAAACATCTCGGGGAAATGGTTAAACATGCTTGGGGTAAATTCG	1020
Db	1177	GCGCACTGTGTGTACCCAAACCAATCAGAAATGTATAGAGCGCCCTGGGGAAATTCG	1236
QY	1021	ATATCCACTATGATGGGTAAACACTTATATGAGGGTCTATTTTCACTTCAATCTTATAG	1080
Db	1237	ATATCCACTATGATGAGCAATATACCTCTCTCAAGAAAGTTTCTTTCAATCAATCTCCAA	1296
QY	1081	CAATATGCCATATGCTGTGTTAAGAAATTTGATGTCATATTTTGTGCCAAGTAAATG	1140
Db	1297	CAATATCCGAGGTGTGTTAAAGATTTGGAAATCTGTGTAAATTAATGATGTCTGGAGTGG	1356
QY	1141	GCTATGTTTGAAGCACACCGCCAGAGACCTTGGAAATGGGTCTTAAATTAAGAAAGCT	1200
Db	1357	GCTACAGTGAAGCAGATGCCCCGGAACCCCTGAGAGGGCTGCCATTTGTAAAGAGCC	1416
QY	1201	CATGTTTACAGAGAAACACCACAGCTGATTAATTTTATGATCTTTGCTCTCACATCTAT	1260
Db	1417	CATGTGATGGGGAACACCTACTCTGGAATATTTTATGAGACTTTGGCTCTATTTCTAT	1476
QY	1261	TTTGGTGTCCCATGATGCTTTTGGTGAATTAAGTTTAAATCAGACACCGGGTACACC	1320
Db	1477	TTTCTTCTTCCCATGATGCTCTTCTCTACAAATTTGCGTTTAAACCAACAGCTGGACCTCC	1536
QY	1321	GTCATCTTGTATGCTTGCATTCGATTCGAGGAAGATCTTATCAATCCCTATCGTATATG	1380
Db	1537	ATTATTTTGTATGCTTTCGATTTTCGATTCGAAAGAAATTAATTAACCCCATGATATATG	1596
QY	1381	CGTAGTGAGAGTGTGTAAAGGTTTAAAGTCAATGCTGATGAATTAACGTAATTTCTTCGG	1440
Db	1597	CGTTTGGCCGTGGCTTAAAGGTGTAACCAATGCGAGAGACTTAACATCTCTTCGG	1656
QY	1441	AATCAATTTGGCCAAACGTATGCTTAAAGATGCGGTGATCAAAAACATTTGAACGTATG	1500
Db	1657	AACATTTTGTGCAAGCCCTGCCAAAGGAAGCGCGGATTAACAAACCATTAAGACGATG	1716
QY	1501	ACTGGTATATGATPACAAATTTGCCACCACTGTAATCCTTATAGCAATGAATTAAGAGT	1560
Db	1717	GTTTGGCTTTTGGAGCGAATTTGCCACACCGCAAAACCTATACGCAATGATATAGCCGCG	1776
QY	1561	ATGGAATGTTTCTCGGGATTCCAATTAAGAAATCGATGAAGTATPACAAGTGTGAT	1620
Db	1777	ATGGAATTCCTCACCTTGGATTCCTATTAATAAATAATCCGATGATGCTATTAATATGTTTAAT	1836
QY	1621	ATTAGTATGAATTAAGAAATGATTTGATGTGCTGAAATGATTAAGATTAACATATGAGG	1680
Db	1837	ATCGCGCATGAATTAAGAAAGTTATGATTTGGCAGAAATGATTAATAATTAACATATGGCA	1896
QY	1681	TCGATGTTTGAAGAAACATAGAGTATATTTTA	1712
Db	1897	AGTATATTCATTAAGAAAGGATTTGTTTA	1928

RESULT	10
AF139082	
LOCUS	
DEFINITION	AF139082 2175 bp mRNA linear INV 20-OCT-2000 Haematobia irritans irritans alpha E7 esterase (AE7) mRNA, complete cds.
ACCESSION	AF139082
VERSION	AF139082.1 GI:6502938
KEYWORDS	
SOURCE	
ORGANISM	Haematobia irritans irritans. Haematobia irritans irritans Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidae; Muscidae; Haematobia. 1 (bases 1 to 2175) Guerrero,F.D. Cloning of a horn fly cDNA, H1alphaE7, encoding an esterase whose transcript concentration is elevated in diazinon-resistant flies Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	
PUBMED	10989298
REFERENCE	2 (bases 1 to 2175) Guerrero,F.D. Direct Submission Submitted (30-MAR-1999) USDA-ARS, Knippling-Bushland U.S. Livestock Insects Research Laboratory, 2700 Fredericksburg Rd., Kerrville, TX 78028, USA
FEATURES	Location/Qualifiers

Query Match	Best Local Similarity	Matches 1242;	Conservative	Score 959.4;	DB 3;	Length 2175;
				Pred. No. 1.1e-201;	Mismatches 471;	Indels 0;
				Gaps 0;		
1	ATGAATTTCACGCTTACGTTGATGAGCAAAATTTAAATGGAAGATTAAATGCATTGGAAT	60				
282	ATGAATTTCAATGTCAGCTTGTGGAGAAATTTAAATGGAATTTAAATGCTGTGGAAT	341				
61	AAGTTTAAACTATCGTTAACTACCAATGAAACGCGTGTAGCTGGAACATGAAATATGCG	120				
Db	342	AAAATTTTAAACTACCGGCTTATTTACCAATGAAGCGCATATTTGCGATAGCGAATATGCA	401			
QY	121	AAAGTGAAGCGCTTAAACGTTTAACTGTATGACATGATTCCTTACTACGTTTGAGCGT	180			
Db	402	AAAAATTTAAAGTGTTAAACGTTTGACATGTACGTACGTGACTATTCCTACAGCTTTGAAGGT	461			

QY 181 ATACCGTACGGCCCAACCCAGTGGGAGCTGAGATTTAAAGCACCACCCACCAACA 240
 DB 462 ATACCATATGCGCAACCTCCTG186GCGAATTAGATTAAAGCTCCACACCTCCCTGTC 521
 QY 241 CCCGGGATGCTGCGCTGATTTGGCAATCATAAAGATAGCTGCAGTGTGATTTT 300
 DB 522 CTTGGGATGAGATTAAAGGATTTGTTCATGCTGCCCTCCGTTGCGGTTCCAAACAGTTTC 581
 QY 301 ATACCGGCAAAAGTGTGCTCAGAGGATGTCATACCTAAGTGTCTATACCAATAT 360
 DB 582 ATATCCGGCACTCAACAGTGTGCGAGGATGTTTATATTGAATGCTATACGATATAT 641
 QY 361 CTAAATCCGCAAACTAAAGCTCCGTTTATATACATACATGCTGCTTTTATATC 420
 DB 642 TTAATAATGATCAAAAGAGTCCCTTTGGTTTCTTCATGCTGCTGCTTCATTTGT 701
 QY 421 GGTGAATAATCATGATATGATGCTGCTGATTTATTTTATTTAAAGAGATGCTGTG 480
 DB 702 GGGGAGCTAATAGAACTATATGCGCTGATTTTTCATTAAGAAAGAGACCTTGTCTTC 761
 QY 481 ATTAACATCAATATGCTTTGGAGCTTATGCTTTTCTAAGTTTAAATTCAGAAACCTT 540
 DB 762 ATAACTGTCAATATGCTTTAGGGGTATAGTTTCTAAGTTTAAATTCGAAATATCTC 821
 QY 541 AATGTCCCGGTAATGCGGCTTAAAGATCAAGTCAATGCGCTGCTTGAATTTAAAT 600
 DB 822 AATGTACCTGTTATGCTGCTGCTTAAAGATCAAGTCAAGTGGCTGCTGATTTAAAT 881
 QY 601 AATGTCCCACTTTGCTGCGCAATCCGATATATATACAGTCTTTGGGAAAGGCGCT 660
 DB 882 AATGTGCGCACTTTGCTGCGCATCCGATTTGATTTATTTGCGGAGAGTCTGGA 941
 QY 661 GCTGCTTACCACTATACATGATTTAACCAACAACTCCGCTTTTCCATCTGTGT 720
 DB 942 GCTGCTTACCACTATATGATGATTTAACTGAACAGCTCTGCTTATTTCCATCTGTGCT 1001
 QY 721 ATACTAATGCTGCTGATGCTATTTGCTCATGCTAATACCAATGCAACATGCTGCT 780
 DB 1002 GTTTTGAATCTGCAACGCTATGCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCT 1061
 QY 781 TTCACTTACCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 1062 TATACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1121
 QY 841 TTTCTTATGAAGCAACCAAGATTTAATAAATCTGAGGAAAGTTTAACTGCTA 900
 DB 1122 TTTCTTATGAAGCAACCAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181
 QY 901 GAAAGGCTGCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 1182 GAGGAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
 QY 961 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 DB 1242 CCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
 QY 1021 ATACCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 DB 1302 ATACCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1361
 QY 1081 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 1362 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421
 QY 1141 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 DB 1422 GTAGTGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1481
 QY 1201 CATGTTAAGGAGAAACCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 DB 1482 TATGTAAGTGAAGCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541

QY 1261 TTCTGTTCCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 DB 1542 TTTTGTATTCATATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1601
 QY 1321 GCT 1380
 DB 1602 ATCAATGCT 1661
 QY 1381 GCT 1440
 DB 1662 GCT 1721
 QY 1441 ATCAATGCT 1500
 DB 1722 ACTATGCT 1781
 QY 1501 ACTGCT 1560
 DB 1782 ATGAGCT 1841
 QY 1561 ATGAGCT 1620
 DB 1842 ATGAGCT 1901
 QY 1621 ATGAGCT 1680
 DB 1902 ATGAGCT 1961
 QY 1681 TCGATGCT 1740
 DB 1962 AGTGTGCT 1994
 RESULT 11
 ARI53445
 LOCUS ARI53445 1710 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 14 from patent US 6235515.
 ACCESSION ARI53445
 VERSION ARI53445.1 GI:15120977
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1710)
 AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
 Robin, G. Charlesde, Quetleville., Claudiano, C., Smyth, K., A.,
 Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 14 22-MAY-2001;
 FEATURES
 Source Location/Qualifiers
 BASE COUNT 498 a 369 c 394 g 449 t
 ORIGIN
 Query Match 55.8%; Score 956.6; DB 6; Length 1710;
 Best Local Similarity 73.4%; Pred. No. 4, 9e-201;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;
 QY 44 TTAATGCTATGAAATTAAGTCTTTTAATGCTATGCTTAACTACCAATGAAGCGTGTAG 103
 DB 44 TTAATGCTATGCTATGCTATGCTTAACTACCAATGAAGCGTGTAG 103
 QY 104 CTGAATGCTATGCTATGCTATGCTTAACTACCAATGAAGCGTGTAG 163
 DB 104 TCGATGCTATGCTATGCTATGCTTAACTACCAATGAAGCGTGTAG 163
 QY 164 ACTAGCTATGCTATGCTATGCTTAACTACCAATGAAGCGTGTAG 223
 DB 164 ACTAGCTATGCTATGCTATGCTTAACTACCAATGAAGCGTGTAG 223
 QY 224 CACCCAGGACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 283

D	b		224	CACCCAGCGGCGTGTACATGGGAGG9GTACGTGATTGCTGTGGGCAGCAACAACAT	283
O	y	284	CAGTCGAAGTGATTTATTAACGGCCAAGAAGTGTGTGCTCAGAGCATTTGCTAATCTAA	343	
D	b	284	CGGTACAGACAGATTTCTATTAAGTGGCAAAACCACAGGTGCGAGGATGTCTAATCTGA	343	
O	y	344	GTCGTATACGAATAATCTAAATCCGGAACATAAAGTCCGCTTTACTATACATACATG	403	
D	b	344	ATGTGTATACCAATGACTTGAACCCAGAACAAAAGGCTCTGTATATGGTTTTCAATCCATG	403	
O	y	404	GTCGTGCTTTTATTAATCGGTAAAAATCATCGTATATGTATGTGCTCTATTAATTCATTA	463	
D	b	404	GCGGAGATTTTATTTTCGGGAGCAAAATCGTACTGGTTGTGCCGACTAATTAAGA	463	
O	y	464	AAAAGATGTGTGTGTGATTAACATCAATATGTGTTGGAGCTCTAGGTGTTCTAACTT	523	
D	b	464	AGAAACCCGTCGTCTGTGTAAACCGTCATATGTGTTGGGTGTGTTGCTTACCC	523	
O	y	524	TAAATTCAGAAAGACCTTAATGTGCCCCGGTAAATGCGGCTTTAAATCAAGTCATGGCT	583	
D	b	524	TGAATGTGGAANAATCTCAAATGTCCCAGGACGCTGCGCTCAAGATCAAGTAATGGCT	583	
O	y	584	TGCGTGTGATTTAAAAATTAATGTGGCAACTTTGGTGGCAATGCCATTAATTAACAGCT	643	
D	b	584	TGAGATGGGTTCAGAGATTAATTTGCCATTTTGGTGTGCGCATTAACATATTAACGCTCT	643	
O	y	644	TTGTGTAAAGTGCCTGGTGTGCTCTACCCACTACATGATGTTAAACGCAACAACTGCG	703	
D	b	644	TGCGCGAAAGTGTGTGGGGGCTCAACCCATTTACATGATGATTAACGCAACGACCGTG	703	
O	y	704	GTCCTTTCATCGTGTGTACTAATGTGCGGTAAATGCTATTTGTCCATTTGCTAATACC	763	
D	b	704	GTTTATTTCCATCGTGTATCATATGTGTGCGGTAAATTCATGTGCTCATGGGCTCTACAG	763	
O	y	764	AATGTCAACATCGGCTTCACTTACCTTAGCCAAATATGGCCGGCTATPAAGGTGGATTAATG	823	
D	b	764	AATGCCAAGTCTGTGCGCTACCATATGCGCAACAGTGTGTGCTATPAAGGAGGGCAATG	823	
O	y	824	ATPAAGATGTTTGGAAATTTCTTATGAAGCCAAAGCCACAGGATTTAATAAACTGTAGG	883	
D	b	824	AAAAAGATATCTGTGATTTCTTAATGAAGCCAAATCCATATGTTGATCAAAAGGAGGC	883	
O	y	884	AAAAAGTTTAACTCTGAAGACCGTACAAATPAAGTCAATGTTTCTTTGTGCCACTG	943	
D	b	884	CACAAGTTTGTACACCCGAAAGAAATCAAAATPAAGTCAATGTTTCTTTGTGACCCACTG	943	
O	y	944	TTGAGCATATACAGCGCTGATTTGTCTTACCCAAACATCTCGGGAAATGTTTAA	1003	
D	b	944	TAGAACCATACAGACGCGGACTGTGTGTACCCAAACCAATCAGAGAAATGTTGAAGA	1003	
O	y	1004	CTGCTTGGGGAATTCGATACCCACATGATGAGGTAAACCTTCATATGAGGCTCTATTTT	1063	
D	b	1004	GGCGCTGGGAATTCGATACCCACATGATGAGCAATCTCTACAGAGGTTTGCTTT	1063	
O	y	1064	TCACTTAATTTCTTAAGCAATGCCATATGCTTGTTPAAGAAATGGAACTGTGTCAATT	1123	
D	b	1064	CCAATCAATGTCCAAACAATATCCGAGAGTGTAAAGATGTGAATCTGTGTGAATTT	1123	
O	y	1124	TTTGGAACAAGTAATGGGATGTTGAAGCACGCGCCACAGACCTTGGAAATGGGCTG	1183	
D	b	1124	ATGTGCTTGGGAGTTGTGTGAAGTAAAGACGATGTGCCCGGAAACCTGTGAGAGGCGTG	1183	
O	y	1184	CTAATAATTTAAAAAGGCTCATGTTAACAGAGAAACACACACACTGATATATTTATGATC	1243	
D	b	1184	CCATTTGTGA AAAAGGCCCATGTGTGAGTGGGAAACACCTACTCTGTGATATTTTATGAGAC	1243	
O	y	1244	TTTGTCTCTACATCTATTTCTGTGCTCCCATGTCATGCTTTGTGCAATTAACGTTCAATC	1303	
D	b	1244	TTTGTCTCTATTTCTATTTCTTCTTCCCATGATGCTGCTTCTCAATATTCGCTTCAAC	1303	
O	y	1304	ACACCTCGGACACCGGCTACTCTATCTATCTGTGACCTTCGATTCGGAAGTCTTAACA	1363	
D	b	1304	ACACAGCTGGACCTCCATTTATTTGTATCTGTTGATTTGCAATTCGGAATAATTAATA	1363	

FEATURES	source
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LOCUS	AY051473
DEFINITION	Drosophila melanogaster 2017 bp mRNA linear INV 27-AUG-2001
ACCESSION	AY051473
VERSION	AY051473.1 GI:15291256
KEYWORDS	FLI_CDNA
SOURCE	Drosophila melanogaster.
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS	1 (bases 1 to 2017) Stapleton, M., Brokstein, P., Hong, L., Abmayyan, A., Carlson, J., Champe, M., Chavez, C., Dorset, V., Farina, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J., Munoo, J., Paolel, J., Paragás, V., Park, S., Phoumenavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M. and Celisner, S.
TITLE	Direct Submission
JOURNAL	Submitted (10-AUG-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA
COMMENT	Sequence submitted by: Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Berkeley, CA 94720
	This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our web site (http://fruitfly.berkeley.edu) or send email to cdna@fruitfly.berkeley.edu .
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	/strain="Y; cn bw sp"
	/db_xref="taxon:7227"
	/map="84D5-84D5"

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BASE COUNT 522 a 487 c 519 g 489 t
ORIGIN
Query Match 39.5% Score 677.2; DB 3; Length 2017;
Best Local Similarity 62.6% Pred. 2.7e-139;
Matches 1073; Conservative 0; Mismatches 638; Indels 3; Gaps 1;
QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAAATGATTTGAAT 60
DB 91 ATGAATGAACCTCGCTTGTGAGCGGTGGGGCCCTCAAAACCATCGAGCAT 150
QY 61 AAGTTTAAACTATCGTTTAACCTACCAATGAAGCGTGTAGCTGAACCTGAATATGCG 120
DB 151 AAATGCAAGCATATCCCAAGTCGACCAATGAACAGTTGCGCCGACGAGTACGGG 210
QY 121 AAATGGAAGCGCTTAAACGTTAACTGATGAGATGATCTACTACAGTTTGAGGGT 180
DB 211 CAATGAGGGGTATCAACGCTATCTCTACGATGTGCGCTTACGCTTCAAGTTTGAG 270
QY 181 ATACCGACGCCCAACGCGCAGTGGTGAAGTGAATTAAGACACCCGACGACCAACA 240
DB 271 ATCCCGTACGCCCAAGCTCGGTGGGGAGTTGCGGTTAAAGCCCGCTCAAGGCCGAT 330
QY 241 CCTGGATGATGCTGCTGATTTGTGCAATCAATGAAGATGAAGTGAAGTTTATTC 300
DB 331 CCTGGAGGAGTGTGCGCATGTCGACGACCGAAGATGAAGCGCGTCAGGTGACGATTC 390
QY 301 ATACGCGCAAGTGTGTGGCTCAGAGATGTCTATACCTAAGTGTCTATACGATATAT 360
DB 391 GTCTTGATTAAGGTAGAGGGCTCCGAGGACTGCTCTATCTCAATGTGACCAACAAT 450
QY 361 CTAATATCCCGAAATGAACGCTCCGCTTTAGTATACATACATGAGTGTGTTTATATTC 420
DB 451 GTGAAGCCCGCAAGAGCTGCGCGGTATGTTGATTCACGGAGGAGGCTCTCATATTC 510
QY 421 GGTGAATATCATCGTATATGTATGCTCTGATTAATTCATTAAGAAAGATGTGTTG 480
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QY 481 ATTACATACATATATGTTGGGAGCTCTAGTATTCTTAATTTAAATTCGAAGACCTT 540
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QY 601 AATGTGCCCACTTTGTGTGCAATCCGATATATTAACAGTCTTTGGTGAAGTGCCTG 660
DB 691 AATGTGCTTAATTTGCGGGAGATCCCAACTGATCACTGTTTGTGAGAGAGTGTGCA 750

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QY 721 ATACTAATGTGCGGTAATGCTATTTGTCCATTTGCG---TAAATGCCAATGTCAACATCT 777
DB 811 ATCTTGACAGTGGGACATGCGCATTTGTCTTGGGCTTACACAGCGGCACATTAACATTAAT 870
QY 778 GCTTTCACCTTAAGCAATTTGCGCGGTATTAAGGTTGAGATTAATGATAGATGTTTGG 837
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QY 838 GAATTTCTTATGAAGCCAAAGCCACAGATTTAATTAATTAATGAGAGAAAGTTTACT 897
DB 931 GAGTTCTTGAGAAACCTAAAGGCCAAGATCTTATTCGGGTGAGAGAAATGCTGACA 990
QY 898 CTGAAGAGGCTCAATTAAGTCAATGCTATTTCTTTTGTGCCACTGTTGAGCAATATGAG 957
DB 991 CTGAGAGAACGATGAACAAGATTAATGTTGCTTGGCCATCCCTGGAACATTTCTCC 1050
QY 958 ACCGCTGATTTGCTCTTACCCAAACATCCTCGGAAATGTTAAAGCTTTGGGGTAAAT 1017
DB 1051 ACCGCCGAATGTGTGATATTCCAAGGCTCCAAAGGATGATGAACCGCTGAGATTAAC 1110
QY 1018 TCGATACCCATATGATGTTGATTAACCTTCAATATGAGGCTATATTTTTCATTTCAATTC 1077
DB 1111 TCCATTCCTATTTTATGAAGAAACATTTGTAAGGAGGCTGTGTGCTTCCAGAGTA 1170
QY 1078 AAGCAATGCTATGCTGTTTAAAGAAATTTGAATTTGTCATATTTTGTCCAAAGTAA 1137
DB 1171 AAGCTTATCCGACAGTGTGTGACGACGCTATGCTGACACCTTTCATTTCCAAAGAA 1230
QY 1138 TTGCGTGAATGTTGAACGACCGCCGACAGACCTTGAATGAGTGTCAATTAATTAAG 1197
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QY 1198 GCTCATGTTTAAAGAGGAACCAACACACATGATTAATTTTATGATCTTTGCTCACATC 1257
DB 1291 GTTCATGCCACATCGCTCGAAGAACACCCGACATTAATTAATGATTTCTTGTGATTTAC 1350
QY 1258 TATTTCTGTTCCCGACATGATGCTTTGTGCAATTAAGTTCATACACCTCCGATACA 1317
DB 1351 TACTTCGTTCCGCGCTGAGGGTGTGTCATTCGACATCCGACCGGATGCGGTGAGCT 1410
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DB 1411 CCAATATATTTCTATGATATGATGATGATTCGAGAGAGCTATTTTCTGATCCGATTT 1470
QY 1378 ATGCGTATGAGAGCTGTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1437
DB 1471 ATGGGTTGGAGCGCGGTGTCAGAGGGGTCAGGCATGCGAGATTTGAGGTACCAATTC 1530
QY 1438 TGAATATATTTGGCAAGATGATGCTTAAGAAATCCGCTGATATCAAAACATTTGAGCT 1497
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DB 1651 GGTATGACACCTGACCAATGATTCAGTTTCCAAATCCGAGAGATATCAAGTGTGCTC 1710
QY 1618 AATATTAATGATTAATTAAGAAATGATGATGATGATGATGATGATGATGATGATGAT 1677
DB 1711 AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1770
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DB 1771 GAGAGCTTCTATGACGACCAACAAAGATTTATTTGT 1804

RESULT 13	AV121675	2660 bp	MRNA	linear	INV 18-JUN-2002
LOCUS	AV121675	2660 bp	MRNA	linear	INV 18-JUN-2002
DEFINITION	Drosophila melanogaster RE24825 full insert cDNA.				
ACCESSION	AV121675				
VERSION	AV121675.1				
KEYWORDS	GI:21464397				
SOURCE	FLI CNA.				
ORGANISM	fruit fly, Drosophila melanogaster				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
AUTHORS	1 (bases 1 to 2660) Stapleton, M., Brokstein, P., Hong, L., Abmayri, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G., Miranda, A., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M., and Celniker, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-JUN-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA				
COMMENT	Sequence submitted by: Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Berkeley, CA 94720				
FEATURES	This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contigility within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcriptase errors that result in single base changes, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to: cdna@fruitfly.berkeley.edu .				
FEATURES	Location/Qualifiers				
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BASE COUNT	724 a 632 c 650 g 654 t				
ORIGIN					

Db 1566 TCCTGAGTGGTGAAGTGGAGAACCTGGCCCTCAAGATGCCACGATGATAGACGCA 1625
 QY 1159 GCGCCAGACCTTGGAAATGGGTCTAAATTAAGAGCGCATGTTACAGAGAAACA 1218
 Db 1626 AGAAAGCGTTTGGAAAGAAAGTACGAGAGCTATATTTGGCGGATAGAGACTCTGGCAGG 1685
 QY 1219 CCACAGCTGATATATTTATGAGCTTGTCTGATCATCTATTTCTGCTCCCATCAT 1278
 Db 1686 AAGACATATTTGAGTACAGGATCTTTCGTCGTAATATTTCTGCAATGACATTCAT 1745
 QY 1279 CGTTTGTGCAATTAACCTTTTAAATCACACCTCCGTTACACCCGCTTACTTGTATGCTTC 1338
 Db 1746 AGGACTTGTCTGCTGCTGCTGCTACACGCCCCCATTTGGCCCAACATTCCTGACGATTC 1805
 QY 1339 GACTTGCATTTGGAAGATCTTATCATATCCCTATGCTATTTATGCGTAGAGAGCGTGT 1398
 Db 1806 GATTTCGACTG---AGCACTTCAATATCATGCAATTTACCTGCGCGCAAGCTG 1862
 QY 1399 AAGGCTGTACTCATCTGATGAAATTAACCTATTTCTTCTGGAATCAATTTGCCAAAGT 1458
 Db 1863 CGCGGACCTTCAACGCGGATGATCTGCTATTTGTTCTCAATTTGGCGCTGCCAAAG 1922
 QY 1459 ATGCTTAAGATCGCGTATACAAACATTTGACGATGATGATGATGATGATGATGATGAT 1518
 Db 1923 CTGAAGAGCGCCACAGCCGAGTTCAGACATTAAGCGTTTGTATGATGATGATGATGATGAT 1982
 QY 1519 TTTGCCACACCTGTTATCTTATTA-----GCAATGAATTTGAAGTATGGA 1566
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 QY 1567 AATGTTTCCGGGATCCCAATTAAGAAATCCGATGATGATGATGATGATGATGATGATGAT 1626
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 QY 1627 GATGAATTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
 Db 2103 CAGAT 2162
 QY 1687 TTTGAAA 1693
 Db 2163 TACGACA 2169

RESULT 14
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 LOCUS Drosophila melanogaster alpha esterase (ae7) gene, partial cds.
 DEFINITION U51050
 ACCESSION U51050
 VERSION U51050.1 GI:1272313
 KEYWORDS
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster.
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 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 2820)
 Robin.C., Medvedsky, K.M., Russell, R.J. and Oakeshott, J.G.
 Duplication and divergence of the genes of the alpha-esterase
 cluster of Drosophila melanogaster
 J. Mol. Evol. (1996) in press
 2 (bases 1 to 2820)
 Robin.C.
 JOURNAL Direct Submission
 REFERENCE Submitted (11-MAR-1996) Charles Robin, Biotechnology, CSIRO div.
 AUTHORS Entomology, Clunies Ross Street, Canberra, ACT 2601, Australia
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 SPPLNTPGNALKDQYLAKWIKNRCASRGEDNCTIVEESGASHTYMMLTDTQ
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 YEGILWPEVKLMPQVLOLDAGTPEIPKELATPESEKELDSMSQIHDVTRTSES
 TPDNYMDCSIVYFVPALRVVSHRAVAAGAPVYRVYDPSEELIPYRIRMRGRC
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 BASE COUNT 777 a 609 c 657 g 776 t 1 others
 ORIGIN

Query Match 21.8%; Score 373.8; DB 3; Length 2820;
 Best Local Similarity 54.6%; Pred. No. 2,9e-72;
 Matches 1054; Conservative 0; Mismatches 612; Indels 263; Gaps 5;

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 Db 890 AGAACCATCGAGATTAAGCCAGCATGTCCGACATGCAATGAACAGTTGTCGCC 949
 QY 106 GAAACTGATATGCAAGTGAAGAGCGTTAAAGTGTAACTGTATGATGATGATGATGATGAT 165
 Db 950 GACACGAGATGAGGCCAAGTGAAGAGGATGATGATGATGATGATGATGATGATGATGAT 1009
 QY 166 TACAGTTTGAAGGATTAACCTGACGCCCAACCGCAGTGGTGAAGTGAAGCA 225
 Db 1010 TTCAGCTTGGAGGATATCCGTCAGCCAGCCGCGTGGGAGATGTCGGTTAAAGGCC 1069
 QY 226 CCCGAGGACCAACACCCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285
 Db 1070 CCTCAGAGGCCCATTCCTCGGAGGAGTTCGCGACTGACGACGCGAAGATGAAGGCC 1129
 QY 286 GTGCAAGTGAATTTAAACGGCAAGTGTGCTGCTGACAGAGATGCTATACCTAAGT 345
 Db 1130 GTCCAGGTGCAAGTTCGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1189
 QY 346 GTCTATACCAATTAAT----- 360
 Db 1190 GTGTACACCAACAAATGTGATTAATTCATTAATCTGTATTAACATTCGTTAAACC 1249
 QY 361 -----CTAAATCCCGAATAACG 380
 Db 1250 GTAATTAACATTTTATTTATTTGTTGTTGATATTTAGTGAAGCCGCAAGAGCTCG 1309
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 Db 1310 CCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1369
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 Db 1370 GTATGCGCCGATTTACTTATTAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1429
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 QY 510 -----AGTTTCTAAGTTTAATTCAGAAGACCTTAATGTGCCGATATGCCGCC 562
 Db 1490 CCTACAGAGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1549
 QY 563 TTAAGATCAAGTCAATGCTGCTGCTGATTAATAAATTAATGGCCCAATTTGCTGTGCA 622

Db	1550	TCAAGGATCAAGGTCTGGCCCTCAAGTGGATCAAGAACAAATTGGCTATGTTTGGCGGAG	1609
OY	623	ATCCGATTAATATTACAGTCTTTGGTGAAGTCCGGTGTGCTCTACCACTATCATGA	682
Db	1610	ATCCCACTGACTACACTGTTTGGTGGAGAGTGTGTGGAGGCGCTCCACTCATCATGA	1669
OY	683	TGTTAACCGAACAACACGCGGCTTTTCCATCGTGGTATACTAATGTCCGGTATGCTA	742
Db	1670	TGCTAACCGATCAGACCACCAAGGCTCTTTTATCGGGGCACTTTGCAGTGCGGAGTGGCA	1729
OY	743	TTTGTCCATTGGC---TAATACCAATGTCAACATGTGTCTTCACCTTTAGCCAAATTGG	799
Db	1730	TTTGTCTTGGGCTTACAAAGGGGACATTACCATTAATCCCTACAGATAGCCAAACTGG	1789
OY	800	CCGGCTATTAAGGTGAGGATATGATTAAGATGTTTGGAAATTTCTATGAAGCAACG	859
Db	1790	TTGGCTACAAAGGGGAGGACAGACAGACAGATGTGTGGAGTTCTTGCAAGACGTAAAG	1849
OY	860	CACAGGTTTAATTAAMACTTGAGGAAAAAGTTTAACTGTAAAGAGGTACAAATANG	919
Db	1850	CCAAAGATCTTAATTCGGCTGGAGAAAAATGTCTCGACACTGGAGAGACGATGAACAAG	1909
OY	920	TCAATGTTCCTTTGGTCCCACTGTTGAGCACTATAGACCCCTATGTGTCTTACCCA	979
Db	1910	TAAATGTTCCGTTGGGCCATCCCTCGAACAATCTCCACGGCCGAAATGTGATATCA	1969
OY	980	AACATCCTCGGGAATGTTTAAACATGCTTGGGGTAAATTCATACCACATATAGTGGTA	1039
Db	1970	AGGCTCCAAAGAGATGATATMAACCGCGCTGGAGTAACTCCATCCCATGTTTATAGAA	2029
OY	1040	ACACTCATATGAGGGCTATTTTTCACATTC-	1075
Db	2030	ACACTGTGTACAGGCGCTACTGTGGGTTCAGAGTTAGATTAAGGAATTTATGAATT	2089
OY	1076	-----TTAAGCAAAATGCTATGCTTGT	1097
Db	2090	TTCTTCAATAGTAATTTAATTTATTTACAGAGAGTAAGCTTAATGCGCAGAGTCT	2149
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OY	1158	CGCCCCAGAGACCTTGGAAATGGGTGCTAAATTAAGAGCTCATGTTACAGAGAAAC	1217
Db	2210	TAAAGAAAACTGGATTCGTGGAGTGCACAGATTCAGATGTTCATCGCAGCGCTCAGA	2269
OY	1218	ACCAACAGCTGATTAATTTATGAT-----	1242
Db	2270	AAGACACCCAGATTAATTCATGATGTAAAGTGTGTCACATTAAGTGCTTACATATAT	2329
OY	1243	-----CTTGGCTCACATCTAATTTCTGTTCCGCCAGCATCTT	1282
Db	2330	AAGCTGAATTTATTTATTCAGCTCTGTTCGATTTACTACTTCGTGTTCCGGCCGAGAG	2389
OY	1283	TGTTGCAATTACGTTTAATCACACCTCCGGTACACCCGCTACTTGTATGCTTGGACT	1342
Db	2390	TGGTTCATTTCCCGACAGCGCTATGCGGCTGGAGACTCCATATTTTCATGATATGACT	2449
OY	1343	TGCAATGGGAAGATCTTAATCAATCCCATGCTTTATATGGGTATGGAGGTGTTAAAG	1402
Db	2450	TGCACTCGAGAGACTATTTTTCCTACCGCATTTATGTGGTATGGGACCGGCTGTCAAG	2509
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OY	1523	CCACACGTGTAATCCTTAATAGCAATGAATTAAGATGAAGAAATGTTTCTGTGGATC	1582
Db	2630	CTGCGACGGTAATCCCTTAACGAGGAAGATCAACGGTATGTGACACTGTGACCATTTATC	2689

Qy	1553	CAATTAGAAATCCGATGAGTATACAGGTTTGAATATTAGTATCAATTTGAAAAATGA	1642
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Qy	1643	TTGATGTGCTCGAATATGATAGATTAAACAATGGGAGCTCGATGTTTGAAAAACATAGAG	1702
Db	2750	TCGATCTGCTCGAAGTGGCCCAATTTAGAGTCTGGAGAGCCTCTATGACGACCAACAAG	2809
Qy	1703	ATTATTATTT	1711
Db	2810	ATTATTATGT	2818

RESULT 15
AC015272/c

LOCUS	AC015272	57335 bp	DNA	linear	HTG 16-NOV-1999
DEFINITION	Drosophila melanogaster, *** SEQUENCING IN PROGRESS *** , in ordered				

ACCESSION	AC015272
VERSION	AC015272.1 GI:6436063

KEYWORDS HIV; HIVS_PHASE2.

SOURCE *Drosophila melanogaster*, *Drosophila melanogaster*.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

REFERENCE
1 (bases 1 to 57335)
AUTHORS Adams, M. and Venter, J.C.

TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,

COMMENT
Rockville, MD, USA
This sequence was identified as CDM:10213452 by the submitter.

* NOTE: This is a 'working draft' sequence.
For further information on this sequence e-mail to lycecelera.com.

- * runs sequence will be replaced
- * by the finished sequence as soon as it is available and

FEATURES

* The accession number will be preserved.

Location/Qualifiers

1 5735

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source
1. .5/335
/organism="Drosophila melanogaster"
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ORIGIN

Query Match	21.5%;	Score 369;	DB 2;	Length 5/335;
Best Local Similarity	54.5%;	Pred. NO. 2.3e-71;		

Matches	1051;	Conservative	0;	Mismatches	615;	Indels	263;	Gaps	5;
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46 AATGCAATGAAAAAAGTCTTTAAACATATCGTTTAACATACCAATGAACGGTGGTAGCT 105

Db 36481 AGAACCAACGAGCAATAAGTCCAGCAGTATCCGAGTCGACCAATGAAACAGATTGTCC 36422

106 GAACTGATATGCGAAGCGAAGCGCTTAAACGTTTAACTGTGTACGATGATTCCTAC 165

DB 36421 GACACCGAGTACGGCCAAAGTGGGGGTATCAACGGTCTATCTCTCTACGATGTCCTTAC 36362

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286 GCGCAAGTGTGATTTATTAACGGGGCAAGTGTGTGGCTCAGGGATTGCTATACCTAAGT 345

DB 30241 GTCACGATCCAGTTCGTCCTCGATTAAGGTAGACGGCTCCGAGGACATCCCTCATCTCAAT 30182

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DB 36181 GGTACACCAACATGTGAGTAATTCATTAACCTGTGTACATAAAMCATCGTTAAACC 36122

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QY 361 -----CTAATCCGAAGTAACG 380
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QY 441 GTATGTCCTGATTTATTTCAATTAAGAGATGTGTGTTGATTAACATACATATCTGTT 500
Db 36001 GTATGCGCCGATTTACTTTATGAAGAAGATGTTGTTCTCTCAGATACAGTACCCACT 35942
QY 501 GGGAGCTCT----- 509
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QY 510 -----AGTTTTCTAAGTTTAATTCAGAAAGACTTAATGTCCCGGTAAATCCGGCC 562
Db 35881 CCTACACAGGATTTATAGCTTTAAGTCCCGGAGCTAAATGTACAGGAATCTGACC 35822
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Db 35821 TCAAGATCAAGTCTGAGCTTCAAGTATCAAGAACAAATTTGGCTAGTTTGGCGAG 35762
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Db 35641 TTTGTCATTGGCCTTACCAAGGCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 35582
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Db 35461 TAAATGTTGCTTTGGCCCACTGTGAGCATATGAGACCGCTGATGTGCTTACCA 35402
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Db 35401 AGCCTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 35342
QY 1040 ACACCTCATATGAGGCTCT----- 1058
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QY 1059 -----ATTTTCACTTCAATTTCTAAGCAAAATGCTTATGCTGT 1097
Db 35281 TTTCTTCAATTAATTAATTTATTTTACAGAGAGTAAAGCTTATGCTGCTGCT 35222
QY 1098 TAAAGAAATGGAACCTGTGCTCAATTTTGTCCAAAGTGAATGCTGATGATGACGAC 1157
Db 35221 GAGCAGAGCTTGTGAGGACACTTTCATTTCCAAAGAAATTTGCTGCGCAGAGGCTG 35162
QY 1158 CGGCCAGAGACTTGGAAATGGGCTTAAATTAAGAGCTCATGTTACAGAGAAAC 1217
Db 35161 TAAAGAAATGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAG 35102
QY 1218 ACCAAGAGCTGATATTTATGAT----- 1242
Db 35101 AAGCAGCCAGATATTTACATGATGATGATGATGATGATGATGATGATGATGATG 35042
QY 1243 -----CTTGTCTCACATCTATTTCTGTTTCCCAATGATGCTT 1282

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QY 1283 TGTTCATTAATGCTTTCAATCACACCTCCGATACCCGCTTACTTATGCTTCACT 1342
Db 34981 TGTTCATTTCCGACAGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 34922
QY 1343 TCGATGAGGAAGATCTATCAATCCATATGCTATATGCTGAGGCTGAGGCTGAGGCT 1402
Db 34921 TCGATGAGGAGATCTATTTTCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 34862
QY 1403 GTGTTAGTATGCTGATGATTAATTAATTTCTTCTGAAATCAATTTGCCCAAGCTATG 1462
Db 34861 GGTTCAGGCTATGCTGAGGATTTGAGTACCAATTTACAGACGCTGCTGCTGCTGCTG 34802
QY 1463 CTAAAGATGCGCTGATATACAAACATTTAGCTATGATGATGATGATGATGATG 1522
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QY 1583 CAATTAAGAAATCGATGAGATATCAAGTGTGATTAATTAATTAATTAATTAATTA 1642
Db 34681 CAGTTCCAAATCCGAGAGGATCATCAAGTGTGCTCAACATCATGATGATGATGATG 34622
QY 1643 TTTGATGCTGAGAAATGATTAAGATTTAAACATGAGGCTGATGATTTGAAAAACAT 1702
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QY 1703 ATTTATTT 1711
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Search completed: April 11, 2003, 06:01:19
 Job time : 3017.03 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:58:21 ; Search time 246.905 Seconds

15624.094 Million cell updates/sec

Title: US-09-776-910-1

Sequence: 1 atgaattcaacgttagtt.....aacatagagatttatttag 1713

Scoring table: IDENTITY_NUC

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
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Maximum DB seq length: 200000000000

Post-processing: Minimum match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1701.8	99.3	1713	16	AAO91561	OP-sensitive esterase
2	1701.8	99.3	1713	18	AAI68596	Ic-alpha-E7 malath
3	1681	98.1	1713	16	AAO91566	OP-resistant esterase
4	1677.8	97.9	1713	16	AAO91564	OP-resistant esterase
5	1677.8	97.9	1713	16	AAO91563	OP-resistant esterase
6	1676.2	97.9	1713	16	AAO91565	OP-resistant esterase
7	1674.6	97.8	1713	16	AAO91562	OP-resistant esterase
8	956.6	55.8	1710	18	AAI68597	Mk-alpha-E7 gene.
9	677.2	39.5	2001	23	AB102067	Drosophila melanog

10	381.8	22.3	1704	23	ABLO20261	Drosophila melanog
11	369	21.5	6175	23	ABLO20266	Drosophila melanog
12	368.2	21.5	1665	23	ABLO20299	Drosophila melanog
13	365.4	21.3	1792	23	ABLO4689	Drosophila melanog
14	323.2	18.9	1593	23	ABLO2103	Drosophila melanog
15	323	18.9	1861	23	ABLO1859	Drosophila melanog
16	311.4	18.2	1791	23	ABLO1033	Drosophila melanog
17	305.8	17.9	1719	23	ABLO2101	Drosophila melanog
18	303	17.7	1878	23	ABLO1947	Drosophila melanog
19	300.4	17.5	3856	23	ABLO10332	Drosophila melanog
20	300.4	17.5	67279	23	ABLO7668	Drosophila melanog
21	269.6	15.7	1809	24	ABAS9060	Drosophila melanog
22.	239.8	14.0	4320	23	ABLO4688	Drosophila cell cy
23	229.6	13.4	1727	23	ABLO1943	Drosophila melanog
24	228.6	13.3	4242	23	ABLO2102	Drosophila melanog
25	224	13.1	5008	23	ABLO2080	Drosophila melanog
26	198.8	11.6	4294	24	ABLO2098	Drosophila melanog
27	198.8	11.6	4294	23	ABLO2100	Drosophila melanog
28	197.6	11.5	1987	19	AAV0762	C. fellis esterase,
29	197.6	11.5	1987	19	AAV0763	C. fellis esterase,
30	193.2	11.3	2613	23	ABLI9064	Drosophila melanog
31	192	11.2	1626	23	ABLO1945	Drosophila melanog
32	191.8	11.2	5132	23	ABLO1858	Drosophila melanog
33	187.4	10.9	1530	19	AAV0764	C. fellis esterase,
34	187.4	10.9	1590	19	AAV0765	C. fellis esterase,
35	179.6	10.5	1540	19	AAV0756	C. fellis esterase,
36	179.6	10.5	1584	19	AAV0757	C. fellis esterase,
37	179.6	10.5	2007	19	AAV0754	C. fellis esterase,
38	179.6	10.5	2007	19	AAV0755	C. fellis esterase,
39	179.6	10.5	2007	22	ABAD1174	Ctenocephalides fel
40	167.6	9.8	4288	23	ABLO1942	Drosophila melanog
41	162.6	9.5	1783	23	ABLO2029	Drosophila melanog
42	148	8.6	4283	23	ABLO1946	Drosophila melanog
43	142.2	8.3	1488	19	AAV0767	C. fellis esterase
44	142.2	8.3	1590	24	AAV0743	C. fellis esterase,
45	142.2	8.3	1590	22	AAVD1169	Ctenocephalides fel

ALIGNMENTS

XX	AAQ91561	standard; cDNA; 1713 BP.	
XX	AAQ91561;		
XX	22-DEC-1995	(first entry)	
XX	OP-sensitive esterase E3	Lc743 clone.	
XX	Esterase; E3:	bioremediation; organophosphate;	
XX	insecticide; pesticide;	water decontamination;	
XX	ss.	meat decontamination.	
XX	Lucilia cuprina.		
XX	Key	Location/Qualifiers	
XX	CDS	1..1713	
XX		/*tag= a	
XX	W09519440-A1.		
XX	20-JUL-1995.		
XX	13-JAN-1995;	95W0-AU00016.	
XX	13-JAN-1994;	94AU-0003347.	
XX	(CSIR)	COMMONWEALTH SCI & IND RES ORG.	
XX	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;		
XX	Parker AG, Robin GC, Russell RJ, Smyth K;		

XX WPI; 1995-263870/34.
DR P-PSDB; AAR78142.
XX
XX
PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
PT eliminate residues of organo-phosphate and carbamate pesticides from
PT water, meat etc.
XX
XX
XX Claim 5; Page 12-17; 38pp; English.
XX
XX cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa. cDNA
CC library was amplified using cluster-specific esterase primers.
CC Isolated clone Lc743, a probable full-length cDNA, was expressed
CC using a baculovirus vector in insect cells and shown to encode
CC an OP-susceptible E3 esterase, useful in bioremediation.
XX
XX Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;

Query Match 99.3%; Score 1701.8; DB 16; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAAATGATTCATTGAAT 60
QY 61 AACTTTTAACTATGCTTTAACTACCAATGAACGGTGTGTAAGTGAATATGCG 120
Db 61 AACTTTTAACTATGCTTTAACTACCAATGAACGGTGTGTAAGTGAATATGCG 120
QY 121 AAAGTGAAGCGGTTAAAGCTTAAGCTGATGATGATTCCTACTACCTTTGAGGT 180
Db 121 AAAGTGAAGCGGTTAAAGCTTTAACTGATGATGATTCCTACTACCTTTGAGGT 180
QY 181 ATACCGTACGCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCACCACCGACACACA 240
Db 181 ATACCGTACGCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCACCACCGACACACA 240
QY 241 CCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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QY 301 ATACGGGCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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QY 361 CTAAATCCGAACTAAAGCTCCGTTTATGATACATACATGCTGCTGCTGCTGCT 420
Db 361 CTAAATCCGAACTAAAGCTCCGTTTATGATACATACATGCTGCTGCTGCTGCT 420
QY 421 GGTGAATAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 421 GGTGAATAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 ATTAACATCAATATGCTTGGAGCTAGCTTCTAAGTTTAAATCAGAAAGCTT 540
Db 481 ATTAACATCAATATGCTTGGAGCTAGCTTCTAAGTTTAAATCAGAAAGCTT 540
QY 541 AATGTCGCCGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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QY 601 AATGTCGCCGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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QY 661 GGTGCTTACCACTACATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 GGTGCTTACCACTACATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 ATACTAATGTCGGGTAATGCTATTTGCTCA/TGGCTAATACCAATGTCAGATGCT 780
Db 721 ATACTAATGTCGGGTAATGCTATTTGCTCA/TGGCTAATACCAATGTCAGATGCT 780

QY 781 TTACCTTAGCAAAATTTGGCGGCTATAGGGTGAAGATATGATAGATGTTTGGAA 840
Db 781 TTACCTTAGCAAAATTTGGCGGCTATAGGGTGAAGATATGATAGATGTTTGGAA 840
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Db 841 TTTCTTATGAAGCAACGACAGATTTAATAAATCCTGAGAAAAGTTTAACTCTA 900
QY 901 GAAGAGGCTCAAAATTAAGTGCATGTTTCTTTTGTCTCCACTGTGAGCCATACAGC 960
Db 901 GAAGAGGCTCAAAATTAAGTGCATGTTTCTTTTGTCTCCACTGTGAGCCATACAGC 960
QY 961 GGTGATGCTGCTTACCAAAATCTCGGGAATGTTTAACTGTTGGGTAATTCG 1020
Db 961 GGTGATGCTGCTTACCAAAATCTCGGGAATGTTTAACTGTTGGGTAATTCG 1020
QY 1021 ATACCCATATGATGAGTAACTCATATAGGGTCTATTTTCACTTCAATTCCTTAAG 1080
Db 1021 ATACCCATATGATGAGTAACTCATATAGGGTCTATTTTCACTTCAATTCCTTAAG 1080
QY 1081 CAATGCTATGATGAGTAACTCATATAGGGTCTATTTTCACTTCAATTCCTTAAG 1140
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QY 1141 GGTGATGCTGCTTACCAAAATCTCGGGAATGTTTAACTGTTGGGTAATTCG 1200
Db 1141 GGTGATGCTGCTTACCAAAATCTCGGGAATGTTTAACTGTTGGGTAATTCG 1200
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QY 1321 GTCTACTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1321 GTCTACTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 CGTAGTGAGAGGCTGTTAAGGCTGTTAGTACATGATGATGATGATGATGATGAT 1440
Db 1381 CGTAGTGAGAGGCTGTTAAGGCTGTTAGTACATGATGATGATGATGATGATGAT 1440
QY 1441 AATCAATTTGGCCAAAGCTATGCTTAAAGATCGCTGAATACAAACATTTGAACGTATG 1500
Db 1441 AATCAATTTGGCCAAAGCTATGCTTAAAGATCGCTGAATACAAACATTTGAACGTATG 1500
QY 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Db 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 ATGGAATAATGTTTCTGCGATGCTCAATTAAGAAATCCGAGAAAGTATACAAAGTGT 1620
Db 1561 ATGGAATAATGTTTCTGCGATGCTCAATTAAGAAATCCGAGAAAGTATACAAAGTGT 1620
QY 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 TCGATGTTTGAAGAAACATGAGATTTATTTTAA 1713
Db 1681 TCGATGTTTGAAGAAACATGAGATTTATTTTAA 1713

RESULT 2
AAT68596
ID AAT68596 standard; DNA; 1713 BP.
XX AAT68596;
AC
XX
DT 08-AUG-1997 (first entry)

DE		Lc-alpha-E7 malathion susceptible esterase clone Lc743.
XX		
KW	Malathion carboxylesterase; organophosphate; insecticide;	
KM	pesticide; remediation; bioremediation; decontamination; esterase;	
KW	ss.	
OS	Lucilia cuprina.	
XX		
FH	Key	Location/Qualifiers
FT	primer_bind	/tag= complement (1..26)
FT		/tag= a
FT		/note= "Lc743 5' primer"
FT	primer_bind	1686..1713
FT		/tag= b
FT		/note= "Lc743 3' primer"
FT	mutation	752
FT		/tag= c
FT		/note= "base 752 is T in resistant clones (TTP to Leu mutation)"
FT	mutation	1344
FT		/tag= d
FT		/note= "base 1344 is C in resistant clones (silent mutation)"
FT	mutation	1362
FT		/tag= e
FT		/note= "base 1362 is C in resistant clones (silent mutation)"
FT	mutation	1599
FT		/tag= f
FT		/note= "base 1599 is T in resistant clones (silent mutation)"
FT	mutation	1629
FT		/tag= g
FT		/note= "base 1629 is T in resistant clones (silent mutation)"
XX		
PN	W09719176-A1.	
XX		
PD	29-MAY-1997.	
XX		
PE	22-NOV-1996; 96WO-AU00746.	
XX		
PR	23-NOV-1995; 95AU-0006751.	
XX		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
PI	Boyce T, Brownlie JC, Campbell PM, Claudianos C;	
PI	Newcomb RD, Oakshott JG, Robin GC, Russell RJ, Smyth K;	
DR	WPI: 1997-298113/27.	
DR	P-PSDB; AAM17765.	
XX		
PT	DNA encoding enzyme that degrades organophosphate pesticides -	
PT	useful for decontamination of soil, water, food etc	
XX		
PS	Claim 4; Fig 1; 52pp; English.	
CC		
CC	DNA molecule Lc743 (AAT66596) codes for an esterase (AAM17765) from	
CC	a malathion susceptible strain of Lucilia cuprina. Comparison	
CC	with a consensus sequence from derived from clones of the	
CC	Lc-alpha-E7 resistant allele (see also AAM17768) indicated only one	
CC	replacement site difference, a TTP to Leu substitution at amino	
CC	acid position 251 (nucleotide position 752). This mutation is an	
CC	excellent candidate for the malathion resistance mutation. The	
CC	resistant enzyme acts as a malathion carboxylesterase and can be	
CC	formulated for use in degrading environmental carboxylester or	
CC	dimethyl general organophosphates.	
XX		
SQ	Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other:	
Query Match	99.3%; Score 1701.8; DB 18; Length 1713;	
Best Local Similarity	99.6%; Pred. No. 0;	

	Matches	1706:	Conservative	0:	Mismatches	7:	Indels	0:	Gaps	0:
QY	1	ATGATTTTCACGTTAGTTTGATGAGCAAAATTAAAAATGCAAGATTAAATGCAATTCGAAAT	60							
Db	1	ATGATTTTCACGTTAGTTTGATGAGCAAAATTAAAAATGCAAGATTAAATGCAATTCGAAAT	60							
QY	61	AAGTTTAAACTATGCTTTAACTACCAATGAACGGGTGTGCGTGAACATGAATATGGC	120							
Db	61	AAGTTTAAACTATGCTTTAACTACCAATGAACGGGTGTGCGTGAACATGAATATGGC	120							
QY	121	AAAGTGAAGGCGTTAAACGTTTAACTGCTGTCAGATTCCTACTACAGTTTGAGGCT	180							
Db	121	AAAGTGAAGGCGTTAAACGTTTAACTGCTGTCAGATTCCTACTACAGTTTGAGGCT	180							
QY	181	ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTTAAAGCACCCAGCGACCAACA	240							
Db	181	ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTTAAAGCACCCAGCGACCAACA	240							
QY	241	CCCTGGGATGGTGTCCGTGATTTGTTCACATCTAAAGATAACTCAGTCAAGTTGATTTT	300							
Db	241	CCCTGGGATGGTGTCCGTGATTTGTTCACATCTAAAGATAACTCAGTCAAGTTGATTTT	300							
QY	301	ATTAAGGGCAAAAGTGTGGCTCAGAGATGTCATATACCTTAAGTGTCTATACGATATAT	360							
Db	301	ATTAAGGGCAAAAGTGTGGCTCAGAGATGTCATATACCTTAAGTGTCTATACGATATAT	360							
QY	361	CTAAATVCCCGAAACTAAACGTCGCCCTTTTATGATACATACATAGTGGTGTATATATC	420							
Db	361	CTAAATVCCCGAAACTAAACGTCGCCCTTTTATGATACATACATAGTGGTGTATATATC	420							
QY	421	GGTGAATAATCATCGTATATATGATGGTCTGATTTATTTCAATTAAGAAGATGTGTGTTG	480							
Db	421	GGTGAATAATCATCGTATATATGATGGTCTGATTTATTTCAATTAAGAAGATGTGTGTTG	480							
QY	481	ATTAACATACATATATCGTTTGGAGCTCTAGATTTCTTAAGTTTAAATCAAGACCTT	540							
Db	481	ATTAACATACATATATCGTTTGGAGCTCTAGATTTCTTAAGTTTAAATCAAGACCTT	540							
QY	541	AATGTGCCCGGATATGCCGGCCTTAAAGATCAAGTCATAGCCCTTGCCTGTGATTAATAAT	600							
Db	541	AATGTGCCCGGATATGCCGGCCTTAAAGATCAAGTCATAGCCCTTGCCTGTGATTAATAAT	600							
QY	601	AATTCGCCCACTTTGGTGGCAATCCCGATATATTAACAGTCTTGTGGTGAAGTGGCGGT	660							
Db	601	AATTCGCCCACTTTGGTGGCAATCCCGATATATTAACAGTCTTGTGGTGAAGTGGCGGT	660							
QY	661	GCTGCGCTACACCTACATATGATGTTAAACCGCAAACTCGGGGCTTTTCCATCGTGT	720							
Db	661	GCTGCGCTACACCTACATATGATGTTAAACCGCAAACTCGGGGCTTTTCCATCGTGT	720							
QY	721	ATACTAATGTGCGGTAATGCTATTTGTCCATTTGGCTAATACCAATGTTCACATCGTGC	780							
Db	721	ATACTAATGTGCGGTAATGCTATTTGTCCATTTGGCTAATACCAATGTTCACATCGTGC	780							
QY	781	TTTCACCTTAGCCAAATTTGGCGGCTATAAAGGTGAGGATATGATATAGGATGTTTGGAA	840							
Db	781	TTTCACCTTAGCCAAATTTGGCGGCTATAAAGGTGAGGATATGATATAGGATGTTTGGAA	840							
QY	841	TTTCTTATGAAGCAAGCAGAGATTTAAATAAACCTGAGAGAAAATTTTAACTCTCA	900							
Db	841	TTTCTTATGAAGCAAGCAGAGATTTAAATAAACCTGAGAGAAAATTTTAACTCTCA	900							
QY	901	GAGAGACGATACAAATTAAGTTCATGTTTCCCTTTGGCCAGCTGTGAGCATATCAGACC	960							
Db	901	GAGAGACGATACAAATTAAGTTCATGTTTCCCTTTGGCCAGCTGTGAGCATATCAGACC	960							
QY	961	GCTGATTTGTGCTTAACCAACATCCTCGGGGAAATGTTAAAACTGCTTGGGGTAAATCG	1020							
Db	961	GCTGATTTGTGCTTAACCAACATCCTCGGGGAAATGTTAAAACTGCTTGGGGTAAATCG	1020							
QY	1021	ATACCCACATATATGGGTACACTTCATATGAGGGCTATTTTTCACCTCAATTCCTTAG	1080							
Db	1021	ATACCCACATATATGGGTACACTTCATATGAGGGCTATTTTTCACCTCAATTCCTTAG	1080							

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QY 1081 CAAATGCTTATGCTTTAAGAAATGGAACCTTGTCAATTTTGTGCAAGTGAATG 1140
DB 1081 CAAATGCTTATGCTTTAAGAAATGGAACCTTGTCAATTTTGTGCAAGTGAATG 1140
QY 1141 GCTGATGTTGAACGACCGCCCGCCAGACCTTGGAAATGGGTGCTAAATTAAGAGCT 1200
DB 1141 GCTGATGTTGAACGACCGCCCGCCAGACCTTGGAAATGGGTGCTAAATTAAGAGCT 1200
QY 1201 CATGTTACAGAGAAACCAACCAACCTGATATTTATGATCTTTGTCTCACAATCTAT 1260
DB 1201 CATGTTACAGAGAAACCAACCAACCTGATATTTATGATCTTTGTCTCACAATCTAT 1260
QY 1261 TTTGTTGTTCCCATGATGCTTTGTTGCAATTTACGTTTCAATCAACCTCCGGTACACC 1320
DB 1261 TTTGTTGTTCCCATGATGCTTTGTTGCAATTTACGTTTCAATCAACCTCCGGTACACC 1320
QY 1321 GTTACTGTTATGCTTGTGATGCTGGAAGATCTTATCATCTCCATGCTATATG 1380
DB 1321 GTTACTGTTATGCTTGTGATGCTGGAAGATCTTATCATCTCCATGCTATATG 1380
QY 1381 CGTAGTGACGTGCTGTTAAGGCTGTTAGTCATGCTGATGAATTAACCTATTTCTGCG 1440
DB 1381 CGTAGTGACGTGCTGTTAAGGCTGTTAGTCATGCTGATGAATTAACCTATTTCTGCG 1440
QY 1441 AATCAATTTGGCCAAACGATGCTTAAAGATCGCGTGAATRCAAAACAATTGAACGTATG 1500
DB 1441 AATCAATTTGGCCAAACGATGCTTAAAGATCGCGTGAATRCAAAACAATTGAACGTATG 1500
QY 1501 ACTGTTATGATGATACATTTTGGCCACCATGCTGATGCTTATGCAATGAAATGGAAGT 1560
DB 1501 ACTGTTATGATGATACATTTTGGCCACCATGCTGATGCTTATGCAATGAAATGGAAGT 1560
QY 1561 ATGGAATATGTTCTCTGGATCCCAATTAAGAAATCGGATGAATCAAGATGTTGGAAT 1620
DB 1561 ATGGAATATGTTCTCTGGATCCCAATTAAGAAATCGGATGAATCAAGATGTTGGAAT 1620
QY 1621 ATTAGTATGATGATGAAATGATGATGCTGCTGAATGATGAATTAACAATGGGAG 1680
DB 1621 ATTAGTATGATGATGAAATGATGATGCTGCTGAATGATGAATTAACAATGGGAG 1680
QY 1681 TCGATGTTTGAACATAGATGATTTATTTAG 1713
DB 1681 TCGATGTTTGAACATAGATGATTTATTTAG 1713

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RESULT 3

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AAQ91566
ID AAQ91566 standard; cDNA; 1713 BP.
XX
AC AAQ91566;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103con.
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
XX insecticide; pesticide; water decontamination; meat decontamination;
XX ss.
XX
OS Lucilia cuprina.
XX
FH Key 1.1713
FT CDS /*tag= a
FT
XX
XX W09519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95W0-AU00016.
XX
XX 13-JAN-1994; 94AU-0003347.
PR

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XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
DR WPI, 1995-263870/34.
XX
PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX
PS
XX
XX Example 4; Page 12-17; 38pp; English.
XX
CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Llandillo 103. 4 isolated clones were
CC sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinon-resistant
CC esterases; a consensus sequence is given in AAQ91566.
XX
XX
SO Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;

Query Match 98.1%; Score 1681; DB 16; Length 1713;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1693; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACCTTGTGATGAGAAATTAATGAGATTAATGCAATGAAAT 60
DB 1 ATGAATTTCAACCTTGTGATGAGAAATTAATGAGATTAATGCAATGAAAT 60
QY 61 AAGTTTAACTATGCTTAACTACCAATGAACGCTGTCGTAATGATGAGC 120
DB 61 AAGTTTAACTATGCTTAACTACCAATGAACGCTGTCGTAATGATGAGC 120
QY 121 AAGTAAAGGCGTTAAACGTTTACTGTGACGATGATCTTACTACAGTTTGAGGT 180
DB 121 AAGTAAAGGCGTTAAACGTTTACTGTGACGATGATCTTACTACAGTTTGAGGT 180
QY 181 ATACGTCAGCCCAACCGCCAGTGGTGAGTGAATTAAGCAGCCAGACACACA 240
DB 181 ATACGTCAGCCCAACCGCCAGTGGTGAGTGAATTAAGCAGCCAGACACACA 240
QY 241 CCCTGGGATGCTGTCGCTGATGTTGCAATCAATAAGATAGTCAGTCAAGTTGATTT 300
DB 241 CCCTGGGATGCTGTCGCTGATGTTGCAATCAATAAGATAGTCAGTCAAGTTGATTT 300
QY 301 ATACGCGCAAGTGTGCTGCTCAGAGATGTCATACCTAAGTGTCTATACGAATAT 360
DB 301 ATACGCGCAAGTGTGCTGCTCAGAGATGTCATACCTAAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCGAATAAAGTCCGCTTTTATGATATCATACATGAGTGGTTATATATC 420
DB 361 CTAAATCCCGAATAAAGTCCGCTTTTATGATATCATACATGAGTGGTTATATATC 420
QY 421 GGTGAAATTCATCGTATGATGCTGCTGATTAATTAATAAAGATGCTGTG 480
DB 421 GGTGAAATTCATCGTATGATGCTGCTGATTAATTAATAAAGATGCTGTG 480
QY 481 ATTAACATACATATGCTTGGGAGCTCTAGTCTTCTAATTTAATTCAGAGACTT 540
DB 481 ATTAACATACATATGCTTGGGAGCTCTAGTCTTCTAATTTAATTCAGAGACTT 540
QY 541 AATGTCGCGGTAATGCCGCGCTTAAGATCAAGTCAATGCGCTGCTTGATTAATAAT 600
DB 541 AATGTCGCGGTAATGCCGCGCTTAAGATCAAGTCAATGCGCTGCTTGATTAATAAT 600
QY 601 AATGCGGCACTTTGGTGGCAATCCGATTAATTAACGCTTTGGTGAAGATGCCGT 660
DB 601 AATGCGGCACTTTGGTGGCAATCCGATTAATTAACGCTTTGGTGAAGATGCCGT 660
QY 661 GCTGCTCTACCCACTACATGATGTTAAACGACAACTGCGGCTTTTCCATCGTGGT 720
DB 661 GCTGCTCTACCCACTACATGATGTTAAACGACAACTGCGGCTTTTCCATCGTGGT 720

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OY 721 ATACTAATGTGGGTAATGCTATTTGTCATTGGCTTAATACCAATGCAACATGCTGCC 780
DB 721 ATACTAATGTGGGTAATGCTATTTGTCATTGGCTTAATACCAATGCAACATGCTGCC 780
OY 781 TTCACCTTAGCCAAATTTGGCCGGCTATAAGGGTGAGGATTAAGATTAAGATTTTGGAA 840
DB 781 TTCACCTTAGCCAAATTTGGCTATAGGGTGAGGATTAAGATTAAGATTTTGGAG 840
OY 841 TTTCTTATGAAGCCAGACGAGATTTAATAAACTTGAGAAAAAAGTTTAACTCTA 900
DB 841 TTTCTTATGAAGCCAGACGAGATTTAATAAACTTGAGAAAAAAGTTTAACTCTA 900
OY 901 GAAGAGCCGACAAATTAAGTCAATGTTCTTTGGTCCACATGTTGACCATATGAGAC 960
DB 901 GAAGAGCCGACAAATTAAGTCAATGTTCTTTGGTCCACATGTTGACCATATGAGAC 960
OY 961 GCTGATTTGTCTTACCCCAACATCCTCGGAAATGGTTAAACCTGTTGGGGTAATTCG 1020
DB 961 GCTGATTTGTCTTACCCCAACATCCTCGGAAATGGTTAAACCTGTTGGGGTAATTCG 1020
OY 1021 ATACCCACTATATGAGGTACACTTATATGAGGGTCTATTTTCTACTTCAATCTTANG 1080
DB 1021 ATACCCACTATATGAGGTACACTTATATGAGGGTCTATTTTCTACTTCAATCTTANG 1080
OY 1081 CAAATGCTATGCTTTTAAGGAATGGAACCTGTGCAATTTTGGCCAGTGAATTG 1140
DB 1081 CAAATGCTATGCTTTTAAGGAATGGAACCTGTGCAATTTTGGCCAGTGAATTG 1140
OY 1141 GCTGATTTGAACGACGCCCCCAGAGACCTTGGAAATGGTCTTAAATTAAGAGCT 1200
DB 1141 GCTGATTTGAACGACGCCCCCAGAGACCTTGGAAATGGTCTTAAATTAAGAGGCT 1200
OY 1201 CATGTTACGAGAAACACCAACAGCTGATATTTATGAGATCTTGGCTCAGATCTAT 1260
DB 1201 CATGTTACGAGAAACACCAACAGCTGATATTTATGAGATCTTGGCTCAGATCTAT 1260
OY 1261 TTTCTGTTCCCATGATGTTTGTGCAATTAACGTTTCAATCACACCTCCGGTACACC 1320
DB 1261 TTTCTGTTCCCATGATGTTTGTGCAATTAACGTTTCAATCACACCTCCGGTACACC 1320
OY 1321 GTCTACTTGTATGCTTTCGACTTCGATTCGATTCGGAAGATCTTATCAATCCCTATATG 1380
DB 1321 GTCTACTTGTATGCTTTCGACTTCGATTCGATTCGGAAGATCTTATCAATCCCTATATG 1380
OY 1381 CCTAGTGCACGTGCTTAAGGGTGTACTCATGCTGATGAATTAACCTATTTCTCTCG 1440
DB 1381 CCTAGTGCACGTGCTTAAGGGTGTACTCATGCTGATGAATTAACCTATTTCTCTCG 1440
OY 1441 AATCAATTTGGCCAAACGATGCTTAAGAGATGCGTGAATACAAACATTTGAACGTATG 1500
DB 1441 AATCAATTTGGCCAAACGATGCTTAAGAGATGCGTGAATACAAACATTTGAACGTATG 1500
OY 1501 ACTGTAATATGATACAAATTTGGCCACTGTAATCCTTAAGCAATGAATTTGAAGGT 1560
DB 1501 ACTGTAATATGATACAAATTTGGCCACTGTAATCCTTAAGCAATGAATTTGAAGGT 1560
OY 1561 ATGGAATAAGTTCTCGGATCCAAATTAAGAAATCCGATGAAGTGAAGTGTGGAAT 1620
DB 1561 ATGGAATAAGTTCTCGGATCCAAATTAAGAAATCCGATGAAGTGAAGTGTGGAAT 1620
OY 1621 ATTAGTATGAATTTGAATTTGATGTCCTGGAATGATTAAGATTTGAAGGT 1680
DB 1621 ATTAGTATGAATTTGAATTTGATGTCCTGGAATGATTAAGATTTGAAGGT 1680
OY 1681 TCGATTTGAAAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATTTGAAAAACATAGAGATTTATTTAG 1713

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RESULT 4
AA091564
ID AA091564 standard; cDNA; 1713 BP.

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XX AC AA091564;
XX DT 22-DEC-1995 (first entry)
XX DE OP-resistant esterase Lc7L103C allele.
XX KW Esterase; E3; bioremediation; organophosphate; carbamate;
XX KW Insecticide; pesticide; water decontamination; meat decontamination;
XX OS Lucilia cuprina.
XX FH Key Location/Qualifiers
XX FT CDS 1..1713
XX FT /*tag= a
XX PN W09519440-A1.
XX PD 20-JUL-1995.
XX PF 13-JAN-1995; 95WC-AU00016.
XX PR 13-JAN-1994; 94AU-0003347.
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX DR WPI: 1995-263870/34.
XX PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX PT eliminate residues of organo:phosphate and carbamate pesticides from
XX PS water, meat etc.
XX PS Example 4; Page 12-17; 38pp; English.
XX CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX CC resistant strain, Llandillo 103. 4 isolated clones were
XX CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
XX CC esterases. The esterases, or cells expressing them, are used
XX CC in bioremediation.
XX SQ Sequence 1713 BP; 512 A; 308 C; 368 G; 525 T; 0 other;

Query Match 97.9%; Score 1677.8; DB 16; Length 1713;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1691; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 1 ATGAATTTACAGCTTACTGTTGATGAGAAATTAATGGAAGTTAATGCATTGAAAT 60
DB 1 ATGAATTTACAGCTTACTGTTGATGAGAAATTAATGGAAGTTAATGCATTGAAAT 60
OY 61 AAGTTTAAACATGATGTTTAACTACCAATGAACGGTGTACTGAACTGAATATGCG 120
DB 61 AAGTTTAAACATGATGTTTAACTACCAATGAACGGTGTACTGAACTGAATATGCG 120
OY 121 AAAGTAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTATACAGTTTGAAGGT 180
DB 121 AAAGTAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTATACAGTTTGAAGGT 180
OY 181 ATACCGTACGCCCAACCGCCAGGCGGTGAGCTGAGATTTAAACACCCGACGACACA 240
DB 181 ATACCGTACGCCCAACCGCCAGGCGGTGAGCTGAGATTTAAACACCCGACGACACA 240
OY 241 CCTGGAGATGCTGCGTATGTTGCAATCATAAAGATAGTCAGTGCAGTGGATTTT 300
DB 241 CCTGGAGATGCTGCGTATGTTGCAATCATAAAGATAGTCAGTGCAGTGGATTTT 300
OY 301 ATACGGGCAAGATGTTGCTCAGAGAGATGTTATACCTAAGTGTCTATAGAAATAT 360
DB 301 ATACGGGCAAGATGTTGCTCAGAGAGATGTTATACCTAAGTGTCTATAGAAATAT 360

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Db 301 ATTAGAGCAAGTGTGTGCTCAGAGATTGTCTATACCTTAAGCCGTATACGAATAT 360
QY 361 CTAATCCCGAACTAAACGTCGGTATTAGTATACATACATGCTGCTTTTATTATC 420
Db 361 CTAATCCCGAACTAAACGTCGGTATTAGTATACATACATGCTGCTTTTATTATC 420
QY 421 GGTGAATATATCGTATATGTCTGTATTTATTTCAATTTAAAGATGGTGTG 480
Db 421 GGTGAATATATCGTATATGTCTGTATTTATTTCAATTTAAAGATGGTGTG 480
QY 481 ATTAGCTACATATGCTTTGGAGCTCTAGTCTTCTAAGTTAAATTCAGAACCTT 540
Db 481 ATTAGCTACATATGCTTTGGAGCTCTAGTCTTCTAAGTTAAATTCAGAACCTT 540
QY 541 AATGCGCCGCTAATGCGGCTTAAAGATCAAGTATGAGCTTGGTGGATTAAT 600
Db 541 AATGCGCCGCTAATGCGGCTTAAAGATCAAGTATGAGCTTGGTGGATTAAT 600
QY 601 AATGGCCCAACTTTGGTGGCAATCCGATATATTTACAGTCTTTGGTGAAGTCCGCT 660
Db 601 AATGGCCCAACTTTGGTGGCAATCCGATATATTTACAGTCTTTGGTGAAGTCCGCT 660
QY 661 GGTGCTCTACCCATACATGATGTATACGGAACAACTCGGCTTTTCATGCTGT 720
Db 661 GGTGCTCTACCCATACATGATGTATACGGAACAACTCGGCTTTTCATGCTGT 720
QY 721 ATACTAATGTCGGTAAATGCTATTTGTCCATGCTTAATACCAATGTCATGCTGC 780
Db 721 ATACTAATGTCGGTAAATGCTATTTGTCCATGCTTAATACCAATGTCATGCTGC 780
QY 781 TTCACCTTAGCAAAATGCGCGCTATAAGGTGAGATATGATTAAGATGTTTGA 840
Db 781 TTCACCTTAGCAAAATGCGCGCTATAAGGTGAGATATGATTAAGATGTTTGA 840
QY 841 TTTCTTAAGAAAGCCAGACAGATTTAAATACTTGAGGAAAGTTTAACTCTA 900
Db 841 TTTCTTAAGAAAGCCAGACAGATTTAAATACTTGAGGAAAGTTTAACTCTA 900
QY 901 GAAGAGCGCAAAATTAAGTATGCTTTCTTTGCTCCACTGTTGAGCCATATCAGCC 960
Db 901 GAAGAGCGCAAAATTAAGTATGCTTTCTTTGCTCCACTGTTGAGCCATATCAGCC 960
QY 961 GCTGATGTGTCTTACCAGCAATCCTCGGGAATGTTAAAGCTGTGGGGTAATTG 1020
Db 961 GCTGATGTGTCTTACCAGCAATCCTCGGGAATGTTAAAGCTGTGGGGTAATTG 1020
QY 1021 ATACCACTATGATGGGTAACACTTCAATATGAGGCTCAATTTTCACTTAATCTTAAG 1080
Db 1021 ATACCACTATGATGGGTAACACTTCAATATGAGGCTCAATTTTCACTTAATCTTAAG 1080
QY 1081 CAAATGCCCTATGCTTTAAGGAATTTGAAACTTGTGCAATTTGTGCCAAGGATTTG 1140
Db 1081 CAAATGCCCTATGCTTTAAGGAATTTGAAACTTGTGCAATTTGTGCCAAGGATTTG 1140
QY 1141 GCTGATGTGTAAGACACCGCCCGCAGAGACCTTGGAATGGGTGCTAAATTAAGAAGCT 1200
Db 1141 GCTGATGTGTAAGACACCGCCCGCAGAGACCTTGGAATGGGTGCTAAATTAAGAAGCT 1200
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATGATGATCTTGTCTCACTATAT 1260
Db 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATGATGATCTTGTCTCACTATAT 1260
QY 1261 TTTCTGTTCCCATGATGCTTTGTGCAATTTACGTTTCAACACCTCCGCTACACCC 1320
Db 1261 TTTCTGTTCCCATGATGCTTTGTGCAATTTACGTTTCAACACCTCCGCTACACCC 1320
QY 1321 GTCTACTTGTATGCTTGCATTCGATTTGGAAGATCTTAATCAATCCCTATCTATTATG 1380
Db 1321 GTCTACTTGTATGCTTGCATTCGATTTGGAAGATCTTAATCAATCCCTATCTATTATG 1380
QY 1381 CGTAGTGAAGCTGTGTTAAGGCTTAAAGCTGATGATGATTAACCTATTTCTCTG 1440
Db 1381 CGTAGTGAAGCTGTGTTAAGGCTTAAAGCTGATGATGATTAACCTATTTCTCTG 1440

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QY 1441 AATCAATGGCCAAACGATATGCTTAAAGATGCGGGAATACAAACAAATGACGTATG 1500
Db 1441 AATCAATGGCCAAACGATATGCTTAAAGATGCGGGAATACAAACAAATGACGTATG 1500
QY 1501 ACTGGTATATGATACATATTTGCCACACTGTGTAATCCTTTATAGCAATGAATGAAGT 1560
Db 1501 ACTGGTATATGATACATATTTGCCACACTGTGTAATCCTTTATAGCAATGAATGAAGT 1560
QY 1561 ATGGAATATGTTTCTGGGATCCATTAAGAAATCCGATGAAGTATGCAAGTGTGTAAT 1620
Db 1561 ATGGAATATGTTTCTGGGATCCATTAAGAAATCCGATGAAGTATGCAAGTGTGTAAT 1620
QY 1621 ATTAGTATGATTAATGAATATGATGCTGCTGAATGATTAAGATTAACAAATGGAG 1680
Db 1621 ATTAGTATGATTAATGAATATGATGCTGCTGAATGATTAAGATTAACAAATGGAG 1680
QY 1681 TCGATGTTTGAATAACATGAGATTTATTATG 1713
Db 1681 TCGATGTTTGAATAACATGAGATTTATTATG 1713

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RESULT 5
AA091565
ID AA091565 standard; cDNA: 1713 BP.
XX
AC AA091565;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103D allele.
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination;
XX
OS Lucilia cuprina.
XX
FH Key 1.1713
FT CDS.
FT /*tag- a
XX
XX W09519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95WO-AU00016.
XX
XX 13-JAN-1994; 94AU-0003347.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI: 1995-263870/34.
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX PT eliminate residues of organo:phosphate and carbamate pesticides from
XX PR water, meat etc.
XX
XX Example 4: Page 12-17; 38pp: English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX CC resistant strain, Llandillo 103. 4 isolated clones were
XX CC sequenced (Lc7L103 A-D. AA091562-65) that encoded diazinin-resistant
XX CC esterases. The esterases, or cells expressing them, are used
XX CC in bioremediation.
XX
XX Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other;
XX
XX Query Match 97.9%; Score 1677.8; DB 16; Length 1713;

```


Qy	1	ATGATTTACAGCGTGGTTGATGAGGAAATTTAAATGGAAGATTAATGATGATTAAT	60
Qy	1	ATGATTTACAGCGTGGTTGATGAGGAAATTTAAATGGAAGATTAATGATGATTAAT	60
Db	1	ATGATTTACAGCGTGGTTGATGAGGAAATTTAAATGGAAGATTAATGATGATTAAT	60
Qy	61	AAAGTTTAAACATGCTGTTAACTACCAATGAAAGCGGTGAGCGAATCAATATGCG	120
Db	61	AAAGTTTAAACATGCTGTTAACTACCAATGAAAGCGGTGAGCGAATCAATATGCG	120
Qy	121	AAAGTAAAGCGGTAAACGTTTAACTGTCGATGATTCCTACTACAGTTTGGAGGT	180
Db	121	AAAGTAAAGCGGTAAACGTTTAACTGTCGATGATTCCTACTACAGTTTGGAGGT	180
Qy	181	ATACCGTAGCCCAACCGCGAGGGGTGAGCGATGATTTAAAGCCACCACGACACACA	240
Db	181	ATACCGTAGCCCAACCGCGAGGGGTGAGCGATGATTTAAAGCCACCACGACACACA	240
Qy	241	CCCTGGAGTGGTGGCTGATTTGTTGCAATCAATTAAGATTAAGTCAGTCAAGTTGATTT	300
Db	241	CCCTGGAGTGGTGGCTGATTTGTTGCAATCAATTAAGATTAAGTCAGTCAAGTTGATTT	300
Qy	301	ATTAACGGCAAAATGTGTGCTCAGAGGATTTGTAATACCTAATGTTGTTAATACGAATAT	360
Db	301	ATTAACGGCAAAATGTGTGCTCAGAGGATTTGTAATACCTAATGTTGTTAATACGAATAT	360
Qy	361	CTAAATCCGAAACTTAAGCTCCCGTTTAAATACATCAATGAGGGGTTTATATATC	420
Db	361	CTAAATCCGAAACTTAAGCTCCCGTTTAAATACATCAATGAGGGGTTTATATATC	420
Qy	421	GGTGAATCATCGTATATGATATGTCCTGATATTTTCATTTAAAGATGTGGTGTG	480
Db	421	GGTGAATCATCGTATATGATATGTCCTGATATTTTCATTTAAAGATGTGGTGTG	480
Qy	481	ATTAACTAACAATATGTTTGGAGCTCTAAGTTTTCTAAGTTTAAATTCAGAGACTT	540
Db	481	ATTAACTAACAATATGTTTGGAGCTCTAAGTTTTCTAAGTTTAAATTCAGAGACTT	540
Qy	541	AAATGGCCCGGTATGCGCGCTTAAAGATCAAGCATGCGCTTGCTGATTTAAAT	600
Db	541	AAATGGCCCGGTATGCGCGCTTAAAGATCAAGCATGCGCTTGCTGATTTAAAT	600
Qy	601	AATGGCCCAACTTGGTGGCAATCCCGATTAATTTACAGTCTTGGTGAAGATGCCGT	660
Db	601	AATGGCCCAACTTGGTGGCAATCCCGATTAATTTACAGTCTTGGTGAAGATGCCGT	660
Qy	661	GCTGCCCTCTACCACTACATGATGTTAACCAGCAAACTCGCGGTCTTTCCATGTGCT	720
Db	661	GCTGCCCTCTACCACTACATGATGTTAACCAGCAAACTCGCGGTCTTTCCATGTGCT	720
Qy	721	ATACTAATGTCGGGTATGCTATTTTCCATTGGCGTAATACCAATGTCACATCTGCC	780
Db	721	ATACTAATGTCGGGTATGCTATTTTCCATTGGCGTAATACCAATGTCACATCTGCC	780
Qy	781	TTCACTTACCCAAATTTGGCGCGCTTAAGGGTGAAGATTAATGATTAAGATTTTGGAA	840
Db	781	TTCACTTACCCAAATTTGGCGCGCTTAAGGGTGAAGATTAATGATTAAGATTTTGGAA	840
Qy	841	TTTCTTATGAAGCCAAAGCCACAGATTTTAATTAATCTTGAGGAAAAAGTTTAACTCTA	900
Db	841	TTTCTTATGAAGCCAAAGCCACAGATTTTAATTAATCTTGAGGAAAAAGTTTAACTCTA	900
Qy	901	GAAAGGCTCAAAATAAGATCATGTTCCCTTTGGGCCACGTTGAGCAATATCAGCC	960
Db	901	GAAAGGCTCAAAATAAGATCATGTTCCCTTTGGGCCACGTTGAGCAATATCAGCC	960
Qy	961	GCTGATTTGCTTACCAACAATCCTCGGAAATGTTTAAACATGCTTGGGGTAAATCG	1020
Db	961	GCTGATTTGCTTACCAACAATCCTCGGAAATGTTTAAACATGCTTGGGGTAAATCG	1020
Qy	1021	ATACCACTATGATGGTAAACCTTCATATAGAGGCTATTTTTCATCTCAATTTCTTAAG	1080

Dd	1021	ATACCCACTATGATGGGTAAACACTTCATATATGAGGGCTATTTTTCACCTTGCTTCTTAAG	1080
Qy	1081	CAATGGCTATGCTTGTTAAGAAGATTGGAACCTGTGTCAATTTTGTGCCAAGGAATG	1140
Dd	1081	CAATGGCTATGCTTGTTAAGAAGATTGGAACCTGTGTCAATTTTGTGCCAAGGAATG	1140
Qy	1141	GCTGATGTTGACGCAACCGGCCCGACGAGACCTTGGAAATGGGTGCTTAAATTAAAAAGCT	1200
Dd	1141	GCTGATGCTGAAACGACCGGCCCGACGAGACCTTGGAAATGGGTGCTTAAATTAAAAAGCT	1200
Qy	1201	CATGTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTTGCTGCACATCTAT	1260
Dd	1201	CATGTTACAGAGAAACACCAACCGCCGATATTTTATGATCTTTGCTGCACATCTAT	1260
Qy	1261	TTCTGGTTCCCAATGATCGTGTGTTGTCATTAACGTTTCAACACACCTCCGGTACACC	1320
Dd	1261	TTCTGGTTCCCAATGATCGTGTGTTGTCATTAACGTTTCAATCACACCTCCGGTACACC	1320
Qy	1321	GTCATCTGTTATGCGCTTCGACTTCGATGTGGGAAGATCTTATCAATCCCTATGCTATTATG	1380
Dd	1321	GTCATCTGTTATGCGCTTCGACTTCGATGTGGGAAGATCTTATTAATCCCTATGCTATTATG	1380
Qy	1381	CGTATGTGACGCTGTGTGTTAAGGGTGTATGATGCTGATGAATTAACCTATTTCTTCGG	1440
Dd	1381	CGTATGTGACGCTGTGTGTTAAGGGTGTATGATGCTGATGAATTAACCTATTTCTTCGG	1440
Qy	1441	AATCAATTTGGCCAAACGATATGCTTAAGAAATCGCGTGAATACAAAACATTTGAACGTATG	1500
Dd	1441	AATCAATTTGGCCAAACGATATGCTTAAGAAATCCCGTGAATACAAAACATTTGAACGTATG	1500
Qy	1501	ACTGGTATATGATACAAATTTGGCCACACGCTGTAATCCCTTATAGCAATGAATTTGAAGT	1560
Dd	1501	ACTGGTATATGATACAAATTTGGCCACACGCTGTAATCCCTTATAGCAATGAATTTGAAGT	1560
Qy	1561	ATGCAAAATGTTTCTCGGATCCCAATTAAGAAATCCGATGAAGTATACAGTGTTCGAT	1620
Dd	1561	ATGCAAAATGTTTCTCGGATCCCAATTAAGAAATCCGATGAAGTATACAGTGTTCGAT	1620
Qy	1621	ATTAGTGAATGAATTAAGAAATGATTGATGTGCTGAAATGGATTAAGATTAAACATGGAG	1680
Dd	1621	ATTAGTGAATGAATTAAGAAATGATTGATGTGCTGAAATGGATTAAGATTAAACATGGAG	1680
Qy	1681	TCGATGTTTGAATAACATAGAGATTATTTTAG	1713
Dd	1681	TCGATGTTTGAATAACATAGAGATTATTTTAG	1713
RESULT 6			
AA091563			
XX	AA091563	standard; cDNA; 1713 BP.	
XX	AA091563;		
DT	22-DEC-1995	(first entry)	
DE	OP-resistant esterase Lc/7L103B allele.		
XX			
XX	Esterase; E3; bioremediation; organophosphate; carbamate;		
KW	insecticide; pesticide; water decontamination; meat decontamination;		
KW	ss.		
XX			
OS	Lucilia cuprina.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	1..1713	
FT		/*tag= a	
XX	W09519440-A1.		
PN			
XX	20-JUL-1995.		
PD			
XX	13-JAN-1995;	95W0-AU00016.	
PF			
XX			

PR 13-JAN-1994: 94AU-0003347.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX BOYCE TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 XX WPI; 1995-263870/34.
 XX
 XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC O-susceptible esterase E3 of L. cuprina) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (LC7L103 A-B, AA091562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used.
 CC In bioremediation.
 CC
 XX
 XX Sequence 1713 BP; 513 A; 308 C; 368 G; 524 T; 0 other;
 SO
 Query Match 97.9%; Score 1676.2; DB 16; Length 1713;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 1690; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Db 661 GCTGCTCTACCCACTACATGATGTAAACGCAAACTCGCGGTCTTTCCATCGTGT 720
 QY 721 ATACTAATGTGGGTAAATGCTATTTGTCATATGGCTATATACCAATGTCACATCGTCC 780
 Db 721 ATACTAATGTGGGTAAATGCTATTTGTCATATGGCTATATACCAATGTCACATCGTCC 780
 QY 781 TTCACTTAGCCAAATTTGGCGCTATAGGGTATAGATTAATGATGATTTTGGAA 840
 Db 781 TTCACTTAGCCAAATTTGGCGCTATAGGGTATAGATTAATGATGATTTTGGAA 840
 QY 841 TTCTTTTGAAGCCCAAGCCACAGATTTAATAAAGCTTGAGAAAAATTTTAACTCTA 900
 Db 841 TTCTTTTGAAGCCCAAGCCACAGATTTAATAAAGCTTGAGAAAAATTTTAACTCTA 900
 QY 901 GAAAGGGTCAAAATTAAGTCAATGTTCTTTGGTCCCACTGTTGGCCATATCAAGC 960
 Db 901 GAAAGGGTCAAAATTAAGTCAATGTTCTTTGGTCCCACTGTTGGCCATATCAAGC 960
 QY 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGTTAAACCTTGCGGTAAATTCG 1020
 Db 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGTTAAACCTTGCGGTAAATTCG 1020
 QY 1021 ATACCACTATGATGGGTAAACCTTCAATATGAGGGTCTATTTTCACTTGTCTTAAAG 1080
 Db 1021 ATACCACTATGATGGGTAAACCTTCAATATGAGGGTCTATTTTCACTTGTCTTAAAG 1080
 QY 1081 CAAATGCCCTATGCTTTGTAAGAAATGTAACCTTGTCAATTTTGCCAAAGGAATTCG 1140
 Db 1081 CAAATGCCCTATGCTTTGTAAGAAATGTAACCTTGTCAATTTTGCCAAAGGAATTCG 1140
 QY 1141 GCTGATGTTGACCGCCAGCCGCCAGAGACCTTGGAATGGGTCTAAATTTAAAGGCT 1200
 Db 1141 GCTGATGTTGACCGCCAGCCGCCAGAGACCTTGGAATGGGTCTAAATTTAAAGGCT 1200
 QY 1201 CATGTTACAGAGAAACACCAAGCTGATATTTTATGATCTTTCCTGTCACATCTAT 1260
 Db 1201 CATGTTACAGAGAAACACCAAGCTGATATTTTATGATCTTTCCTGTCACATCTAT 1260
 QY 1261 TTTGTTTCCCATGATGCTTTGTTGCAATTTAGCTTTCATGACACCTCGGATACACC 1320
 Db 1261 TTTGTTTCCCATGATGCTTTGTTGCAATTTAGCTTTCATGACACCTCGGATACACC 1320
 QY 1321 GTCTACTTGTATGCTTCCGACTTGCATTTGCGAAGATCTTATCAATCCCTATCGATATG 1380
 Db 1321 GTCTACTTGTATGCTTCCGACTTGCATTTGCGAAGATCTTATCAATCCCTATCGATATG 1380
 QY 1381 CGTAGTGAGCTGCTGTTAAGGGGTAGTCATGCTGATGAATTAACCTATTTCTTCTG 1440
 Db 1381 CGTAGTGAGCTGCTGTTAAGGGGTAGTCATGCTGATGAATTAACCTATTTCTTCTG 1440
 QY 1441 AATCAATTTGGCCAAAGCTATGCTTAAGAAATCGGCTGAATACAAACATTTGAACGTATG 1500
 Db 1441 AATCAATTTGGCCAAAGCTATGCTTAAGAAATCGGCTGAATACAAACATTTGAACGTATG 1500
 QY 1501 ACTGCTATGATGATACAAATTTGGCCACCACTGTAATCCTTATGCAATGAATTTGAAGT 1560
 Db 1501 ACTGCTATGATGATACAAATTTGGCCACCACTGTAATCCTTATGCAATGAATTTGAAGT 1560
 QY 1561 ATGGAATAATGTTTCTGCGGATCCAAATTAAGAATTCGATGAAGTATACAAGTCTTTGAAT 1620
 Db 1561 ATGGAATAATGTTTCTGCGGATCCAAATTAAGAATTCGATGAAGTATACAAGTCTTTGAAT 1620
 QY 1621 ATTATGATGAATTTGAATATGATGATGCTGGAATTTGAATTAACAATGGAG 1680
 Db 1621 ATTATGATGAATTTGAATATGATGATGCTGGAATTTGAATTAACAATGGAG 1680
 QY 1681 TCGATGTTGAAAAACATAGATTTATTTAG 1713
 Db 1681 TCGATGTTGAAAAACATAGATTTATTTTAG 1713
 RESULT 7

AA091562
ID AA091562 standard; cDNA; 1713 BP.
XX
AC AA091562;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103a allele.
XX
XX Esterase; E3; bioremediation: organophosphate; carbamate;
KM insecticide; pesticide; water decontamination; meat decontamination;
KM ss.
XX
XX Lucilia cuprina.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..1713
FT /tag- a
XX
XX MO9519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95WO-AU00016.
XX
XX 13-JAN-1994; 94AU-0003347.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI; 1995-263870/34.
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX
XX Example 4; Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Llandillo 103. 4 isolated clones were
CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
CC in bioremediation.
XX
XX
XX Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;
SO
Query Match 97.88; Score 1674.6; DB 16; Length 1713;
Best Local Similarity 98.68; Pred. No. 0;
Matches 1689; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 301 ATAAAGGCAAAAGTGTGCTCAGAGATTCTATACCTAAGTCTATACGAATAT 360
DB 301 ATTAAGGCAAAAGTGTGCTCAGAGATTCTATACCTAAGTCTATACGAATAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTGTTTATATACATACATGCTGCTTATATC 420
DB 361 CTAAATCCCGAACTAAACGTCCTGTTTATATACATACATGCTGCTTATATC 420
QY 421 GGTAAATATCATGCTGATATGATGTCCTGATATTTTCAATTAAGATGCTGTTG 480
DB 421 GGTAAATATCATGCTGATATGATGTCCTGATATTTTCAATTAAGATGCTGTTG 480
QY 481 ATTAACATACATATGCTGTTGAGCTCTAGCTTTCTAAGTTAAATTCAGAACCTT 540
DB 481 ATTAACATACATATGCTGTTGAGCTCTAGCTTTCTAAGTTAAATTCAGAACCTT 540
QY 541 AATGTCGCCGTAATGCGGCTTAAGATCATGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 AATGTCGCCGTAATGCGGCTTAAGATCATGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AATGTCGCCGTAATGCGGCTTAAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 AATGTCGCCGTAATGCGGCTTAAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GCTGCTCTACCCACTACATGATGTTAAACGAAACAACTCCGCTCTTTCATGCTGCT 720
DB 661 GCTGCTCTACCCACTACATGATGTTAAACGAAACAACTCCGCTCTTTCATGCTGCT 720
QY 721 ATTAATATGCTGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCT 780
DB 721 ATTAATATGCTGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCT 780
QY 781 TTCACTTACGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 TTCACTTACGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 TTCTTTATGAAGCAAGCCACAGATTTAATAAAGTGAAGAAAGTTTAACTGTA 900
DB 841 TTCTTTATGAAGCAAGCCACAGATTTAATAAAGTGAAGAAAGTTTAACTGTA 900
QY 901 GAAGAGGCTAATTAAGTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 GAAGAGGCTAATTAAGTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GCTATGCTGCTTACCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 GCTATGCTGCTTACCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 ATACCACTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 ATACCACTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 CAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 CAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 CATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 CATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 CGTAGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440

Db 1381 CBTAGGACGCTGCTTAAAGGCTTACATGCTGATGAATTAACCTATTTCTCTCG 1440
 QY 1441 AATCAATTTGGCAACGTAATGCTTAAGAATCGCGTAATACAAACATTTGAACGTATG 1500
 Db 1441 AATCAATTTGGCAACGTAATGCTTAAGAATCGCGTAATACAAACATTTGAACGTATG 1500
 QY 1501 ACTGCTATTTGATACATTTGGCCACCACTGCTATCTTATAGCAATGAATTTGAAGGT 1560
 Db 1501 ACTGCTATTTGATACATTTGGCCACCACTGCTATCTTATAGCAATGAATTTGAAGGT 1560
 QY 1561 ATGGAATATGCTTCCGGATCCCAATTAAGAAATCCGATGAATATACAAAGTCTTGAT 1620
 Db 1561 ATGGAATATGCTTCCGGATCCCAATTAAGAAATCCGATGAATATACAAAGTCTTGAT 1620
 QY 1621 ATTATGATGAATTTGAATTTGATGCTGCTGAATGAATGAATTTAAACATGGAG 1680
 Db 1621 ATTATGATGAATTTGAATTTGATGCTGCTGAATGAATGAATTTAAACATGGAG 1680
 QY 1681 TCGATGTTGAAAACATAGAGATTTATTTAG 1713
 Db 1681 TCGATGTTGAAAACATAGAGATTTATTTAG 1713

RESULT 8

AA168597 standard; DNA; 1710 BP.

AA168597;

08-AUG-1997 (first entry)

Md-alpha-E7 gene.

Malathion carboxylesterase; organophosphate; insecticide; pesticide; remediation; bioremediation; decontamination; ds.

Musca domestica Rutgers strain.

Key Location/Qualifiers

FT mutation 752

FT /tag= a /note= "Trp-251 TGG codon is altered to a Ser codon in resistant mutants"

WT

PN WO9719176-A1.

PD 29-MAY-1997.

XX 22-NOV-1996; 96MO-AU00746.

XX 23-NOV-1995; 95AU-0006751.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

PI Boyce T, Brownlie JC, Campbell PM, Claudianos C, Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

DR WPI; 1997-298113/27.

XX P-PSDB: AAW17767.

PT DNA encoding enzyme that degrades organophosphate pesticides -

PT useful for decontamination of soil, water, food etc

PS Claim 6; Fig 3; 52pp: English.

CC A 1710 bp DNA molecule (AA168597) comprises the Md-alpha-E7
 CC coding sequence of the Musca domestica Rutgers strain. It was
 CC isolated by amplification of genomic DNA using alpha-esterase
 CC consensus primers (see also AA168598-99) and use of a 534 bp
 CC amplicon to screen a genomic library of M. domestica. A
 CC mutation of the gene, resulting in substn. of serine for tryptophan
 CC at amino acid position 251 (see also AAW17767), confers malathion

CC resistance. The resistant enzyme acts as a malathion
 CC carboxylesterase and can be formulated for use in degrading
 CC environmental carboxylester for dimethyl general organophosphates.

SO Sequence 1710 BP; 498 A; 369 C; 394 G; 449 T; 0 other:

Query Match 55.8%; Score 956.6; DB 18; Length 1710;
 Best Local Similarity 73.4%; Pred. No. 8.8e-253;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

QY 44 TTTAATGCAATGAAATTAAGTTTAACTATGCTTAACATGCAATGAACGCTGTAG 103
 Db 44 TTTAATGCAATGCAATTAATATACACAACTACCGTGTGATACAAATGAACCAATATA 103
 QY 104 CTGAATGCAATATGCAACAAAGTGAAGGGTTAAACGTTTAACGTGTGATGATTCCT 163
 Db 104 TCGATATCTGAATATGCAACAAATTAAGGGTTTAAGGAATGACCGTCTGATGATTCCT 163
 QY 164 ACTACAGTTTGAAGGTTATACCGTACGCCAACCGCAAGTGGTGAAGTATTAAG 223
 Db 164 ACTACAGTTTGAAGGTTATACCGTACCGCCAACCGCAAGTGGTGAAGTATTAAG 223
 QY 224 CACCCGAGGACCAACACCCCTGGATGGTGGTGGTATGTCATTCATTAAGATAGT 283
 Db 224 CACCCGAGGACCAACACCCCTGGATGGTGGTGGTATGTCATTCATTAAGATAGT 283
 QY 284 CAGTCAAGTTGATTTTATACGCGCAAGTGTGGCTCAGAGATGTCTATACCTAA 343
 Db 284 CAGTCAAGTTGATTTTATACGCGCAAGTGTGGCTCAGAGATGTCTATACCTAA 343
 QY 344 GGTCTATACGATTAATCTTAATCCCGAACTTAACGTCCTGTTTATGATACATCATG 403
 Db 344 GGTCTATACGATTAATCTTAATCCCGAACTTAACGTCCTGTTTATGATACATCATG 403
 QY 404 GTGGTGTGTTTATATATGCTGTAAGAAATCATGCTGATATGATGCTGCTATATCATTA 463
 Db 404 GTGGTGTGTTTATATATGCTGTAAGAAATCATGCTGATATGATGCTGCTATATCATTA 463
 QY 464 AAAAGATGCTGTTGATTAATCAATCAATATCGTTTGGAGCTGATGTTTCTAAGT 523
 Db 464 AAAAGATGCTGTTGATTAATCAATCAATATCGTTTGGAGCTGATGTTTCTAAGT 523
 QY 524 TAAATTCAGAAAGCTTAATGTCGGGTAATGCGGCTTAAGTCAAGTCAATGCGCT 583
 Db 524 TAAATTCAGAAAGCTTAATGTCGGGTAATGCGGCTTAAGTCAAGTCAATGCGCT 583
 QY 584 TGGGTTGATTAATAAATAATATGCGCAACTTGTGCAATCCGATTAATATACGCT 643
 Db 584 TGGGTTGATTAATAAATAATATGCGCAACTTGTGCAATCCGATTAATATACGCT 643
 QY 644 TTGGTGAAGTGGCGGTGCTGCTTACCCACTACATGATGTTAACGCAACAACTCGCG 703
 Db 644 TTGGTGAAGTGGCGGTGCTGCTTACCCACTACATGATGTTAACGCAACAACTCGCG 703
 QY 704 GTCTTTCCATGCTGTGTATACATATGTGGGTAATGCTATTTGTCATTTGGCTAATACC 763
 Db 704 GTCTTTCCATGCTGTGTATACATATGTGGGTAATGCTATTTGTCATTTGGCTAATACC 763
 QY 764 AATGTCACATGCTGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 823
 Db 764 AATGTCACATGCTGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 823
 QY 824 ATAAGATGTTTGAATTTCTTATGAAGCAAGCCACAGATGTTAATAAACCTTGAGG 883
 Db 824 ATAAGATGTTTGAATTTCTTATGAAGCAAGCCACAGATGTTAATAAACCTTGAGG 883
 QY 884 AAAAATTTTAATCTTGAAGCAAGCCACAGATGTTAATAAACCTTGAGG 943
 Db 884 AAAAATTTTAATCTTGAAGCAAGCCACAGATGTTAATAAACCTTGAGG 943
 QY 944 TTGAGCATATGACAGCGGATGTTGTTGTTACCCAAATCTCGGGAATGTTAATAA 1003
 Db 944 TTGAGCATATGACAGCGGATGTTGTTGTTACCCAAATCTCGGGAATGTTAATAA 1003


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Db 695 AATGGCCCTAGTTTCGGCGGAGATCCCACTGCATCACTGTTTTTGGAGAGAGTGCGGA 754
OY 661 GCTGCTCTACCCACTCATGATGTTTAACGCAACAACTGCGGCTCTTTCATCGTGT 720
Db 755 GGGCCCTCCACTCCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 814
OY 721 ATACTAATGTCGGGTAATGCTATTTGTCATGTGC--TATATCCCAATGTCATCATGT 777
Db 815 ATCTTGAGTCGGGCACTGTCATTTGTCCTGGCCCTACAAGCGGCATTTACCATTAAT 874
OY 778 GCCTTACCTTAGCAATTTGCGCGCTATTAAGGTAGATATGATTAAGATGTTTG 837
Db 875 CCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 934
OY 838 GAATTTCTTATGAAGCCACACAGATTTAATAAATTGAGAAAAAGTTTACT 897
Db 935 GAGTTCTTGAGAAACGTAAGGCCAAGATCTTATCGCTGGAGAAAAATGTCCTGACA 994
OY 898 CTGAGAGAGCGTACAAATAAGTCATGTTTCTTTGGTCCACTGTTGAGCCATATCAG 957
Db 995 CTGAGAGAGCGATGAAGATATGTTTGCCTTGGCCATCCCTGGAACCATCTCC 1054
OY 958 ACCGCTGATGTCCTTACCAACATCTCGGGAATGTTAACTGCTTGGGGTAT 1017
Db 1055 ACCGCGAATGTCATATCAAGCCCTCAAGAGATGATGAAGACCGCTGAGATAC 1114
OY 1018 TCGATACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
Db 1115 TCGATCCCATGTTTATGAGAAACATCTGCTAGAGAGGCTGCTGGGTTCCAGAGTA 1174
OY 1078 AAGCAATGCTTATGCTTGTAAAGATTTGAACCTGTGTCATTTTGTGCCAAGTGA 1137
Db 1175 AAGCTTATGCGCAGAGTGCTGACAGCTGATGCTGACACCTTCAATTCCTCAAGAA 1234
OY 1138 TTGGCTGATGTTGAAGCCCGCCAGAGACCTTGAATGGCTGCTAAATTAAG 1197
Db 1235 TTGCTGGCCAGGAGCCGATTAAGAAAACTGATTCGTGAGTCACAGATTCAGAT 1294
OY 1198 GCTCATGTTACAGAGAACACCAACAGCTGATATTTTATGATCTTCTCATC 1257
Db 1295 GTTCATGCGACGTCGTCAGAAAGCCCGCATTAATTAATGATGATGATGATGATGAT 1354
OY 1258 TATTTGCTGCTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
Db 1355 TACTTGTGTTCCGGCCCTGAGAGGTGTCATTCCTCCGACCGCTGAGGCTGAGCT 1414
OY 1318 CCCGCTACTTGTGATGCTTGCATTCGATTCGAGATCTTATCAATCCCTATG 1377
Db 1415 CCGATATATTTCTATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1474
OY 1378 ATGCGTAGTGACGTCGTGTAAGGTGTTAGTATGATGATGATGATGATGATGATGAT 1437
Db 1475 ATGCGGTTGGGACGCGGTCAAGGGGTGACGATGCGGAGATTTGAGCTACCAATTC 1534
OY 1438 TGGAAATCAATTTGGCCAAAGCTATGCTAAAGATGCGGTAATCAAAACATTAAGCT 1497
Db 1535 AGAGGCTCTGCTGCTGCGGCTGCGAAGAAAGTCGAGATGAGGAATCTGAAACA 1594
OY 1498 ATGACGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
Db 1595 ACCGTGGGATCTGAGCCAGATTTGTCGCAAGGGTATCCCTACAGCAAGAGATCAAC 1654
OY 1558 GGTATGGAATGTTTCTGCGGATTCGAATTAAGAAATCCGATGATGATGATGATGAT 1617
Db 1655 GGTATGACACTCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1714
OY 1618 AATATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
Db 1715 AATATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1774
OY 1678 GAGTCATGTTTGAAGAAACATGAGATTTATTTT 1711

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Db 1775 GAGAGCCTTATGACGACCAACAAAGATTTATGCT 1808
RESULT 10
ABL02081
ID ABL02081 standard; cDNA; 1704 BP.
XX
AC ABL02081;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 725.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
DR P-PSDB; ABB57978.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 725; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 1704 BP: 417 A; 445 C; 460 G; 382 T; 0 other:
Query Match 22.3%; Score 381.8; DB 23; Length 1704;
Best Local Similarity 54.0%; Pred. No. 1.2e-94;
Matches 879; Conservative 0; Mismatches 727; Indels 21; Gaps 4;
OY 85 ACCAATGAAAGCGTGGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 144
Db 64 ACCAATGAAAGCGTGGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 123
OY 145 ACTGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 204
Db 124 TCCATCTAGGCAACAACTAGTACAGCTTTCGAGGCGATCCCTTCCCAAGCGCGGTG 183
OY 205 GGTGAGCTGAGATTTAAAGCACCACGACCAACACCCTGGGATGCTGCGGATTTGT 264
Db 184 GCGGAGCTCCGCTCAAGCGCCCGCTGAGCCAGGACACTGTCAGATGTCAGGCGTGC 243
OY 265 TGCATCAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 324
Db 244 ACACATGTTGCGGCAAGCCCTGCGAGGTCAACATGCTTTCGAGACGATGACGAGGACG 303

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Oy 325 GAGATGTCATATACCTAAGTGTCTATACGAATAATCCGGAACCTAAAGTCC 384
 Db 304 GAGGACGTCTGTAACCTAATGCTACACAGGAGTGTACATCCACAGACTTTGGCG 363
 Oy 385 GTTTAGTATACATACATGCTGTGTGTTTATTCGCTGAATAATCATCGTATATGAT 444
 Db 364 GTTCGTGTTGGATCTATAGGGGTGGATTCGAATGGGAGAGATCCGGGATCTGTAC 423
 Oy 445 GGTCTGATTTATTCATTTAAAAAGAGTGTGTTGATTAAACATATCATATGTTGGGA 504
 Db 424 AGCCCGGCTCATATATGATGGAACATGCTACTGCTGTAATATCCTATGCTTAGGA 483
 Oy 505 GCTAGATTTTCAATTAATTAATTCAGAAAGCTTAATGTCGCGGTAATGCGGCTT 564
 Db 484 GCCCTGGATTCCTTAGTCTGTCAGACAGAAAGATGATGTTCTGGAAGACCGGACTA 543
 Oy 565 AAGATCAAGTATGAGCTGCTGCTGTTGATTAATAATTAATGCGCACTTTGTTGCAAT 624
 Db 544 AAGGATCAAGTATGAGCTGCTGCTGTTGATTAATAATTAATGCGCACTTTGTTGCAAT 603
 Oy 625 CCCGATATATACATGCTGTTGTAAGTGGCGTGTGCTGCTACCATACATGATG 684
 Db 604 CCCGATATATACATGCTGTTGTAAGTGGCGTGTGCTGCTACCATACATGATG 663
 Oy 685 TTAACCGAACAACCTGCGGCTGTTTCCATGCTGATTAATGCTGATTAATGCTGAT 744
 Db 664 CTGACGATCAAGGCTGAGGCTGATTTTACAGACTATTAATGCTGAGGATCCGACTG 723
 Oy 745 TGTCATTTGCTTAATACCAATGTCA--ACATGCTGCTTACCTTACCAATTTGGCC 801
 Db 724 GCACCTTGCGGCGAGACCCCAACCAATTAATGCGCTTATGCTGCGACAGGCCACT 783
 Oy 802 GGTATTAAGGCTGAGATGATGATAGAGATTTTGGATTTCTTATGAAGCCAGCCA 861
 Db 784 GGTATTAAGGCTGAGATGATGATAGAGATTTTGGATTTCTTATGAAGCCAGCCA 843
 Oy 862 CAGATTTAATAAATCTGAGAAAGTAACTTAATCTAGAAAGCTGTAATAATGCT 920
 Db 844 AGTACATGCTGAAAGTGTGCGGAGATATCATCATGAGAGAGACACAGCGGTTG 903
 Oy 921 --CATGTTTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 978
 Db 904 AACATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
 Oy 979 AAACATCTCTGCGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
 Db 964 AAGTCCGCTGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
 Oy 1039 AACATCTCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098
 Db 1024 GGAATCTCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
 Oy 1099 AAGCAATTTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1158
 Db 1084 TGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
 Oy 1159 GCCCAGAGCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1218
 Db 1144 AGAAAGGCTTTGGAAGAAAGTACGAGATATATTTGCGGAGTAGAGCTCTGCGAGG 1203
 Oy 1219 CCACAGCTGATTAATTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1278
 Db 1204 AAGACATATTTGAGATACAGGATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263
 Oy 1279 CGTTTGTGCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1338
 Db 1264 AAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1323
 Oy 1339 GACTTCGATTTGGAAGATCTTATCATATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1398
 Db 1324 GATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

Oy 1399 AAGGCTTTAGCATGCTGATGATTAACCTATTCTTCTGGAATCAATTTGGCAAGCT 1458
 Db 1381 CGCGGACCTGTACGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 Oy 1459 ATGCTAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1518
 Db 1441 CTGAAGCCGCGACGCGGAGTGTCAAGCAATTAAGCTTTGCTGCTGCTGCTGCTGCT 1500
 Oy 1519 TTTGCTACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
 Db 1501 TTTGCTACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 Oy 1567 AATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1626
 Db 1561 CGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 Oy 1627 GATGAATTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
 Db 1621 CACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
 Oy 1687 TTTGAA 1693
 Db 1681 TACGACA 1687

RESULT 11
 ABL02066
 ID ABL02066 standard; cDNA; 6175 BP.
 XX
 AC ABL02066;
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 680.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmacological; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 WO200171042-A2.
 XX
 PN 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2001; 2000US-191637P.
 PR 23-MAR-2001; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 EL Venter JC, Adams M, Li PMD, Myers EW;
 DR WI: 2001-656860/75.
 DR P-PSDB; ABB57963.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 PS Claim 1; SEQ ID NO 680; 21bp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 779.
 DE
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 XX
 XX
 PD 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR P-PSDB; ABB57996.
 XX
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX
 PS Claim 1; SEQ ID NO 779; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 CC
 XX
 XX Sequence 1665 BP; 397 A; 446 C; 468 G; 354 T; 0 other;
 SQ

Query Match 21.5%; Score 368.2; DB 23; Length 1665;
 Best Local Similarity 52.4%; Pred. NO. 6.7e-91;
 Matches 861; Conservative 0; Mismatches 773; Indels 9; Gaps 2;

QY 53 TTGAATAATAGTTTAACTATGTTTAACTACCAATGAAGCGTGTAGCTGAACGTG 112
 DB 5 TCGACTTTAAAGTCCACACAGAGATACAGACCAGGAAAGACTCTGTCAGACCA 64
 QY 113 AATATGCAAGTGAAGAGCGTTAAAGCTTAACTGTGTAGATGATTCCTACTACGTT 172
 DB 65 CCFACGACCCATCAAGAGGTGTAAAGAGAGTCACTACGCGCAGTCTACTACT 124
 QY 173 TTGAGGATATACCGTACGCCCAACCGCAGTGGTGAAGTATTAAGACCCGACG 232
 DB 125 TCGAGCGGATCCCTTCGCAACACCGGAGGCGAGCTACGTCACAAAGCTCCCGACG 184
 QY 233 GACCAACACCTGGGATGTTGCGTGTATGTCATCATTAAGATGAATGATGAGTGAAG 292
 DB 185 CCCCAGAGGTGTGAGAGAGTCAAGAGCTCACCCTCCAGAGGTCACAAAGCAGCTGCA 244
 QY 293 TTGATTTTAAAGCGGCAAGTGTGTGCTCAGAGATTTGTCTATACCTAAAGTGTATA 352
 DB 245 AGCACTTGCTGTGAGATGACCGATGGCTCGAGAGACTGCTCTACTCATGTCTACA 304
 QY 353 CGAATATCTTAATCCGAACCTAAGCTCCCGTTTATGTTATACATCATGTGTGTT 412
 DB 305 CAAGAATTTTATCCACCAACCAATGCCGATGATGCTGTGATGTATGCGGTGCT 364

QY 413 TTATATCGTGAAATATCATGTATATGATGCTGATTAATTTTCAATTAAGAGATG 472
 DB 365 TCCAGTTTGGGAGAGCCCTCAGAGGATGTATACAGTCGGATATTTGCTGGTGAAGATG 424
 QY 473 TGTGTTGATTAACATATATATGCTTTGGAGCTCTAGTTTCTTAAGTTAAATTCAG 532
 DB 425 TGTGTGTCATTTCTATCACTAAGTATGAGTGGAGCAGCTGGATTTCTGTGCTGACGATG 484
 QY 533 AAGACCTTAATGTCGCGGTATGCGGCTTAAAGATCAATGATGCGCTTGGTGA 592
 DB 485 CCGAATCTGATGCGCGGCAATGCGGATCAAGAGATGATGTTGCGCTGCGCTGG 544
 QY 593 TTAATAATATGCGCCCAACTTTGGTGCAATCCCGATATATTAATCACTTTTGGTGAA 652
 DB 545 TCAAGGCCAATGTTTGGGTTTCCGAGGCGATTCGCGCAATATATCAATTTTGGGACA 604
 QY 653 GTGCGGTGCTGCTCTACCACTACATGATGTTAAACCAACAACTGCGGCTTTTCC 712
 DB 605 GTGCGGGAAGTGCCTGCTGATCAATGATGATCAAGACAGACGATGAGACTTTTCC 664
 QY 713 ATCGGTATATATGTCGGGTAAATGCTATTTGTCATTTGGCTATATCCCAATGTCAC 772
 DB 665 ACAAGCCATCTGCAATGCGGTATATGCTTTCCCTGCGCAGTACTCTCAGAGAA 724
 QY 773 ATCGTCCCTTACCTTACCAAAATTTGGCGGCTATTAAGGTGAGATATGATAAGATG 832
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 QY 833 TTTTGAATTTCTATGAAAGCCAAAGCCACAGATTTAATTAATCTGAGGAAAGTTT 892
 DB 785 TCTGGAGTCTCTGAAAGCCCAAGGATCCGAATATCAAAAGCCATGAGAGACT 844
 QY 893 TAACCTGAAAGAGGCTCAATATAGTATGTTTCTTTTGGTCCCTGTTGAGCAT 952
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 QY 953 ATCAAGCCGCTGATGTTGCTTACCACCAATCTCGGGAATATGTTAAACTGCTTGG 1012
 DB 905 ATGTAACAGCACGCTGTGTGGTGGAGGAAGAACCCATGAAATATGTAAGACCGCTG 964
 QY 1013 GTAATTCATATCCCATCTATGATGGTAAACACTTCAATGAGGATATTTTCACTTAA 1072
 DB 965 GCATTAATATCCCACTTATCATTCGAGGCGTTTCCAAAGGAGGCGTCTCTTGTACTAG 1024
 QY 1073 TTCTTAAGCAATGCTGTGCTGTTGTAAGAAATGTAAGTGTCAATTTTGGCAA 1132
 DB 1025 AGACCAAGACGATCCGAATGTCTAAAGAGTTGGAGACGCTGCGTTTGTGGCTTA 1084
 QY 1133 GTGAATGGCTGATGTTGAAGCAGCCG-----CCAGAGACCTTGGAAATGGGTGCTA 1186
 DB 1085 TCGAATTAATATGACAGGGAAGAGTGCCTGTGCGGGAGTACGGCATCAGCTGAGAGC 1144
 QY 1187 AAATTAAGGCTCATGTATACAGAGAAACACCAACAGCTGATATATTTATGATCTTT 1246
 DB 1145 AGTGTACTAGCGGATTAAGAGCGCCAGTCTGAGACCCCTGATATATACCTTCAGATGG 1204
 QY 1247 GCTCACAATATTTTGTGTTCCCATGATGCTTTTGTGCAATTTAGCTTTCAATCA 1306
 DB 1205 TTTCCAGAGATCTTGTGTTTCCCAATATACCGCAGATATTTGCGCGTCAAGTACG 1264
 QY 1307 CCTCCGAGTACACCGCTTACTTGTATCGTCTGATCGATTTGGAATCTTATCAATC 1366
 DB 1265 CTGCGAGTGGCCGACGATTTTGTACCGCTTGATGATGCTGCTGCTGCTGCTGCTG 1321
 QY 1367 CCTATGATTAATGCGTATGAGTGAAGTGTGTTAAGGCTGTATGCTGATGATGAATTA 1426
 DB 1322 ACCTGCGCATCTGATGTTGCGCAAAAGGTGAGGAGGACGACGCGACGCGATCTGT 1381
 QY 1427 CCTATTTCTTGAATATATTTGGCCAAAGTATGCTTAAAGATTCGGGTGAATCAAAA 1486
 DB 1382 CCTACTGTTTATACAACTGCTGGGAGGAAGCTCAAAACACACAGCGGAGTATCAAGT 1441
 QY 1487 CAATTGAAGTATGACTGCTATGATGATACAAATTTGGCACCAGCTGATCTTATACGA 1546

QY 1190 TTAAGAGCTCATGTTTACAGAGAACACCAAGCTGATATTTATGATCTTTCT 1249
 Db 1281 TCTACTTACACAGAGATGACAGATTCGATGAGATGTTTGAGGCCCTGATATATTT 1340
 QY 1250 CTCACATCTATTTTGTGTTCCCATGCAATGCTTTGTCATTAATGCTTCAACACCT 1309
 Db 1341 CGCATCGCAATTTGGCAGATACGATCGCTTATTCGCGCCGTCATCTATATGCC 1400
 QY 1310 CCGGTACACCGCTCTACTTGTATGCTTCCGACTTCGATTCGGAAGATCTTTCATCCCT 1369
 Db 1401 CCAAAAGCCCACTATCTATATCTGTTTGAATCTGACTC---CCCGCACTTCAATCAAT 1457
 QY 1370 ATCTATATGCTGATGAGAGCTGATGTTAAGAGCTGATGATGATGATGATTAACCT 1429
 Db 1458 TTCGCCGACTGCTGTGGCGCATGCGATTCGCGGAGTAGCCATGCGGATATCATATAT 1517
 QY 1430 ATTTCTCTGATCAATTCGCAACGATGCTTAAGAATCCGATGATACAAACAA 1489
 Db 1518 ACTGTTCTACACATCTATACCTCCAACTGATTAAGTCAATGATGATGATACAAACCA 1577
 QY 1490 TTGAACGATACCTGATATGATACAAATTTGCCACACGATGATATCTTATAGCAATG 1549
 Db 1578 TTGAGAGATGTTGGCATGTGGAGCTGTTGCCCTCCAGTGGAGATCCAAATTCGCCAG 1637
 QY 1550 AATTTGAAGTATGTAAGAAATGTTCCCTGATCCAAATTAAGAATCCGATGATATCA 1609
 Db 1638 AACTGGGATCTGCCAAATGGAGAGCCGTCACG-----TTAAAGAAATCCGATGAGA 1691
 QY 1610 AGTGTGTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662
 Db 1692 AGTGTGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1744

RESULT 14

ABL02103 standard; cDNA; 1593 BP.

AC ABL02103;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 791.

KW Drosophila; developmental biology; cell signalling; insecticide;

KX pharmaceutical; gene; ss.

OS Drosophila melanogaster.

PN W0200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR P-PSDB: ABB58000.

PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

CC Claim 1; SEQ ID NO 791; 21bp + Sequence Listing; English.
 The invention relates to an isolated nucleic acid detection reagent
 capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://ipo.int/pub/published_pct_sequences.

Sequence 1593 BP; 417 A; 394 C; 405 G; 377 T; 0 other;

Query Match 18.9%; Score 323.2; DB 23; Length 1593;

Best Local Similarity 52.4%; Pred. No. 1,66-78; Matches 821; Conservative 0; Mismatches 723; Indels 24; Gaps 4;

QY 111 TGAATATGCAAGTGAAGGCGTTAAAGTTTAACTGTGATGATGATGATGATGATGAT 170
 Db 6 TGACTGCGGCTGCTGCGGAGATGAGAAACACATCTGGGAGAGAGCTACTTACG 65
 QY 171 TTTGAGGATATACCGTACGCCCAACCCGACAGTGGGTAGCTGAGATTTAAAGCACCCCA 230
 Db 66 TTTGAGAGATATCCCTTGCAAAAGCTCCGTTGGAGATCTGCGCTTCAAGGCCCGGA 125
 QY 231 GCGACCAACACCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 290
 Db 126 AGCAGTGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 185
 QY 291 AGTGTATTTTAAAGGCGCAAGTGTGCTCAGAGATGATGATGATGATGATGATGATGAT 350
 Db 186 GACACACATGTTTTCAGAAATATACCGGCGCTCAGAGATGATGATGATGATGATGATGAT 245
 QY 351 TACGATATATCTAAATCCCGAAACCTAAACGTCCTTTAGTATACATACATGATGATGAT 410
 Db 246 TGTCAAGATCTGACGCGGATTAACCTGCTCCGATGATGATGATGATGATGATGATGAT 305
 QY 411 TTTTATATGCGTGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 470
 Db 306 CTATCAATTTGGCGAAGCTTCTCGGATATGATGATGATGATGATGATGATGATGATGAT 365
 QY 471 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530
 Db 366 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
 QY 531 AGAAGCTTATATGCGCGGATATGCGGCTTAAAGATCAAGTATGCGCTTCCGTTG 590
 Db 426 TCCCAACTAAACCTTCCCGAAGATGATGATGATGATGATGATGATGATGATGATGAT 485
 QY 591 GATTAAATATATGCGCAACTTGTGCGCAATCCGATATATATGATGATGATGATGATGAT 650
 Db 486 GGTGCAAAACATCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
 QY 651 AAGTCCGCTGCTGCTTACCCACTACATGATGATGATGATGATGATGATGATGATGATGAT 710
 Db 546 AAGTCCGCGGAGGCTGACCCACTTCTGCACTAAGTCCCAACTGAAGGCTTAT 605
 QY 711 CCATGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770
 Db 606 CCACAAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 665
 QY 771 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
 Db 666 TAATGCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
 QY 831 TGTGGAATTTCTTATGAAAGCCACAGGATTTAATTAATTAATTAATTAATTAATTAAT 890
 Db 726 GATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 785
 QY 891 TTTAAGTATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 950
 Db 786 TCTGCAAGCATGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 845
 QY 951 ATATCAGACCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1010

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Db      846  ATATACACGACACACATGTCCTTAACACACCCTGAACCTATGACAGATGCTG 905
QY      1011  GGGTAATTCGATACCCACTATGATGGTAACACTTATAGAGGCTCTATTTTCACCTC 1070
Db      906  GAGTCACAGATATCCCATGATGTTTGAGGACAGACCTTCGAGAGTTCATCTATCTACC 965
QY      1071  AATTCTTAAGCAATATGCTTGTGTAAGAAATGGAAACTGTGTCAATTTTGTGCG 1130
Db      966  AGAGGTTTCAAGGCGGCACCAACCTCGATGAGGTGGTAAGTGAAGATGCTGCTACC 1025
QY      1131  AAGGATTTGGTATGATGTAAGCACCAGCCAGAGACCTTGAAGATGGGCTCTAAAT 1190
Db      1026  GACGAGATCT---CGTCTTAACCTAGATCCCAACAGCTCGAAGACTACGCGCTTGAACG 1082
QY      1191  TAAAAAGCTCATGTTACAGAGAAACACACAGCTGATATTTATGATCTTTGCTC 1250
Db      1083  GAAGAAAGGCTATTTGCGGCACGACACCTGTAAACAGGCAACATGATGAAGTTTCTCGA 1142
QY      1251  TCACATCTATTTCTGCTTCCCATGATCGTTTGTGTCATTAACGTTTCAATCAGACCC-- 1308
Db      1143  GCTATGCTCATATCGAGATTTGCGACCCCTATATACAGGCAAGCTTGAACCGTGTGCG 1202
QY      1309  ---TCCGATACACCCCTCTACTGTTATCGCTTGCAGCTTGATGGAAGATCTTATCAA 1364
Db      1203  GCATTCAGGACGCCACCGATCTGTATCGATTCGATCAGATTCACAA---CTGTGCAA 1259
QY      1365  TCCTATCTATTTATGCTGATGAGACTGCTGTTAAGGGTGTAGTCTGCTGAT 1424
Db      1260  CGCATTAAGATGATGCTTGTGCGGCATCAGATCGAGGTGTGTATGATGATGATCT 1319
QY      1425  AACCTATTTCTTCTGGAATCAATGAGCAACAGTATGCTTAAGAAATCGGTGATACAA 1484
Db      1320  GTGCTATATTTTCCACAGCATGTTGTGCAATTCGCTCCGATCTCCGGAACCAA 1379
QY      1485  AACATTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1544
Db      1380  GGTATTAACCGGATGTCGACGTTTGGACGAGTTTCCAGCCGACGAGATCCCAACTG 1439
QY      1545  CAATGAATTTGAAGTATGGAATGTTTCTGAGTCAATTAAGAAATCCGATGAAGT 1604
Db      1440  CGAAGATTAATCACTCAAGTTTGCACCCATGGAAGCACTAACAATTT----- 1491
QY      1605  ATACAGTGTGTAATATTAAGTGAATGAATGAATGAATGAATGAATGAATGAATGA 1664
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QY      1665  GATTAAAC 1672
Db      1548  AATCGAAC 1555

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RESULT 15

ABLO1859
ID ABLO1859 standard; cDNA: 1863 BP.

ABLO1859:

26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 59.

XX Drosophila: developmental biology; cell signalling; insecticide;

XX pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

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PR      23-MAR-2000; 2000US-191637P.
PR      11-JUL-2000; 2000US-0614150.
XX      (PEKE ) PE CORP NY.
XX      Venter JC, Adams M, Li PWD, Myers EW:
XX      WPI: 2001-656860/75.
XX      P-PSDB: ABB57756.
XX      New isolated nucleic acid detection reagent for detecting 1000 or more
XX      PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX      interactions -
XX      Claim 1; SEQ ID NO 59; 21pp + Sequence Listing; English.
XX      The invention relates to an isolated nucleic acid detection reagent
XX      CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX      CC useful in developmental biology and in elucidating cell signalling and
XX      CC cell-cell interactions in higher eukaryotes for the development of
XX      CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX      CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
XX      CC sequences (AB101840-AB16175) and the encoded proteins
XX      CC (ABB57737-ABB72072).
XX      CC The sequence data for this patent did not form part of the printed
XX      CC specification, but was obtained in electronic format directly from WIPO
XX      CC at ftp.wipo.int/pub/published_pcl_sequences.
XX      SO Sequence 1863 BP; 425 A; 493 C; 523 G; 422 T; 0 other:
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XX      Query Match      18.9%; Score 323; DB 23; Length 1863;
XX      Best Local Similarity 52.4%; Pred. No. 1.9e-78;
XX      Matches 812; Conservative 0; Mismatches 725; Indels 14; Gaps 4;
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QY      1  ATGAATTTCAAGCTTGAATGAGAAATTAATGAAGATTAATGATGAAAT 60
Db      166  ATGAGATGCGAGTGGGAGTGGCGATGCTGAAATGAGGCCAAGCTATTGGCCAC 225
QY      61  AAGTTTAAACATGCTTTAACTACCAATGAACGCTGATGAACTGAATTTGGC 120
Db      226  AAGATGCTCAGATGATGCTTGGCACAAGCAGAGAGTGTGTCACCAAGGATGAGC 285
QY      121  AAGTGAAAGGCGTTAAGCTTAACTGCT---AGATGATTCCTACTACAGTTTGA 177
Db      286  CAGGTGGCGGACATGCGGCAAGACACTCTACGAGAGAGATGATCTTGGCTTCGAG 345
QY      178  GGTATACCGTACGCCCAACCGCAGTGGTGAAGTTTAAGACACCCAGCAGCA 237
Db      346  GAATGCCCTTTGACAGCGCGGAGGAGAGCTGCTCCGACCCGCCAGCCAGCA 405
QY      238  ACACCCGAGATGCTGCTGATGTTGTGCAATCAATGAAGTCAAGTTCAT 297
Db      406  CATCCCTGTTGGGGGAGGATGACCTATTCGCGGGGCCAAGCCGATGCAAAAGCAC 465
QY      298  TTATTAACGGGCAAGTGTGTGCTCAGAGATGTTCTATACCTAAGTGTCTATAGGAAT 357
Db      466  TTGCTGCTCAGACATGCTGCAAGGAGAGATTTGCTGATGAACGATATTTCCAG 525
QY      358  AATCTAAATCCGAATAACGCTCCGCTTTAGTATACATACATGATGATGATGATGAT 417
Db      526  CCGCTGAGATCGACAGCGCGCTGCGTGTGATGATGATGATGATGATGATGATGATG 585
QY      418  ATCGGTAATAATCATGCTGATATGATGATGATGATGATGATGATGATGATGATGATG 477
Db      586  TTGCGCAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 645
QY      478  TTGATTAACATACATATGCTTTGGGAGCTCTAGGTTTCTAAGTTTAATTCAGAGAC 537
Db      646  GTTGTCAATTCATTTATAGGTTGGCGCATTTGGCTCTCAGCGTCGCGGATTCGGAC 705
QY      538  CTTAATGTGCCGGTAAATGCGGCTTAAAGATCAATGATGATGATGATGATGATGATG 597
Db      706  TTGATGTGCGCGGAATGCTGCTCAGAGACCAAGTATGATGATGATGATGATGATGATG 765

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GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1663.49 seconds
(without alignments)
16677.553 Million cell updates/sec

Title: US-09-776-910-1

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Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: em_estba: *
2: em_esthum: *
3: em_estln: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_hiv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_man: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	313.6	18.3	778	9	A1062034 GH01076.5
2	282.4	16.5	649	9	A1388926 GH1977.5
3	265.2	15.5	688	9	A1403569 GH23036.5
4	256.6	15.0	671	9	A1517692 GH28740.5
5	254.4	14.9	569	13	B1609541 RH14337.5
6	250	14.6	674	13	B1628316 RH56682.5

7	249.4	14.6	676	13	B1635372 SD16705.5
8	248.6	14.5	660	13	B1639486 SD22067.5
9	248.4	14.5	673	13	B1614181 RH43493.5
10	246.8	14.4	672	13	B1614443 RH43812.5
11	246.4	14.4	670	13	B1233202 RE29491.5
12	245	14.3	648	9	A11133763 GH10213.5
13	245	14.3	648	9	A1403098 GH22464.5
14	243.4	14.2	646	9	A1109901 GH09292.5
15	243.4	14.2	646	9	A1293416 LP06524.5
16	241	14.1	526	9	A1108080 GH06811.5
17	239.8	14.0	516	9	A1108156 GH06911.5
18	239.2	14.0	658	13	B1564586 RH61888.5
19	238.4	13.9	656	13	B1619037 RH44296.5
20	236.8	13.8	656	13	B1614821 RH44296.5
21	236.6	13.8	669	13	B1588370 RH29561.5
22	236.2	13.8	666	13	B1621302 RH52624.5
23	233.2	13.6	628	9	A1109573 GH08808.5
24	232.2	13.6	630	9	A1403830 GH23353.5
25	231.4	13.5	619	9	A1516869 GH27454.5
26	231	13.5	638	13	B1564361 RH37254.5
27	230.8	13.5	628	13	A1513346 GH26524.5
28	230	13.4	614	12	B641228 SD12519.5
29	230	13.4	647	13	B1575862 RH32195.5
30	229.6	13.4	614	9	A1107729 GH05557.5
31	229.6	13.4	614	9	A1134360 GH11805.5
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33	228	13.3	633	13	B1370683 RH57396.5
34	221	12.9	670	9	A1389766 GH21022.5
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36	219.2	12.8	615	13	B1588504 RH29849.5
37	218.6	12.8	587	9	A1517539 GH28541.5
38	218.6	12.8	588	13	B1638519 SD20822.5
39	218.6	12.8	607	13	B1624437 RH63994.5
40	218.6	12.8	609	13	B1667389 RH37771.5
41	218.6	12.8	609	13	B1607309 RH74350.5
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ALIGNMENTS

RESULT 1
LOCUS A1062034 778 bp mRNA
DEFINITION GH01076.5prime GH Drosophila melanogaster head pot2 Drosophila melanogaster cDNA clone GH01076 5prime similar to U51050:
Drosophila melanogaster alpha esterase (aet) gene, partial cds,
mRNA sequence.

ACCESSION A1062034
VERSION A1062034.1 GI:3337873
KEYWORDS EST.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 778)

AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project

Unpublished (2001)

COMMENT Contact: Stapleton, M.

TITLE

JOURNAL

COMMENT

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
Plate: 10 row: G column: 4
High quality sequence stop: 363.
Location/Qualifiers

Matches	376:	Conservative	0:	Mismatches	199:	Indels	0:	Gaps	0:
QY	1	ATGAATTTCAACGTTAGTTGATGGAAATTAATGAACATTGAATGCAATTTGAAT	60						
Db	95	ATGAATTAAGAACCTCGGCTTTGTGGAGCCTTGCGCGCTCAAAACATCGAGCAT	154						
QY	61	AAGTTTAACTATTCGTTTAACATCCATGAACGGTGTGCTGAACATGAATATGCG	120						
Db	155	AAAGTCACACACTATCCGACAGTCGACCAAGAAAGTTGCGCACGAGATGAGGC	214						
QY	121	AAAGTGAAGCGGTTAAACGTTTAATCTGTAGATGATTCCTACTACAGTTTGAAG	180						
Db	215	CAAGTAGAGGCTATCAAGGCTATCTCTAGAGATGCGCCCTACTACGTTGAGGCT	274						
QY	181	ATACGCTACGCCACACCGCAGTGGGTGAGCTGAGATTAAAGACACCCAGGACCA	240						
Db	275	ATCCCTACGCGCCAGCCTCCGCGGAGATTGCGGTTAAGGCCCTCAGAGGCCAT	334						
QY	241	CCCTGGATGTTGCTGCTGATTTGTCATATCAATGAATAGTCAGTGAAGTTGAT	300						
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Db	455	GTCAGGCCACACAGGCTCCCGGTTATGTTGATTCACGAGAGAGGCTTCATATC	514						
QY	421	GCTGAATATCATGCTATATGATGTCTGATTTATTTCAATTAAGATGTGCTTG	480						
Db	515	GGGAGGCGCAATCGGATGTATGCGCCGATTTACTTTATGAAGATGTGTTCTTC	574						
QY	481	ATTAACATACAAATATGTTGGAGCTCTAGTCTTCTAATTAATTAATGAGACCT	540						
Db	575	GTCAGCTATAGTACCTACTTGGGCTTGGATTTATGATCTTAAGTCCCCGAGCTA	634						
QY	541	AATGTCCCGTATGCGCGCTTAAGATCAAGT	575						
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DEFINITION	RH14337.5prlme RH Drosophila melanogaster normalized Head pR1c-1								
	Drosophila melanogaster cDNA clone RH14337.5 similar to alpha-Est7:								
	Fban0001112 GO: [carboxylesterase (GO:0004091), carboxylesterase								
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ACCESSION	BI609541								
VERSION	BI609541.1	GI:15505066							
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SOURCE	Drosophila melanogaster								
ORGANISM	fruit fly.								
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;								
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;								
	Ephydroidea; Drosophilidae; Drosophila.								
REFERENCE	1 (bases 1 to 569)								
AUTHORS	Stapleton, M., Broksstein, P., Hong, L., Tyler, D., Berman, B., Carlson								
	J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Fiske, E., George								
	M., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,								
	Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,								
	Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin								
	G.M.								
TITLE	BDGP/HMT RH Drosophila EST Project								
JOURNAL	Unpublished (2001)								
COMMENT	Contact: Stapleton, M.								
	BDGP								
	Lawrence Berkeley National Lab								
	One Cyclotron Rd, Berkeley, CA 94720, USA								
	Fax: 510 486 6798								
	Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu								

FEATURES	Source	Plate: RH.143 row: D column: 1	High quality sequence stop: 447.
		Location/Qualifiers	
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		/lab_host="DH5-alpha Tona"	
		/note="Organ: head; Vector: pR1c; Site: 1; XhoI; Site: 2; BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."	
BASE COUNT	126 a 147 c 167 g 129 t		
ORIGIN			
Query Match	14.9%; Score 254.4; DB 13; Length 569;		
Best Local Similarity	65.5%; Pred. No. 2.9e-58;		
Matches	372: Conservative 0: Mismatches 196: Indels 0: Gaps 0:		
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QY	137	AACGTTAACTGTACATGATTCCTACTACAGTTTGAAGGTTATACGCTACGCCAAC	196
Db	121	AGGCTATCTCTCAAGATGTGCGCTTACTTCACTTGAAGGATATCCGTAAGGCCAAC	180
QY	197	CGCAGTGGGTAGCTGAGATTAATGAACACCCAGGACCAACACCTGGATGTGTC	256
Db	181	CTCCGCTGGGAGATGGCGGTTTAAGGCCCCCAAGAGGCCAATCCCTGGAGGAGTTC	240
QY	257	GTCATTTGTCATCATTAAGATTAAGTCACTGACGTCAGTATTTATACGGCAAGTCT	316
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QY	317	GTCGCTCAGAGATTTGCTATCTAATCTAATCTAATCTAATCTAATCTAATCTAATCTA	376
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QY	377	AACGTCCTGTTTATGATACATACATGATGTGTTTATATATGCGTGAATATCATGCTG	436
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DEFINITION	RH5682.5prlme RH Drosophila melanogaster normalized Head pR1c-1		
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	Fban0001112 GO: [carboxylesterase (GO:0004091), carboxylesterase		
	(GO:0004091)] located on: 3R 84D5-84D5;: 08/22/2001, mRNA sequence.		
ACCESSION	BI628316		
VERSION	BI628316.1	GI:15530524	

KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota:
Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
REFERENCE
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
, J., Champagne, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S. and Rubin
, G.M.
TITLE BDGP/HHMI RH Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: RH.566 Row: G column: 10
High quality sequence stop: 558.
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/lab_host="DH5-alpha Tona"
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BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
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Qy 421 GGTGAATATCATCTGATATGTATGTCTGATTTATTTCAATTAAGATGTGTGTG 480

Db 531 GGCGAGCCCAATCGGAGATGATGCGCGGATTTACTTATGAAGAGATGTGTCTC 590
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, mRNA sequence.
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Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
REFERENCE
AUTHORS 1 (bases 1 to 676)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
TITLE BDGP/HHMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: SD.167 Row: A column: 5
High quality sequence stop: 641.
location/Qualifiers
1. 676
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culture port2"
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/note="Vector: port2; Site.1: EcoRI; Site.2: XhoI; Sized
fractionated cDNAs were directly ligated into port2.
Plasmid cDNA library."
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Query Match 14.6%; Score 249.4; DB 13; Length 676;
Best Local Similarity 65.2%; Pred. No. 7.1e-57;
Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
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Db 114 ATGATTAAGAAGCTGCGCTTGTGAGCGCTTGTGCGCTTAAGCAATCGACAT 173
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Db 174 AAGTCCAGCAGTATCGGCGAGTGCACCAATGAACAGTTGTGCGCAGACGAGTACGGC 233
Qy 121 AAGTGAAGCGCTTAAAGCTTAACTGTAGTGAATGATTCCTACTACAGTTTGGAGGT 180
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Qy 181 ATACCGTACGCCCAACCCCGAGTGTGAGTGAATTAAGCAAGCCGACGACCAACA 240

Db 294 ATCCGTCAGCCCAAGCCCTCCGCTGGGGAGTTGGGTTTAAAGGCCCTCAGAGCCCAATT 353
QY 241 CCTGGAGATGTCGCTGATTTGTCATCATTAAGATAGTCAGATGTTGATTT 300
Db 354 CCTGGAGAGGATTCGCGCTGACAGCCAGAGGATTAAGCCCTCCGAGGAGTTTC 413
QY 301 ATTAAGGGGAAAGCTGTGGCTCAGAGATTTCTATACCTAGTGTCTATACGAATAT 360
Db 414 GTCTTGATTAAGTAGAGGCTCCGAGAGCTGCTCTATCTATCATGTATACCAACAAAT 473
QY 361 CTAAATCCCAAACTAAACGTCCTGTTTATATATACATACATGCTGTGTTTATATAC 420
Db 474 GTGAAGCCGCAACAAGCTGCCCGGTTATGTTGATTCACGAGAGAGCTTCATATAC 533
QY 421 GGTGAATAATATGCTGATATGATGCTGCTGATTTATTTCAATTAAGATGCTGTG 480
Db 534 GCGCAGGCAATGCGGAGTGTATGCGCCGATTTACTTTGAAGAAGATGTTGTTCTC 593
QY 481 ATTAACATACAAATGCTTTGGAGCTCTAGCTTTTCTAAGTTTAAATTCAGAGACCTT 540
Db 594 GTCAAGATACAGTACCACTTGGGCTTTGGATTTATGATCTTATAGTCCCGAGACTA 653
QY 541 AATGTGCCCCGTAATGCCGCT 563
Db 654 AATGTACAGGAATGCTGCT 676

RESULT 8
BI639486
LOCUS
DEFINITION
SD22067.5prime SD Drosophila melanogaster Schneider L2 cell culture
POT2 Drosophila melanogaster cDNA clone SD22067 5 similar to
alpha-Est7: Fban0001112 GO: [carboxyesterase (GO:0004091)];
carboxyesterase (GO:0004091) located on: 3R 84D5-84D5... 05/19/2001
, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BI639486
BI639486.1 GI:15541696
EST.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 660)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G. M.,
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP

FEATURES
SOURCE
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: SD.220 row: F column: 7
High quality sequence stop: 546.
Location/Qualifiers
1..660

/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD22067"
/clone_id="SD Drosophila melanogaster Schneider L2 cell
culture POT2"
/lab_host="DH5-alpha"
/note="Vector: POT2; Site1: EcoRI; Site2: XhoI; Sized
fractionated cDNAs were directly ligated into POT2.
Plasmid cDNA library."
BASE COUNT 169 a 170 c 176 g 145 t
ORIGIN

Query Match 14.5%; Score 248.6; DB 13; Length 660;
Best Local Similarity 64.3%; Pred. No. 1.2e-56;
Matches 390; Conservative 0; Mismatches 214; Indels 3; Gaps 1;

QY 535 GACCTTAATGTCCTCCGATGATCCGCTTAAGATCAAGTCATGCTTGGCTTGAT 594
Db 9 GACCTTAATGTCACAGAAATGCTGCTCAGAGATCAGGCTGCTCAAGTGATC 68
QY 595 AAAATTAATGCGCAACTTGTGGCAATCCCGATATATATACAGTCTTGTGTAAGT 654
Db 69 AAGAACAAATGGCGTAGTTTCGCGGAGATCCCACTGCATCCTGTTTGGAGAGAT 128
QY 655 GCGGTGTCCTCTACCATACATGATGTTACCGAACAACCTGGGCTTTCCAT 714
Db 129 GCTGAGGCGCTCCACTCATATGATGTTACCGATCAACCCAGGCTCTTTCAT 188
QY 715 CGTGTATCTAATGTCGGGTAATGCTATTTGCTATGGC---TAATACCAATGCA 771
Db 189 CGGCGATCTTGAGAGTGGGCAATGCTATTTGCTTGGCTTACAGCGGCAATTACC 248
QY 772 CATCGTCCCTCACCTTACCGCAATTGGCGGCTAATAGGAGATGATATAGAT 831
Db 249 CATTAATCCCTACAGGATACCCAGTGTGGCTACAGGCGGACACAGACAGAT 308
QY 832 GTTTGGAAATTTCTTATGAAGCCACAGATTTAATAAATGAGGAAAAAGTT 891
Db 309 GTCTGAGATTTCTTGCAAGAACGTAAGGCAAGATCTTATTCGCTGAGAAATGTC 368
QY 892 TTAAGCTAGAGAGCGTCAAAATTAAGTATGTTTCTTTGGTCCACTGTAGCCA 951
Db 369 CTGACACTGAGAGACGATGAACAAGATATGTTGCTTGGCCATCCCTGAGCA 428
QY 952 TATCAGACCGCTGATGTTGCTTACCCAAACATCCTGGAAATGTTAAACTGTTGG 1011
Db 429 TTCTCCAGGCCCAATGTTGATATCCAAAGGATGATGAAGACCGCTG 488
QY 1012 GGTAAATCGATACCACTATGATGTTGATACCTTCAATATGAGGCTATATTTCACTTCA 1071
Db 489 AGTAAGTCCATCCCATGTTATAGGAACACTTCTAGAGGCGCTGCTGGTTCCA 548
QY 1072 ATTCTAAGCAAAATGCTATGCTTGTTAAGATTTGGAACCTGTCAATTTGTGCCA 1131
Db 549 GAGTAAAGCTTATGCGCGAGGTGTCAGCAGCTGATGCTGACACCTTTCAITCCC 608
QY 1132 AGTGAAT 1138
Db 609 AAGGATT 615

RESULT 9
BI614181
LOCUS
DEFINITION
BI614181
673 bp. mRNA linear EST 07-SEP-2001
RH43493.5prime RH Drosophila melanogaster normalized Head pfic-1:
Drosophila melanogaster cDNA clone RH43493 5 similar to alpha-Est7:
Fban0001112 GO: [carboxyesterase (GO:0004091)]; carboxyesterase
(GO:0004091) located on: 3R 84D5-84D5... 08/18/2001, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BI614181
BI614181.1 GI:15509706
EST.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 673)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S.,
Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phonaknavorong, S., Wan, K., Yu, C., Lewis, S.E., Ceiniker, S. and Rubin
G.M.

BDGP/HHMI RH Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST/est@fruitfly.berkeley.edu>
 Plate: RH.434 row: H column: 9
 High quality sequence stop: 553.

FEATURES

Source

Location/Qualifiers

1. 673

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone_lib="RH.43493"

/sex="male and female"

/dev_stage="Adult"

/lab_host="DH5-alpha Tona"

/note="Organ: head; Vector: pF1c1; Site: 1: XhoI; Site: 2: BamHI. Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

BASE COUNT 153 a 169 c 195 g 155 t 1 others
 ORIGIN

Query Match

Best Local Similarity 65.0%; Pred. No. 1.3e-56;
 Matches 366; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 1 ATGATTTCAACGTTACTTGTATGAGAAATTAATGAAGATTAAATGATTAATGAAAT 60
 DB 111 ATGATTAAGAAACCTGGCTTTGTGAGCGCTTGGCGGCCCTCAAAACCATGACAT 170
 QY 61 AAGTTTAAACATATCTTAACATCAATGAACGCTGTGAGTGAACATGATATGCG 120
 DB 171 AAGTTCACAGATATCCAGTGCACCAATGAACATGTTGCGCCGACAGGATACGCG 230
 QY 121 AAGTGAAGCGCTTAACGTTTACTGTGATGATCTTCTACTACGTTTGAAGGT 180
 DB 231 CAAGTGAAGGATTAACAGCTTATCTCTACTGATGCTTCTACTGATGAGGT 290
 QY 181 ATACCGAGCGCCCAAGCGGAGTGGAGTGAAGTTTAAAGCCCGCCAGCCACACA 240
 DB 291 ATCCCGTACGCCAGCTCCGCTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 350
 QY 241 CCTGGGATGCTGTGCTGATTTGTCATCATTAAGATTAAGTCAAGTGAATTTT 300
 DB 351 CCTGGGAGGAGTGTGCGACTGACAGCCAGGAGATTAAGGCGCTTCAAGTCACTTC 410
 QY 301 ATTAAGGCGAAAGTGTGTGCTCAGAGATTTCTTATACCTAAGTGTCTATACGAAT 360
 DB 411 GTCTTCATTAAGTGAAGGCTCCGAGACTGCTTATCTCATGTGTACACCAAT 470
 QY 361 CTAAATCCGAACTAAGCCGCTTTTATGATACATACATGATGATGATTAATATC 420
 DB 471 GTGAAGCCGCAAGGCTCGCGCTTATGATGATGATGATGATGATGATGATGATG 530
 QY 421 GGTGAATATCATGCTGATGATGATGCTGATGATTTTCAATTAAGAGATGCTGTG 480
 DB 531 GCGGAGGCAATCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 590
 QY 481 ATTAACATACATATGCTGTGAGCTCTAGAGTTTCTAAGTTAAATTCAGAACCTT 540
 DB 591 GTCCGATTAAGTACAGTACAGTGTGGGCTTTGGATTTAGTGTGATGATGATGATG 650
 QY 541 AATGTCCCGGATATGCGGCGCT 563
 DB 651 AATGTACAGGAATGCTGCGCT 673

RESULT 10
 BIG14443 672 bp mRNA linear EST 07-SEP-2001
 LOCUS
 DEFINITION RH43812.5:prime RH Drosophila melanogaster normalized Head pF1c-1
 Drosophila melanogaster cDNA clone RH43812.5: similar to alpha-Est7:
 Fban0001112 GO: [carboxylesterase (GO:0004091); carboxylesterase

ACCESSION

(GO:0004091) located on: 3R 84D5-84D5; 08/18/2001, mRNA sequence.

VERSION

BIG14443.1 GI:15509968

KEYWORDS

EST.

SOURCE

fruit fly.

ORGANISM

Drosophila melanogaster

REFERENCE

Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha: Phyllophaga: Drosophilidae: Drosophila.

AUTHORS

1 (bases 1 to 672)
 Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Gurin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nuno, J., Pacle, J., Paragas, V., Park, S., Prounnavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.

TITLE

BDGP/HMI RH Drosophila EST Project

JOURNAL

Unpublished (2001)

COMMENT

Contact: Stapleton, M.

COMMENT

Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST/est@fruitfly.berkeley.edu>
 Plate: RH.438 row: A column: 12

High quality sequence stop: 554.

FEATURES

Location/Qualifiers

1. 672

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone_lib="RH43812"

/sex="male and female"

/dev_stage="Adult"

/lab_host="DH5-alpha Tona"

/note="Organ: head; Vector: pF1c1; Site: 1: XhoI; Site: 2: BamHI. Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

BASE COUNT 154 a 169 c 194 g 155 t
 ORIGIN

Query Match

Best Local Similarity 64.9%; Pred. No. 3.6e-56;
 Matches 365; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 1 ATGATTTCAACGTTACTTGTATGAGAAATTAATGAAGATTAAATGATTAATGAAAT 60
 DB 111 ATGATTAAGAAACCTGGCTTTGTGAGCGCTTGGCGGCCCTCAAAACCATGACAT 170
 QY 61 AAGTTTAAACATATCTTAACTAATCAATGAACGCTGTGAGTGAACATGATATGCG 120
 DB 171 AAGTTCACAGATATCCAGTGCACCAATGAACATGTTGCGCCGACAGGATACGCG 230
 QY 121 AAGTGAAGCGCTTAACGTTTACTGTGATGATGATCTTCTACTACGTTTGAAGGT 180
 DB 231 CAAGTGAAGGATTAACAGCTTATCTCTACTGATGCTTCTACTGATGAGGT 290
 QY 181 ATACCGAGCGCCCAAGCGGAGTGGAGTGAAGTTTAAAGACCCAGCAGACACA 240
 DB 291 ATCCCGTACGCCAGCTCCGCTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 350
 QY 241 CCTGGGATGCTGTGCTGATTTGTCATCATTAAGATTAAGTCAAGTGAATTTT 300
 DB 351 CCTGGGAGGAGTGTGCGACTTGTGAGATGATGATGATGATGATGATGATGATGATG 410
 QY 301 ATTAAGGCGAAAGTGTGTGCTCAGAGATTTATATACCTAAGTGTCTATACGAATAT 360
 DB 411 GTCTTCATTAAGTGAAGGCTCCGAGACTGCTTCTATCTCATGTGTGTACACCAAT 470
 QY 361 CTAAATCCGAACTAAGCTCCGCTTTTATGATATACATACATGATGATGATGATGATG 420

Db 471 GTGAAGCCGACAGGCTCCGCGGTATGTTGGATTGACGAGAGGAGCTTCATTATC 530
QY 421 GGTGAATATCATCGTATGATATGATGCTCTGATTTATTTCAATTAAGAGATGCGTGG 480
Db 531 GGGGAGGCGCAATCGGAAATGATGCGCCGAGATTACTTATTAAGAAAGATGTTGCTC 590
QY 481 ATTAACATATCATATGTTGGAGCTGAGCTTTTCTAAGTTTAATTCACAGACCTT 540
Db 591 GTCAGATACATACGAGACTTGGGGCTTTGGGATTATAGCTTAAGTCCCGGAGCTA 650
QY 541 AATGTGCCCGGTAATGCCGCC 562
Db 651 AATGTACCAAGAAATGCTGGCC 672

RESULT 11
LOCUS B1233202 670 bp mRNA linear EST 11-JUL-2001
DEFINITION RE29491.5prime RE Drosophila melanogaster normalized Embryo pF1c-1
Drosophila melanogaster cDNA clone RE29491.5 similar to alpha-Est7:
Fban0001112 located on: 3R 84D5-84D5:: 04/12/2001, mRNA sequence.
ACCESSION B1233202 GI:14700784
VERSION B1233202.1
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 670)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
J., Champagne, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S.,
Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
G.M.
TITLE BDGP/HMI RE Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: RE.294 row: H column: 7
High quality sequence stop: 534.
Location/Qualifiers
FEATURES
source 1..670
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RE29491"
/clone_1lb="RE Drosophila melanogaster normalized Embryo
pF1c-1"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha Tona"
/note="Organ: embryo; Vector: pF1c; site_1: XhoI; site_2:
BamHI; Library was kindly generated by Piero Carinici at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library." 1 others

BASE COUNT 152 a 168 c 194 g 155 t
ORIGIN
Query Match 14.4%; Score 246.4; DB 13; Length 670;
Best Local Similarity 64.9%; Pred. No. 4.6e-56;
Matches 364; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 1 ATGAATTCACAGCTAGTTGATGAGAAATTAATGAAGATTAATGCAATTAAT 60
Db 110 ATGAATTAAGAACTCGGCTTTTGAGAGCGCTTGGGGCGCTCAAAACATCGAGCA 169
QY 61 AAGTTTAACTAATGTTTAACTACCATGAAGAGCGTGTACTGAACACTGATATGC 120

Db 170 AAGTCCAGCACTATGCCAGTCGACCAATGAAGAGTGTGCCGACAGGATACGGC 229
QY 121 AAGTGAAGAGCGGTAAGAGCTTTAACTGATGATGATGATGATGATGATGATGATGAT 180
Db 230 CAAGTGAAGAGGATTAAGAGCTTATCTCTAAGATGAGGCTTACTTACTTACTTACTT 289
QY 181 ATACGTCAGCCCAACCGGCACTGGGTAGCTGAGATTTAAAGCACCCAGGACCAACA 240
Db 290 ATCCGTAGCCCAACCGGCTGGGGAGTGTGGTTTAAAGCCCTCAGAGGCCCAT 349
QY 241 CCCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 350 CCCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 409
QY 301 ATACGAGGCAAGTGTGCTCAGAGATGCTATGATGATGATGATGATGATGATGATGAT 360
Db 410 GCTCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
QY 361 CTAATTCCTGAAAGTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 470 GTGAAGCCGACAGGCTCCGCGGTATGTTGATTCACGAGGAGGCTTCATATATC 529
QY 421 GGTGAATATCATCGTATGATATGATGCTCTGATTTATTTCAATTAAGAGATGCTG 480
Db 530 GGGGAGGCGCAATCGGAAATGATGCGCCGAGTATCTTATGANAAGAGATGTTCTC 589
QY 481 ATTAACATATCATATGTTGGAGCTGAGCTTTCTAAGTTTAATTCAGAGACCTT 540
Db 590 GTCAGATACATACGAGACTTGGGGCTTTGGGATTATAGAGCTTAAGTCCCGGAGCTA 649
QY 541 AATGTGCCCGGTAATGCCGCC 561
Db 650 AATGTACCAAGAAATGCTGGCC 670

RESULT 12
LOCUS A1113763 648 bp mRNA linear EST 19-APR-2001
DEFINITION GH10213.5prime GH Drosophila melanogaster head port2 Drosophila
melanogaster cDNA clone GH10213.5prime similar to us1050:
Drosophila melanogaster alpha esterase (aef) gene, partial cds,
mRNA sequence.
ACCESSION A1113763 GI:3514566
VERSION A1113763.1
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 648)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: 102 row: B column: 1
High quality sequence stop: 435.
Location/Qualifiers
FEATURES
source 1..648
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH10213"
/clone_1lb="GH Drosophila melanogaster head port2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: port2; Site_1: EcoRI; Site_2:


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VERSION      A1109901.1  GI:3478225
KEYWORDS     EST.
SOURCE       fruit fly.
ORGANISM     Drosophila melanogaster
              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 646)
AUTHORS      Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
              Lewis, S. and Rubin, G.M.
TITLE        BDGP/HMI Drosophila EST Project
JOURNAL      Unpublished (2001)
COMMENT      Contact: Stapleton, M.
              BDGP
              Lawrence Berkeley National Lab
              One Cyclotron Rd, Berkeley, CA 94720, USA
              Fax: 510 486 6798
              Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
              Plate: 92 row: H column: 8
              High quality sequence stop: 513.
              Location/Qualifiers
                1..646
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /clone_lib="GH Drosophila melanogaster head POT2"
                /sex="male and female"
                /dev_stage="adult"
                /lab_host="DH5 - alpha"
                /note="Organ: head; Vector: POT2; Site_1: EcoRI; Site_2:
                XhoI; Sized fractionated cDNAs were directly ligated into
                POT2. Plasmid cDNA library."
                152 a 163 c 182 g 149 t
BASE COUNT   152 a 163 c 182 g 149 t
ORIGIN
Query Match      14.2%; Score 243.4; DB 9; Length 646;
Best Local Similarity 64.8%; Pred. No. 3e-55;
Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAATGAAGATTAAATGATGAAAT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 89 ATGATTAAGAAGCTCGCTTGTGGAGCGCTGCGCGCCCTCAAAACCATGAGCAT 148
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 AAGTTTAAACTATGCTTAACTACCAATGAACGCTGAGTGAACCTGAATATGGC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 149 AAGTCCACAGATATGCGAGTCGACCAATGAAGATTGTGCGCGACACGAGTACGC 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 AAGTGAAGGCGTTAAAGCTTAACTGTGATGATGATGATGATGATGATGATGAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 209 CAAGTGAAGGATATCAAGCTATCTATCTATGCTATGCTATGCTATGCTATGCT 268
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 ATACCTACGCCCAACGCCGATGAGTGAAGTTAAAGCAACCCAGCAGCACACA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 269 ATCCCTAGCCAGCCTCGGCGGAGGAGTTCGCGTTAAAGCCCTCAGAGGCCATT 328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 CCTGGATGATGTCGCTGATTTGTCATCATTAAGATTAAGTCAAGTCAAGTATTT 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 329 CCTGGAGAGGATTTGGCGATGACCAAGCCGAAAGATTAAGCCGTCAGTGTTC 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 301 ATAAAGGCAAGATGTGTGCTCAAGAGATTTGCTATTAAGTCAAGTCAAGTATAT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 389 GTCTGATTAAGTGAAGGCTCCGAGGAGCTGCTATCTCAATGTGTACCAACAT 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 361 CTAAATCCCAACTAAGCTCCGTTTATGATATACATCAATGATGATGATGATGAT 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 449 GTAAAGCCCAAGAGCTCCCGGCTTATGTTGATTCACGAGAGAGGCTTCAATATC 508
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 421 GGTGAATCAATCGTATATGATGCTGATATTTATTAATTAAGATGTGCTG 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 509 GGGAGAGCAATCGGAAATGATGCGCGGATTAAGTAAAGAAATGTTGTTCTC 568
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 481 ATTAACATCAATATGCTTTGGAGGCTGATGTTTCTAAGTTAAATTCAGAACCTT 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 569 CTCACGATACAGTACCCAGCTTGGGGCTTTGGGATTATGATGCTTAAGTCCCGAGCTA 628
OY 541 AATGCCCCGTAATGC 557
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 629 AATGTACCAAGAAATGC 645
RESULT 15
A1293416 646 bp mRNA linear EST 19-Apr-2001
LOCUS LP06524.Sprime LP Drosophila melanogaster larval-early pupal POT2
DEFINITION Drosophila melanogaster cDNA clone LP06524 Sprime similar to
            Drosophila melanogaster alpha esterase (aE7) gene, partial
            cds, mRNA sequence.
ACCESSION A1293416
VERSION A1293416.1 GI:3942823
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
          Ephydroidea; Drosophilidae; Drosophila.
          1 (bases 1 to 646)
          Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
          Lewis, S. and Rubin, G.M.
          BDGP/HMI Drosophila EST Project
          Unpublished (2001)
          Contact: Stapleton, M.
          BDGP
          Lawrence Berkeley National Lab
          One Cyclotron Rd, Berkeley, CA 94720, USA
          Fax: 510 486 6798
          Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
          Plate: 65 row: B column: 12
          High quality sequence stop: 493.
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            /db_xref="taxon:7227"
            /clone_lib="LP06524"
            /clone_lib="LP Drosophila melanogaster larval-early pupal
            POT2"
            /sex="male and female"
            /dev_stage="larvae-pupae"
            /lab_host="DH5-alpha"
            /note="Organ: whole body; Vector: POT2; Site_1: EcoRI;
            Site_2: XhoI; Sized fractionated cDNAs were directly
            ligated into POT2. Plasmid cDNA library."
BASE COUNT 151 a 163 c 184 g 148 t
ORIGIN
Query Match      14.2%; Score 243.4; DB 9; Length 646;
Best Local Similarity 64.8%; Pred. No. 3e-55;
Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAATGAAGATTAAATGATGAAAT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 89 ATGATTAAGAAGCTCGCTTGTGGAGCGCTGCGCGCCCTCAAAACCATGAGCAT 148
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 AAGTTTAAACTATGCTTAACTACCAATGAACGCTGAGTGAACCTGAATATGGC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 149 AAGTCCACAGATATGCGAGTCGACCAATGAAGATTGTGCGCGACACGAGTACGC 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 AAGTGAAGGCGTTAAAGCTTAACTGTGATGATGATGATGATGATGATGATGAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 209 CAAGTGAAGGATATCAAGCTATCTATCTATGCTATGCTATGCTATGCTATGCT 268
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 ATACCTACGCCCAACGCCGATGAGTGAAGTTAAAGCAACCCAGCAGCACACA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 269 ATCCCTAGCCAGCCTCGGCGGAGGAGTTCGCGTTAAAGCCCTCAGAGGCCATT 328
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OY 241 CCTGGATGATGTCGCTGATTTGTCATCATTAAGTCAAGTCAAGTATATTT 300
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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	1706.6	99.6	1713	4	US-09-068-960-5
5	1701.8	99.3	1713	2	US-08-669-524-1
6	1701.8	99.3	1713	2	US-09-068-960-7
7	1676.6	97.9	1713	2	US-08-669-524-2
8	956.6	55.8	1710	4	US-09-068-960-14
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23	142.2	8.3	1792	3	US-08-747-221B-18
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C	32	138.6	8.1	2144	3	US-08-747-221B-59	Sequence 59, Appl
C	33	138.6	8.1	2144	4	US-09-005-051-57	Sequence 57, Appl
C	34	138.6	8.1	2144	4	US-09-005-051-59	Sequence 59, Appl
C	35	138	8.1	1515	3	US-08-747-221B-16	Sequence 16, Appl
C	36	138	8.1	1515	3	US-08-747-221B-17	Sequence 17, Appl
C	37	138	8.1	1515	4	US-09-005-051-16	Sequence 16, Appl
C	38	138	8.1	1515	4	US-09-005-051-17	Sequence 17, Appl
C	39	138	8.1	1982	3	US-08-747-221B-13	Sequence 13, Appl
C	40	138	8.1	1982	3	US-08-747-221B-15	Sequence 15, Appl
C	41	138	8.1	1982	4	US-09-005-051-13	Sequence 13, Appl
C	42	138	8.1	1982	4	US-09-005-051-15	Sequence 15, Appl
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C	44	88.8	5.2	2989	1	US-07-927-851-1	Sequence 1, Appl
C	45	88.8	5.2	2989	1	US-08-453-323-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-068-960-1
; Sequence 1, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
; ORGANISM: Lucilia cuprina
US-09-068-960-1

Query Match	100.0%	Score 1713;	DB 4;	Length 1713;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1713;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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QY	61	AAATTTTAAACGTTAACTAATCAATGAAGAAAGGTTAGTGAATGAATATGCG	120	
DB	61	AAATTTTAAACGTTAACTAATCAATGAAGAAAGGTTAGTGAATGAATATGCG	120	
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DB	121	AAATTTTAAACGTTAACTAATCAATGAAGAAAGGTTAGTGAATGAATATGCG	180	
QY	181	ATACCGTACGCGCCCAACGCGGAGTGTGAGTGAATTAAGACCCGACGACACA	240	
DB	181	ATACCGTACGCGCCCAACGCGGAGTGTGAGTGAATTAAGACCCGACGACACA	240	
QY	241	CCCTGGATGCTGCTGCTGATTTGTCATCAATCAATGAAGTCAAGTCAAGTTT	300	
DB	241	CCCTGGATGCTGCTGCTGATTTGTCATCAATCAATGAAGTCAAGTCAAGTTT	300	
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Qy 541 AATGCTCCGCGTAATGCGCGCTTAAGAATCAAGTCAGCTTGGCTTGAATTAAT 600
Db 541 AATGCTCCGCGTAATGCGCGCTTAAGAATCAAGTCAGCTTGGCTTGAATTAAT 600
Qy 601 AATGCGCCCACTTTGGTGGCAATCCCGAATATTAACAGTCTTGGTGAAGTCCGCT 660
Db 601 AATGCGCCCACTTTGGTGGCAATCCCGAATATTAACAGTCTTGGTGAAGTCCGCT 660
Qy 661 GCTGCTCTACCCATACATGATATGATACCGAACAACCTGCGGCTTTTCATGCTGT 720
Db 661 GCTGCTCTACCCATACATGATATGATACCGAACAACCTGCGGCTTTTCATGCTGT 720
Qy 721 ATACTAATGTGCGGTAATGCTATTTGCTCCATTTGGCTAATACCCAAATGTCACATGCTGCC 780
Db 721 ATACTAATGTGCGGTAATGCTATTTGCTCCATTTGGCTAATACCCAAATGTCACATGCTGCC 780
Qy 781 TTCACCTTAGCAAAATGCGCGCTAATAGGTAAGGATATGATTAAGATGTTTGGAA 840
Db 781 TTCACCTTAGCAAAATGCGCGCTAATAGGTAAGGATATGATTAAGATGTTTGGAA 840
Qy 841 TTTCTTATGAAGCCAGCCAGATTTAATAAATCTTAGGAAAAGTTTAACTCTA 900
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Db 1501 ACTGGAATATGATATCAATTTGCGACACAGTAACTCTTATAGCAATGAATGAAGCT 1560

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; Sequence 5, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLSTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068, 960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-5

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 ATGAATTTCAACGTTAGTTGATGAGGAATTAATGGAAGATTTAATGCAATTTGAAAT 60
Qy 61 AAGTTTAACTATGCTTTAACTACCAATGAACGCTGATGCTGAACTGAATATGCG 120
Db 61 AAGTTTAACTATGCTTTAACTACCAATGAACGCTGATGCTGAACTGAATATGCG 120
Qy 121 AAAGTGAAGCGCTTAAACGTTAACTGTTGATGATGATTTCTACTACAGTTTGGGCT 180
Db 121 AAAGTGAAGCGCTTAAACGTTAACTGTTGATGATGATTTCTACTACAGTTTGGGCT 180
Qy 181 ATACCGTACCGCCACACCGCCAGGCGTACAGATTTAAACGACCCAGCAGCAACA 240
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Qy	781	TTACACCTTAGCCAAATTTGGCGGCTATAAAGGTGAGAGATATGATAGAGATTTTGGAA	840
Db	781	TTACACCTTAGCCAAATTTGGCGGCTATAAAGGTGAGAAATTAAGATAGATTTTGGAA	840
Qy	841	TTTCTATTAGAAAGCCAGCCAGGATTAATTAACCTGAGGAAAAAGTTTAACTCTA	900
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Qy	1081	CAAAATGCCATATGCTTTGTTAAGAAATTTGAAACCTTGTCATATTTGTGCCAATGAATG	1140
Db	1081	CAAAATGCCATATGCTTTGTTAAGAAATTTGAAACCTTGTCATATTTGTGCCAATGAATG	1140
Qy	1141	GCTGATGTTGAAGCACCAGCCGCCAGAGACCTTGGAAATGGTGTAAATTTAAAAAGCT	1200
Db	1141	GCTGATGTTGAAGCACCAGCCGCCAGAGACCTTGGAAATGGTGTAAATTTAAAAAGCT	1200
Qy	1201	CATGTTACAGAGAAACACCAACAGCTGATATTTATGATCTTTGCTCTCACATCTAT	1260
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Qy	1261	TTTGTGTTCCCAATGCATCTTTGTTGGCAATTAACGTTTCAACACACCTCCGGTACACC	1320
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Qy	1381	CGTAGTGCAGCTGGTGTAAAGGGTGTAGTCATGCTGATGAATTAACCTATTCTTCGG	1440
Db	1381	CGTAGTGCAGCTGGTGTAAAGGGTGTAGTCATGCTGATGAATTAACCTATTCTTCGG	1440
Qy	1441	AATCAATTTGGCCAAACGTATAGCCTTAAAGATGCGGTATACAAAACAATTBACGTATG	1500
Db	1441	AATCAATTTGGCCAAACGTATAGCCTTAAAGATGCGGTATACAAAACAATTBACGTATG	1500
Qy	1501	ACTGATATATGATACAAATTTGCCACACCTGTAATCTTTATAGCAATGAATTAAGAGT	1560
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Qy	1561	ATGGAATATTTCTCGGATCCAAATTAAGAAATCGATGAAGTATACAAAGTGTGAAT	1620
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Db      1561  ATGGAATGTTTCTCGGAGATCCCAATTGAAGAAATCCCATGAAGTATACAACTGTTTGAT 1620
QY      1621  ATTACTGATGAATTGAAGAAATGATTGATGTGCTCGTAATGATTAAGATTAAACATGGAG 1660
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Db      1621  ATTAGTGATGAATTGAAGAAATGATTGATGTGCTCGTAATGATTAAGATTAAACATGGAG 1660
QY      1681  TCGATGTTGAAGAAACATAGACATTATTTAG 1713
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Db      1681  TCGATGTTGAAGAAACATAGACATTATTTAG 1713

RESULT 5
US-08-669-524-1
; Sequence 1, Application US/08669524
; Patent No. 5843758
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, Robyn J.
; APPLICANT: NEWCOMB, Richard D.
; APPLICANT: ROBIN, Geoffrey C.
; APPLICANT: BOYCE, Thomas M.
; APPLICANT: CAMPBELL, Peter M.
; APPLICANT: PARKER, Anthony G.
; APPLICANT: OAKESHOT, John G.
; APPLICANT: SMYTH, Kerrie A.
; TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe Price Leblanc & Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 1451-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-669-524-1

Query Match          99.3%; Score 1701.8; DB 2; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY      1  ATGATTTTCAACGCTAGTTGATGAGAAATTAATAATGAGAGATTAAATGCAATGAAAT 60
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Db      1  ATGATTTTCAACGCTAGTTGATGAGAAATTAATAATGAGAGATTAAATGCAATGAAAT 60
QY      61  AAGTTTAAACTATCGTTTAACTACCAATGAACGCTGTAGCTGAACATGAATATGGC 120
      |||||||
Db      61  AAGTTTAAACTATCGTTTAACTACCAATGAACGCTGTAGCTGAACATGAATATGGC 120
QY      121  AAAGTGAAGGCGTTAAACGTTTAACTGTATGATGATGATTCCTACTACAGTTTGAGGCT 180
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Db      121  AAAGTGAAGGCGTTAAACGTTTAACTGTATGATGATGATTCCTACTACAGTTTGAGGCT 180

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QY	1261	TTTCGGTCCCCATGCATCGTTTGTGCAATTACGTTTCATTCACACTCCGGTACACC	1320
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QY	1321	GTCTACTTGTATWCCCTTCGACTTCGATTCGGAAAGATCTTATCAATCCCTATCGTATTATG	1380
Db	1321	GTCTACTTGTATWCCCTTCGACTTCGATTCGGAAAGATCTTATCAATCCCTATCGTATTATG	1380
QY	1381	CGTGTGGAGCTGGTGTAAAGCGGTGTAGCATCTGTATGAATTAACCTATTTCTTCTGG	1440
Db	1381	CGTGTGGAGCTGGTGTAAAGCGGTGTAGCATCTGTATGAATTAACCTATTTCTTCTGG	1440
QY	1441	AATCAATTTGGCCAAACGCTATGCTCTTAAGAAATCCGGGTAAATACAAACAATTTGAACGTATG	1500
Db	1441	AATCAATTTGGCCAAACGCTATGCTCTTAAGAAATCCGGGTAAATACAAACAATTTGAACGTATG	1500
QY	1501	ACTGCGTATATGATGATACAAATTTGGCCACACGCTGTATATCCCTATATAGCAATGAATTTGAAGGT	1560
Db	1501	ACTGCGTATATGATGATACAAATTTGGCCACACGCTGTATATCCCTATATAGCAATGAATTTGAAGGT	1560
QY	1561	ATGGAATAATGTTTCCCTGGGATCCAAATTAAGAAATCCGATGAAGTATCAGTGTGTTGAAT	1620
Db	1561	ATGGAATAATGTTTCCCTGGGATCCAAATTAAGAAATCCGATGAAGTATCAGTGTGTTGAAT	1620
QY	1621	ATTAGTGATGAATTTGAATAATGATTTGATGTGCTGTAATGATTAAGATTAAACAATGGGAG	1680
Db	1621	ATTAGTGATGAATTTGAATAATGATTTGATGTGCTGTAATGATTAAGATTAAACAATGGGAG	1680
QY	1681	TTGATGTTTGGAAAAACATAGAGATTTATTTTAG	1713
Db	1681	TTGATGTTTGGAAAAACATAGAGATTTATTTTAG	1713
RESULT	6		
US-09-068-960-7			
Sequence 7, Application US/09068960A			
Patent No. 6235515			
GENERAL INFORMATION:			
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.			
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE			
FILE REFERENCE: Attorney Docket No. 6235515 50179-051			
CURRENT APPLICATION NUMBER: US/09/068,960A			
CURRENT FILING DATE: 1998-05-20			
EARLIER APPLICATION NUMBER: PCT/NU96/00746			
EARLIER FILING DATE: 1996-11-22			
EARLIER APPLICATION NUMBER: AU 6751			
EARLIER FILING DATE: 1995-11-23			
NUMBER OF SEQ ID NOS: 43			
SOFTWARE: Patent In Ver. 2.0			
SEQ ID NO 7			
LENGTH: 1713			
TYPE: DNA			
ORGANISM: Lucilia cuprina			
US-09-068-960-7			
Query Match	99.3%	Score 1701.8;	DB 4; Length 1713;
Best Local Similarity	99.6%	Pred. No. 0;	
Matches 1706; Conservative	0;	Mismatches	7; Indels 0; Gaps 0;
QY	1	ATGAATTTCAACGTTAGTTGATGAGAAATTAATGGAAGATTAAATGATGAAAT	60
Db	1	ATGAATTTCAACGTTAGTTGATGAGAAATTAATGGAAGATTAAATGATGAAAT	60
QY	61	AAGTTTAACTATCGTTTAACTACCAATGAACGCTGTGTGCTGAAACTGAATATGCT	120
Db	61	AAGTTTAACTATCGTTTAACTACCAATGAACGCTGTGTGCTGAAACTGAATATGCT	120
QY	121	AAAGTGAAGGCGTTAAAGCGTTTAACTGTGTGCAATGATTTCTACTACAGTTTAAAGGCT	180
Db	121	AAAGTGAAGGCGTTAAAGCGTTTAACTGTGTGCAATGATTTCTACTACAGTTTAAAGGCT	180
QY	181	ATACGTCAGCCCAACGCGCACTGGGTAGCGATTTAAAGCAACCCAGAGCAACCA	240

Db 181 ATACCGTACGCCAACCCGACGAGTGGGTGAGCTGAGATTTAAAGCACCCGACGACACACA 240
 Qy 241 CCGTGGATGGTGGCGGTGATGTTGGCAATCAATAAAGTAAGTCAAGTCAGAGTTGATTTT 300
 Db 241 CCGTGGATGGTGGCGGTGATGTTGGCAATCAATAAAGTAAGTCAAGTCAGAGTTGATTTT 300
 Qy 301 ATACGGGCAAGTGTGGGCTCAGAGAGTGTCTATACCTAAGTGTCTATACCAATAT 360
 Db 301 ATACGGGCAAGTGTGGGCTCAGAGAGTGTCTATACCTAAGTGTCTATACCAATAT 360
 Qy 361 CTAAATCCGAACCTAAACGTCGCCGTTTGTATATACATACATAGTGTGTGTTTATATC 420
 Db 361 CTAAATCCGAACCTAAACGTCGCCGTTTGTATATACATACATAGTGTGTGTTTATATC 420
 Qy 421 GGTGAAATTCATCGTATATGATGTCCTGATTTTCAATTAAGAGATGTGTGTG 480
 Db 421 GGTGAAATTCATCGTATATGATGTCCTGATTTTCAATTAAGAGATGTGTGTG 480
 Qy 481 ATTAACATACATATGCTTGGAGCTCTAGTGTCTTCAAGTTTCAAGAACCTT 540
 Db 481 ATTAACATACATATGCTTGGAGCTCTAGTGTCTTCAAGTTTCAAGAACCTT 540
 Qy 541 AATGTCGCCGTAATGCGGCTTAAGATCAAGTCAAGTGGCTTGGATTAATAAT 600
 Db 541 AATGTCGCCGTAATGCGGCTTAAGATCAAGTCAAGTGGCTTGGATTAATAAT 600
 Qy 601 AATGTCGCCGTAATGCGGCTTAAGATCAAGTCAAGTGGCTTGGATTAATAAT 660
 Db 601 AATGTCGCCGTAATGCGGCTTAAGATCAAGTCAAGTGGCTTGGATTAATAAT 660
 Qy 661 GCTGCTCTACCCACTATCATGATGTTAACCAACAACTCGCGGCTTTCCATCGTGT 720
 Db 661 GCTGCTCTACCCACTATCATGATGTTAACCAACAACTCGCGGCTTTCCATCGTGT 720
 Qy 721 ATACTAATGTCGGGTATGCTATGTTGTCATGCTTAATACCAATGTCACATCGTCC 780
 Db 721 ATACTAATGTCGGGTATGCTATGTTGTCATGCTTAATACCAATGTCACATCGTCC 780
 Qy 781 TTCACCTAGCAAAATTTGGCGGCTATTAAGGTGAGATTAATGATTAAGATGTTTGA 840
 Db 781 TTCACCTAGCAAAATTTGGCGGCTATTAAGGTGAGATTAATGATTAAGATGTTTGA 840
 Qy 841 TTTCTTATGAAGCCCAACAGAGATTTAAACTTGAAGAAAGTTTAACTCTA 900
 Db 841 TTTCTTATGAAGCCCAACAGAGATTTAAACTTGAAGAAAGTTTAACTCTA 900
 Qy 901 GAAGAGCTACAAATTAAGGTATGTTCTTTGCTCCACTGTGAGCCATATCAGAC 960
 Db 901 GAAGAGCTACAAATTAAGGTATGTTCTTTGCTCCACTGTGAGCCATATCAGAC 960
 Qy 961 GCTGATGTCCTTACCAACATCTCGGGGAAATGTTAAACGCTTGGGTAATTCG 1020
 Db 961 GCTGATGTCCTTACCAACATCTCGGGGAAATGTTAAACGCTTGGGTAATTCG 1020
 Qy 1021 ATACCACTATGATGGTAACTTCAATATGAGGCTATTTTCACTTCAATCTTAA 1080
 Db 1021 ATACCACTATGATGGTAACTTCAATATGAGGCTATTTTCACTTCAATCTTAA 1080
 Qy 1081 CAATAGCTATGCTTGTAAAGAAATGGAACCTTGTCAATTTTGTCCAAATGTA 1140
 Db 1081 CAATAGCTATGCTTGTAAAGAAATGGAACCTTGTCAATTTTGTCCAAATGTA 1140
 Qy 1141 GCTGATGTTGAAGCGACGCGCCAGAGACCTTGAATGGGTGCTAAATTAAGAGCT 1200
 Db 1141 GCTGATGTTGAAGCGACGCGCCAGAGACCTTGAATGGGTGCTAAATTAAGAGCT 1200
 Qy 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTGTCTCACATCTAT 1260
 Db 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTGTCTCACATCTAT 1260
 Qy 1261 TTTCTGTTCCCATGATGCTTTTGTGAATTAAGTTCAATCAGACCTCGGATACACC 1320
 Db 1261 TTTCTGTTCCCATGATGCTTTTGTGAATTAAGTTCAATCAGACCTCGGATACACC 1320

Qy 1321 GCTACTGTATTCGCTTCGACCTGATGTTGGAAGATCTTATCATCCATGATTAAT 1380
 Db 1321 GCTACTGTATTCGCTTCGACCTGATGTTGGAAGATCTTATCATCCATGATTAAT 1380
 Qy 1381 CGTAGTGAAGTGTGTTAAGGCTGTATGTCATGCTGATGAATTAACCTATTTCTTGG 1440
 Db 1381 CGTAGTGAAGTGTGTTAAGGCTGTATGTCATGCTGATGAATTAACCTATTTCTTGG 1440
 Qy 1441 AATCAATGGCCAAACGATAGCTTAAGAAATCGCTGATACAAACAAATGACGTATG 1500
 Db 1441 AATCAATGGCCAAACGATAGCTTAAGAAATCGCTGATACAAACAAATGACGTATG 1500
 Qy 1501 ACTGCTATGATGATCAATTTTCCACCACTGCTATCTTATAGCAATGAATTAAGT 1560
 Db 1501 ACTGCTATGATGATCAATTTTCCACCACTGCTATCTTATAGCAATGAATTAAGT 1560
 Qy 1561 ATGAAATGTTTCTCGGATCCATTAAGAAATCGATGAAGTATACAGTGTGTAAT 1620
 Db 1561 ATGAAATGTTTCTCGGATCCATTAAGAAATCGATGAAGTATACAGTGTGTAAT 1620
 Qy 1621 ATTAGTATGAATTAAGAAATGATGATGCTGTAATGATTAAGATTAACATGGAG 1680
 Db 1621 ATTAGTATGAATTAAGAAATGATGATGCTGTAATGATTAAGATTAACATGGAG 1680
 Qy 1681 TCGATGTTGAAACATAGATTAATTTAG 1713
 Db 1681 TCGATGTTGAAACATAGATTAATTTAG 1713

RESULT 7

US-08-669-524-2

Sequence 2, Application US/08669524

Patent No. 5843758

GENERAL INFORMATION:

APPLICANT: RUSSELL, Robyn J.

APPLICANT: NEWCOMB, Richard D.

APPLICANT: BOYCE, Geoffrey C.

APPLICANT: CAMPBELL, Peter M.

APPLICANT: PARKER, Anthony G.

APPLICANT: OAKSHOTT, John G.

APPLICANT: SMYTH, Kerrie A.

TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lowe Price Leblanc & Becker

STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/669,524

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Price, Robert L.

REGISTRATION NUMBER: 22,685

REFERENCE/DOCKET NUMBER: 1451-021

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-684-1111

TELEPHONE: 703-684-1124

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1713 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: Linear
MOLECULE TYPE: DNA (genomic)
US-08-669-524-2

Query Match 97.9%; Score 1676.6; DB 2; Length 1713;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAAATGCAATGAAAT 60
DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAAATGCAATGAAAT 60
QY 61 AAGTTTAACTATGCTTTAACTACCAATGAACGGGTGATGCTGAAGATATGCG 120
DB 61 AAGTTTAACTATGCTTTAACTACCAATGAACGGGTGATGCTGAAGATATGCG 120
QY 121 AAGTGAAGGCGTTAAAGCTTACGTACGATGATGCTCTCTACAGTTTGAGGCT 180
DB 121 AAGTGAAGGCGTTAAAGCTTACGTACGATGATGCTCTCTACAGTTTGAGGCT 180
QY 181 ATACCGTACGCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCAGCACACA 240
DB 181 ATACCGTACGCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCAGCACACA 240
QY 241 CCCTGGATGGTGGCGGATGTTGCAATGATTAAGTAAAGTACGACGATGATTT 300
DB 241 CCCTGGATGGTGGCGGATGTTGCAATGATTAAGTAAAGTACGACGATGATTT 300
QY 301 ATAAAGGCGCAAGTGTGTGCTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
DB 301 ATAAAGGCGCAAGTGTGTGCTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTGTTTACTATACATACATGCTGCTGTTTATATC 420
DB 361 CTAAATCCCGAACTAAACGTCCTGTTTACTATACATACATGCTGCTGTTTATATC 420
QY 421 GGTAAATATCATGCTGATGATGATGCTGATGATGATGATGATGATGATGATG 480
DB 421 GGTAAATATCATGCTGATGATGATGCTGATGATGATGATGATGATGATGATG 480
QY 481 ATTAACATACATATGCTGTTGGAGCTCTAGGTTTCTAAGTTTAAATGGAAGACTT 540
DB 481 ATTAACATACATATGCTGTTGGAGCTCTAGGTTTCTAAGTTTAAATGGAAGACTT 540
QY 541 AATGTCGCCGTATATGCGGCTTTAAAGATCACTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 AATGTCGCCGTATATGCGGCTTTAAAGATCACTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AATGTCGCCGTATATGCGGCTTTAAAGATCACTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 AATGTCGCCGTATATGCGGCTTTAAAGATCACTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GCTGCTCTACCACTACATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 GCTGCTCTACCACTACATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 ATACTATATGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 780
DB 721 ATACTATATGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 TTACCTTATGACCAATTTGCGGCTATGAAGGTGAGATGATGATGATGATGATG 840
DB 781 TTACCTTATGACCAATTTGCGGCTATGAAGGTGAGATGATGATGATGATGATG 840
QY 841 TTTCTTATGAAAGCAAGCAGGATTTATTAATAAAGTGAAGAAAGCTTTAACTCTA 900
DB 841 TTTCTTATGAAAGCAAGCAGGATTTATTAATAAAGTGAAGAAAGCTTTAACTCTA 900
QY 901 GAAGACGCTACAAATGAAGTATGCTGCTTGGTCCAGCTGAGCATATGACGAC 960
DB 901 GAAGACGCTACAAATGAAGTATGCTGCTTGGTCCAGCTGAGCATATGACGAC 960
QY 961 GCTGATGCTGTCTTACCAACATCCTCGGAATGTTAAACTCTGCGGTATGCTG 1020

DB 961 GCTGATTTGTCTTACCAACATCTCTCGGAATGTTAAANNCTGTGGGTAAATTCG 1020
QY 1021 ATACCACATATGATGGGTATACACTTATATGAGGTCTATTTTACCTCAATTCCTTAAG 1080
DB 1021 ATACCACATATGATGGGTATACACTTATATGAGGTCTATTTTACCTCAATTCCTTAAG 1080
QY 1081 CAATGGCTATGCTGTTAAGGATTTGAAACTGTCTCAATTTTGTGCCAAGTGAATG 1140
DB 1081 CAATGGCTATGCTGTTAAGGATTTGAAACTGTCTCAATTTTGTGCCAAGTGAATG 1140
QY 1141 GCTGATGTTGAAGCAGCCAGCCAGAGACCTTGAATGGGTGCTAAATTTAAAGAGCT 1200
DB 1141 GCTGATGTTGAAGCAGCCAGCCAGAGACCTTGAATGGGTGCTAAATTTAAAGAGCT 1200
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATATGATCTTGTCTCATCTAT 1260
DB 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATATGATCTTGTCTCATCTAT 1260
QY 1261 TTCTGTTCCCATGATGATGCTGTTGCTGATGATGATGATGATGATGATGATGATG 1320
DB 1261 TTCTGTTCCCATGATGATGCTGTTGCTGATGATGATGATGATGATGATGATGATG 1320
QY 1321 GTCTACTTGTATGCTTGCACCTTCGATTCGAGATCTTATCAATCCCTATCGTATTAAG 1380
DB 1321 GTCTACTTGTATGCTTGCACCTTCGATTCGAGATCTTATCAATCCCTATCGTATTAAG 1380
QY 1381 CGTAGTGAGCTGCTGTTAAGGCTGTAGTACATGCTGATGATGATGATGATGATGATG 1440
DB 1381 CGTAGTGAGCTGCTGTTAAGGCTGTAGTACATGCTGATGATGATGATGATGATGATG 1440
QY 1441 ATCAATTTGGCCAAAGCTATAGCTTAAAGATGCGGATATACAAACATTTGAAGCTATG 1500
DB 1441 ATCAATTTGGCCAAAGCTATAGCTTAAAGATGCGGATATACAAACATTTGAAGCTATG 1500
QY 1501 ACTGATATGATGATACATTTGCGCACCTGCTGATTCCTTATGCAATGAATGGAAGCT 1560
DB 1501 ACTGATATGATGATACATTTGCGCACCTGCTGATTCCTTATGCAATGAATGGAAGCT 1560
QY 1561 ATGGAATATGCTTCTGCGGATGATGATGATGATGATGATGATGATGATGATGATG 1620
DB 1561 ATGGAATATGCTTCTGCGGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
DB 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 TCGATGTTGAAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTGAAAACATAGAGATTTATTTAG 1713

RESULT 8
US-09-068-960-14
Sequence 14, Application US/09068960A
Patent No. 623515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 623515 50179-051
CURRENT APPLICATION NUMBER: US/09/068, 960A
EARLIER FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 1710
TYPE: DNA
ORGANISM: Musca domestica
US-09-068-960-14

Query Match 55.8%; Score 956.6; DB 4; Length 1710;
 Best Local Similarity 73.4%; Pred. No. 6.9e-268;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

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QY 44 TTAATGCAATGAAATTAAGTTTAACTATCGTTTAACCAATGAACGGTGTAG 103
DB 44 TTAATGCAATGAAATTAAGTTTAACTATCGTTTAACCAATGAACGGTGTAG 103
QY 104 CTGAATCGAATATGGAAGGCTTAAACGTTTAACGTGTACATGATTTCT 163
DB 104 CTGAATCGAATATGGAAGGCTTAAACGTTTAACGTGTACATGATTTCT 163
QY 164 ACTACAGTTTGGAGGTATACCGTACGCCAACCGCGGTGAGTGAATTAAG 223
DB 164 ACTACAGTTTGGAGGTATACCGTACGCCAACCGCGGTGAGTGAATTAAG 223
QY 224 CACCCACGACCAACACCCCTGGAGGTGTGCTGATTTGCAATGAAGTAAGT 283
DB 224 CACCCACGACCAACACCCCTGGAGGTGTGCTGATTTGCAATGAAGTAAGT 283
QY 284 CAGTCCAGTTGATTTTAAACGGCAAGTGTGTGCTCAGAGATTTGTATACCTAA 343
DB 284 CAGTCCAGTTGATTTTAAACGGCAAGTGTGTGCTCAGAGATTTGTATACCTAA 343
QY 344 GTGCTATACGAATTAATCCGCAACTAAACGTCCTGTTTATGATATACATACATG 403
DB 344 GTGCTATACGAATTAATCCGCAACTAAACGTCCTGTTTATGATATACATACATG 403
QY 404 GTGTGTTTTATTAATCGGTGAATATCATGATATGATGTCCTGATTAATTTCAATTA 463
DB 404 GTGTGTTTTATTAATCGGTGAATATCATGATATGATGTCCTGATTAATTTCAATTA 463
QY 464 AAAAGATGTGTGTGATTAACATACATATCGTTTGGAGCTTACGTTTCTAACTT 523
DB 464 AAAAGATGTGTGTGATTAACATACATATCGTTTGGAGCTTACGTTTCTAACTT 523
QY 524 TAAATTCGAAGACCTTAATGTGCCGTAATGCGCGCTTAAAGATCAAGTACGCT 583
DB 524 TAAATTCGAAGACCTTAATGTGCCGTAATGCGCGCTTAAAGATCAAGTACGCT 583
QY 584 TGCGTGAATTAATAATATGCGCAACTTGTGSCAATCCGATATATTAACATCT 643
DB 584 TGCGTGAATTAATAATATGCGCAACTTGTGSCAATCCGATATATTAACATCT 643
QY 644 TTGCTGAAGTGGCGGTGCTGCTACCCATACATGATGTTAAGCAACCAACTCCG 703
DB 644 TTGCTGAAGTGGCGGTGCTGCTACCCATACATGATGTTAAGCAACCAACTCCG 703
QY 704 GTCTTTCCATCGTGTATTAATGTCGGTAATGCTATTGTCATTTGGCTAATACCC 763
DB 704 GTCTTTCCATCGTGTATTAATGTCGGTAATGCTATTGTCATTTGGCTAATACCC 763
QY 764 AATGTCACATCGTCCCTTACACCTTAAGCCAAATTTGGCGCTATAAGGCTGAAGTATG 823
DB 764 AATGTCACATCGTCCCTTACACCTTAAGCCAAATTTGGCGCTATAAGGCTGAAGTATG 823
QY 824 ATAAGGATGTTTGAATTTCTTATGAAGCCACACGAGATTTAATAAATCTTGAGG 883
DB 824 ATAAGGATGTTTGAATTTCTTATGAAGCCACACGAGATTTAATAAATCTTGAGG 883
QY 884 AAAAGATATCTGGAATTCCTAAATGAAGCAATCCCTATGATTTGATCAAAAGGAGC 883
DB 884 AAAAGATATCTGGAATTCCTAAATGAAGCAATCCCTATGATTTGATCAAAAGGAGC 883
QY 944 TTGAGCCATPACAGACCGCTGATTTGCTTACCCAAACATCTCTGGGAAATGTTAA 1003
DB 944 TTGAGCCATPACAGACCGCTGATTTGCTTACCCAAACATCTCTGGGAAATGTTAA 1003
QY 1004 CTGCTTGGGGAATTCGATACCCATATGATGGGTAACACTTTCATATGAGGTCTATTTT 1063
DB 1004 CTGCTTGGGGAATTCGATACCCATATGATGGGTAACACTTTCATATGAGGTCTATTTT 1063

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QY 1064 TCACCTCAATTCCTTAAGCAAAATGCTATGCTTAAAGCAATTTGAACACTGTGCAATT 1123
DB 1064 CCAATCAATTTGCGCAAAACATATTCGGAGGTTTAAAGAGTTGCAATTCCTGTGCAATT 1123
QY 1124 TTGTGCCAAGTGAATTTGGCTGATGTTGAACGCGACCCCGACAGACCTTGAATGGGTG 1183
DB 1124 ATGTGCTTTGGAGGATTTGGCTGACATGAAACGACGATGCGCCGAAACCTCGAGAGGCTG 1183
QY 1184 CTAAATTAATAAAGGCTCATGTTACAGAGAAACCAACCAACACTGATATTTTATGATC 1243
DB 1184 CCATTTGTAATAAAGGCTCATGTTACAGAGAAACCAACCAACACTGATATTTTATGATC 1243
QY 1244 TTGCTCTCACATCTATTTCTGTTCCCATGCACTGTTTGTGCAATTTACCTTCAATC 1303
DB 1244 TTGCTCTCATTTCTATTTCTGTTCCCATGCACTGTTTGTGCAATTTACCTTCAATC 1303
QY 1304 ACACCTCGGTACACCCGCTACTATGTTATGCTTGCACCTTGATTTGGAAGATCTTATCA 1363
DB 1304 ACACAGCTGGCACTCCCATTTTATTTGATGCTTGTGATTTGATTTCCCAAAATTAATTA 1363
QY 1364 ATCCCTATGTAATTTATGCTAGTGAACGCTGTTAAAGGCTTATGCTATGCTATGAT 1423
DB 1364 ACCCTATGTAATTTATGCTAGTGAACGCTGTTAAAGGCTTATGCTATGCTATGAT 1423
QY 1424 TAACCTATTTCTTGAATCAATTTGCCCAACGATGCTTAAAGATGCGTGAATACA 1483
DB 1424 TAACCTATCTCTTGAATCAATTTGTGGAACGCTTGCCTCAAAAGAAACCGCGAATACA 1483
QY 1484 AAACATTTGAACGATGATGCTATATGATACAAATTTGCCACACACTGCTAATCTTATA 1543
DB 1484 AAACATTTGAACGATGATGCTATATGATACAAATTTGCCACACACTGCTAATCTTATA 1543
QY 1544 GCAATGAATTTGAAGTATGGAATATGTTTCTGCGATTCATTTAAGAAATCCGATGAAG 1603
DB 1544 GCAATGAATTTGAAGTATGGAATATGTTTCTGCGATTCATTTAAGAAATCCGATGAAG 1603
QY 1604 TATACAGTGTGTAATATTAATGATGAATTAATAATGATTAATGCTGCTGAATGATA 1663
DB 1604 TATACAGTGTGTAATATTAATGATGAATTAATAATGATTAATGCTGCTGAATGATA 1663
QY 1664 AGATTAACATGGAAGTGCATGTTGAAAAACATGAGATTTATTT 1710
DB 1664 AGATTAACATGGAAGTGCATGTTGAAAAACATGAGATTTATTT 1710

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RESULT 9
 US-08-747-221B-51
 ; Sequence 51, Application US/08747221B
 ; Patent No. 6063610
 ; GENERAL INFORMATION:
 ; APPLICANT: Silver, Gary W.
 ; TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
 ; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESS: Heska Corporation
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: WordPerfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/747,221B
 ; FILING DATE: No. 6063610e1ember 12, 1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1584
US-08-747-221B-51

Query Match 10.5%; Score 179.6; DB 3; Length 1584;
Best Local Similarity 56.2%; Pred. No. 2.3e-42;
Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

QY 116 ATGCGAAGTGAAGCGGTTAAAGCTTAACTGTACATGATTCCTACTACAGTTTG 175
DB 29 AAGGTACTTTAAAGGAAAGCAATATGTGAAAAAGGAAATGTCTCATAGTTATT 88
QY 176 AAGGTATACGCTACGCCCAAGCGGCTGAGTGAAGTAAAGCAACCCAGGAC 235
DB 89 CTGGAATTCATATGCCAAGCTCTCTGTAGTATCTAAGATTTAAAGCCACCTG 148
QY 236 CAACACCCCTGGATGCTGCGTGTGTTGCAATCATAAAGATAGTCAGTCAGTTG 295
DB 149 CAGAACCTGTGAGGTTCTTGATGCTAGTAAAGAGGAATAGTTAGATCAGTAC 208
QY 296 ATTTTATACGGGCAAGTGTGGCTCAGAGATGTCTATACCTAAGTCTATACGA 355
DB 209 ATTTTATTAATAAATTAAAGTAGAGGCTGAAGATGTGTTATACCTCAATGTCTATG 268
QY 356 ATATCTAATATCCGAATTAACGTCCTTTAGTATACATACATGATGTTGTTTAA 415
DB 269 CAAACATCAGAGAAATCACTCTTCCACTAATGTATGATATACATGAGAGGCTTCT 328
QY 416 TTATCGGTGAATCATCGTATATGTATGCTGCTGATTTTCAATTAAGAGATGTG 475
DB 329 TCATGGATCTGGAATATGATATGTATGCTGATATTTGATGATTAATGGAATG 388
QY 476 TGTGATTAACATACATATCGTTGGAGCTGATGTTTCTAAGTTTAAATCAGAG 535
DB 389 TTCTGGTACTTCAATATTCGATTAGGTGTTTGGGATTTTGAACCTGGGAATAGAG 448
QY 536 ACCTTAATGTCGCGGTAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTA 595
DB 449 AA-----GGCGCTGGCAATGTTGTTGAATGACAGGTTGAAGCTCTAAATGCTAA 502
QY 596 AAAATTAATGCGCACTTTGGTGGCAATCCGATATATTAACGCTCTTGGTGAAGTG 655
DB 503 AAAACAATATTTGATCTTGGTGGTGAACCCCAACATGTGACATTTTGGAGAAACAG 562
QY 656 CCGGTGCTGCTACCACTACATGATGTTAAACGAACAACTCGGCGTCTTTCCATC 715
DB 563 CAGGTGCTGACAGTGTCTATTTGATGATTCAGATCTTTCCAAAGGACCTTTTCATA 622
QY 716 GTGTATACATAATGTCGGGTAATGCTATTTGTCATTGGC 755
DB 623 AAGGATCTCACAAGTAGAGGTCTTTTAATCCTGGGC 662

RESULT 10
US-08-747-221B-52/C
; Sequence 52, Application us/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.

APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESS: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-747-221B-52

Query Match 10.5%; Score 179.6; DB 3; Length 1584;
Best Local Similarity 56.2%; Pred. No. 2.3e-42;
Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

QY 116 ATGCGAAGTGAAGCGGTTAAAGCTTAACTGTACATGATTCCTACTACAGTTTG 175
DB 1556 AAGGTACTTTAAAGGAAAGCAATATGTGAAAAAGGAAATGTCTCATAGTTATT 1497
QY 176 AAGGTATACGCTACGCCCAAGCGGCTGAGTGAAGTAAAGCAACCCAGGAC 235
DB 1496 CTGGAATTCATATGCCAAGCTCTCTGTAGTATCTAAGATTTAAAGCCACCTG 1437
QY 236 CAACACCCCTGGATGCTGCGTGTGTTGCAATCATAAAGATAGTCAGTCAGTTG 295
DB 1436 CAGAACCTGTGAGGTTCTTGATGCTAGTAAAGAGGAATAGTTAGATCAGTAC 1377
QY 296 ATTTTATACGGGCAAGTGTGCTCAGAGATGTCTATACCTAAGTCTATACGA 355
DB 1376 ATTTTATTAATAAATTAAAGTAGAGGCTGAAGATTTTATACCTCAATGTCTATG 1317
QY 356 ATATCTAATATCCGAATTAACGTCCTTTAGTATACATACATGCTGTTGTTTAA 415
DB 1316 CAAACATCAGAGAAATCACTCTTCCACTAATGTATGATGATTAACAGGAGGCTTCT 1257
QY 416 TTATCGGTGAATCATCGTATATGTATGCTGCTGATTTTCAATTAAGAGATGTG 475
DB 1256 TCATGGATCTGGAATATGATATGTATGCTGCTGATATTTGATGATTTATGGAATG 1197
QY 476 TGTGATTAACATACATATCGTTGGAGCTGATGTTTCTCAAGTTTAAATTCAGAG 535
DB 1196 TTCTGGTACTTCAATATTCGATTAGGTGTTTGGGATTTTGAACCTGGGAATAGAG 1137
QY 536 ACCTTAATGTCGCGGTAATGCGGCTTAAAGATCAAGTCATGAGCTTGGATTA 595
DB 1136 AA-----GGCGCTGGCAATGTTGTTGAATGACCAAGTTGAAGCTCTAAATGGGTAA 1083

NAME/KEY: CDS
LOCATION: 11..1594
US-09-005-051-36

Query Match 10.5%; Score 179.6; DB 4; Length 2007;
Best Local Similarity 56.2%; Pred. No. 2.6e-42;
Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

OY 116 ATGGCAAAAGTGAAGGCGTTAAAGCTTTAACTGTAGCATGATGCTTCTACTACAGTTTG 175
DB 39 AAGGTACTTTAAAGAGAAAGACCAATTAAGTAAAGAGAAATGTTCTCAGATTATT 98
OY 176 AAGGTATACCTGACGCCCAAGCCAGTGGTGGAGCTGAGATTAAAGCACCAGCGAC 235
DB 99 CTGGAAATTCATATGCCCAACCTCCTGTAGCATTAAGATTAAAGCCACCTCAACCTG 158
OY 236 CAACACCCCTGGGATGCTGCGGTGATGTTGACATATAAGTAAAGTCAAGTCAAGTTG 295
DB 159 CAGAACCTTGGTCAAGGTGCTTGTAGTGTAGTAAAGAGGGAATGTTGTAGATCAGTAC 218
OY 296 ATTTTAAACGGGCAAGTGTGCTCAGAGGATTTGTCTATACCTAAGTGTCTATACGA 355
DB 219 ATTTTAAACAAATTAAGTAAAGTGGGCTGAGATGTTTATACCTCAATGCTATGTAC 278
OY 356 ATAACTAAATCCCGAAGTAAAGTCCGCTTTAGTATACATACATAGTGTGTTTAA 415
DB 279 CAAGAACATCAGAAATATCCTTCCAGTAATGATGATACATGAGAGAGCCTTCT 338
OY 416 TTATCGGTGAATATCATCGTATGATGTCCTGATTTATTTCAATTAAGAGATGTG 475
DB 339 TCATGGGATCTGGAATATGATATGATGTGCTGAAATATTTGATGATTAAGAAATTG 398
OY 476 TGTGATTAAATACATATATCGTTTGGAGCTTAGTGTTCCTAAGTTTAAATTCAGAA 535
DB 399 TTCTGTACTTCAATATGATGATGATGTTTGGATTTTGAACCTGGGAATAGAA 458
OY 536 ACCTTAATGTGCGCGGTAAATGCGCGCTTAAGATCAAGTCAATGCGCTTGGATTA 595
DB 459 AA-----GCGCCTGGCAATGTTGTTGATGGACAGGTGAAGCTTAAATGGGTAA 512
OY 596 AAAATTAATGGCGCACTTGGTGGCAATCCGATTAATATTAAGTCTTGGTGAAGTG 655
DB 513 AAACAAATTTGATCTCTTGGTGGTGGACCCCAACATGACTATTTTGGAGAAATCAG 572
OY 656 CCGGTGCTGCTCTTACCACTACATGATGTTAAACGAACAACCTCGGCTTTTCCATC 715
DB 573 CAGGTGCTGCAAGTGTCAATTTATGATGTTATCAGATCTTCCAAAGACTTTTCAAT 632
OY 716 GTGCTATCTAATGTGCGGTAAATGCTATTTGCTCATTTGGC 755
DB 633 AAGCATCTCACAAGTGAAGTCTTTAAATCCTTGGGC 672

Search completed: April 11, 2003, 08:51:10
Job time : 47.5118 secs

GenCore version 5.1.4 p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 01:07:17 ; Search time 94.5276 Seconds
(Without alignments)
15895.765 Million cell updates/sec

Title: US-09-776-910-1

Perfect score: 1713

Sequence: 1 atgaattcaacgttagttt.....aacatagagattatttttag 1713

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCOT_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88.8	5.2	1691	9	US-10-083-590-13
2	77.2	4.5	1611	9	US-09-738-626-1254
3	62.2	3.6	1967	10	US-09-748-739A-1
4	62.2	3.6	2381	10	US-09-880-107-2271
5	62.2	3.6	2416	10	US-09-748-739A-3
6	62.2	3.6	2416	10	US-09-748-739A-5
7	62.2	3.6	2416	10	US-09-748-739A-7
8	62.2	3.6	2416	10	US-09-748-739A-16
9	62.2	3.6	2444	9	US-09-893-519A-112
10	57.8	3.4	657	10	US-09-974-500-1107
11	57.6	3.4	2508	10	US-09-934-323-3
12	57.6	3.4	4667	10	US-09-934-323-1
13	56.8	3.3	2191	9	US-09-954-531-1038
14	56.8	3.3	2191	10	US-09-880-107-3854
15	56.8	3.3	2484	9	US-10-103-806-271
16	55.4	3.2	1641	10	US-09-895-860-3
17	55.4	3.2	2087	10	US-09-895-860-1
18	55.4	3.2	2428	9	US-09-418-176-1
19	55.4	3.2	2428	10	US-09-969-347-220

20	55.4	3.2	3824	9	US-10-036-041-22	Sequence 22, Appl
21	55.4	3.2	3824	9	US-10-028-072-541	Sequence 541, App
22	55.4	3.2	3824	9	US-10-038-855-22	Sequence 22, Appl
23	55.4	3.2	3824	9	US-10-121-049-541	Sequence 541, App
24	55.4	3.2	3824	9	US-10-123-904-541	Sequence 541, App
25	55.4	3.2	3824	9	US-10-140-470-541	Sequence 541, App
26	55.4	3.2	3824	9	US-09-931-836-22	Sequence 22, Appl
27	55.4	3.2	3824	9	US-10-175-746-541	Sequence 541, App
28	55.4	3.2	3824	9	US-10-176-918-541	Sequence 541, App
29	55.4	3.2	3824	9	US-10-176-921-541	Sequence 541, App
30	55.4	3.2	3824	9	US-10-227-884-209	Sequence 209, App
31	55.4	3.2	3824	9	US-10-036-214-22	Sequence 22, Appl
32	55.4	3.2	3824	9	US-10-137-865-541	Sequence 541, App
33	55.4	3.2	3824	9	US-10-140-474-541	Sequence 541, App
34	55.4	3.2	3824	9	US-10-035-719-22	Sequence 22, Appl
35	55.4	3.2	3824	9	US-10-142-431-541	Sequence 541, App
36	55.4	3.2	3824	9	US-10-143-114-541	Sequence 541, App
37	55.4	3.2	3824	9	US-10-230-163-209	Sequence 209, App
38	55.4	3.2	3824	9	US-10-140-002-541	Sequence 541, App
39	55.4	3.2	3824	9	US-10-036-160-22	Sequence 22, Appl
40	55.4	3.2	3824	9	US-10-142-419-541	Sequence 541, App
41	55.4	3.2	3824	9	US-10-218-631-209	Sequence 209, App
42	55.4	3.2	3824	9	US-10-230-338-209	Sequence 209, App
43	55.4	3.2	3824	9	US-10-035-958-22	Sequence 22, Appl
44	55.4	3.2	3824	9	US-10-036-150-22	Sequence 22, Appl
45	55.4	3.2	3824	9	US-10-123-262-541	Sequence 541, App

ALIGNMENTS

RESULT 1
US-10-083-590-13
Sequence 13, Application US/10083590
Publication No. US20030027257A1

GENERAL INFORMATION:

APPLICANT: IATROU, Kostas

APPLICANT: FARRELL, Patrick J.

APPLICANT: BEHE, Leo A.

TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF

FILE REFERENCE: 028722-207

CURRENT FILING DATE: 2002-02-27

PRIOR FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/136,421

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/056,871

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 13

LENGTH: 1691

TYPE: DNA

ORGANISM: Heliothis virescens

US-10-083-590-13

Query Match 5.2%; Score 88.8; DB 9; Length 1691;
Best Local Similarity 53.6%; Pred. No. 7.2e-13;
Matches 211; Conservative 0; Mismatches 177; Indels 6; Gaps 1;

QY	368	CCGAACCTAACGTCGCCGTTTATGATACATACATGCTGCTTTATTAATCGCGA	427
DB	380	CCACACCTTTAGCGCTTACGCTGCTTATACATACATGCTGAGAGATTGCTTCGCTCG	439
QY	428	ATCATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	487
DB	440	GCCACGAGACCTACACGACGACGACGACGACGACGACGACGACGACGACGACGACG	499
QY	488	TACATATGCTTTGGAGCTGAGCTTCTAAGTTTAAATTCAGAACGCTTAATGTC	547
DB	500	TTAATATACGATTAACGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	553

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QY 548 CCGGTAATGCCGCGCTTAAGATCATAGTGGCCCTTGGCTGGATTAATAATATTGCG 607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 554 CCGGGAATGCCGCGCTCCGGATCAGGTAACCCCTGTTGGCGTGGTGCAAAAGAACGCCA 613
QY 608 CCAACTTTGGGGAATCCCGATATATATACAGTCTTTGGGAAAGTCCGGTCTGCT 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 614 AGAATTTGGGAGAGACCCAGACATCACATAGCGGGGCAAGAGCGCTGGTCATCAG 673
QY 668 CTACCCACTACATGATGTTAAACCGAACACTCGCGCTTTTCCATCGTGATACGTA 727
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 674 CTGGGCACTACATGACCTTTCTTAACCTACTGAAAGTCTTTTCAAAAGACGATTCTGA 733
QY 728 TGTGGGTAATGCTATTGTTCATTGGCTATAC 761
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Db 734 TGAGCGGAACAGAAATGAGCTACTTCTTACTAC 767

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RESULT 2

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US-09-738-626-1254
; Sequence 1254, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHITO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1254
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-1254

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Query Match 4.5%; Score 77.2; DB 9; Length 1611;
Best Local Similarity 50.2%; Pred. No. 7e-10;
Matches 277; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

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QY 177 GGGTATACGCTAGCCCAACCGCAGTGGGTGAGTGAATTTAAAGCACCCAGCGACC 236
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Db 78 GGGAAATCCCTACGCGCGGAACACGTGGGAAATATCCCTCCGGGCAACCCGCGCCG 137
QY 237 AACACCCCTGGATGTGTGCTGATGTTGCA---ATCATAAAGATTAAGTCAGTCAAGT 293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 CAAAGAAATGGAGCGCGGATGCTCAATGTTCCGGTGAAGTACGTTCTCAGCCAAC 197
QY 294 TGATTTTAAAGGGCAAGTGTGCTCAGAGATGTTCTATACCTAAGTGTCTATAC 353
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 GTACTCTCTGAGAGATMAATTCGCGTTACAGAACTGCTTAACCTGATGTCTGGC 257
QY 354 GATATATCTAAATCCGGAATAAGTCCGTTTAAATATACATCATGATGTGTGTT 413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 G-----CTGATTCGGAAGAAAGCTTCTGTGTGTGTATCTCCAGCGGTTCTT 311
QY 414 TATATCGGTGA---AATCATGTGATATGATATGCTCTGATTTATTTCAAAAAGA 470
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Db 312 CATCATGGGCTCATCAAGCGAAGAAAGCGCTGGCGGATATATACCTGTCACAAACATGAA 371
QY 471 TGTGCTGTGATTAACATACATATCTGTTGGAGCTCTAGTGTTTTAAGTTAATTC 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 372 TGTGCTTACGTGTCTTAATTTTCGCTGCGGCTTTGGGCTATCTAATCTGCGTTC 431
QY 531 AGAAGACCTTAATGTGCGCGCTAATGCGGCTTAAGATCAAGTCAATGCGCTTGGT 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 432 CGTGGGGAGGATTTGCTTACCAACCCCGGCTCCACAGATCAGCTCTGCGCTGCACTG 491
QY 591 GATTAAATAATTTGCGCCCAACTTTGGTGCATCCGATTAATTAACATCTTTGGTGA 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 492 GGTACGCCGTAATATCGAACCATTCGGTGGGATCTCGAACAGTCACTCCATCATGGGCGA 551
QY 651 AAGTGGCGGTGCTGCTCTACCCACTACATGATGTTAAACGAACAACTCGCGCTTTT 710
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Db 552 ATCCGCGGGCGCTGACAGCATGTTGCATCTATGTGTGTCGCCGCTGACAGAGACTATT 611
QY 711 CCATCGTGTAT 722
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Db 612 CCAACCGGCCAT 623

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RESULT 3

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US-09-748-739A-1
; Sequence 1, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1967
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
; NAME/KEY: CDS
; LOCATION: (86)...(1891)
; US-09-748-739A-1

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Query Match 3.6%; Score 62.2; DB 10; Length 1967;
Best Local Similarity 54.8%; Pred. No. 6e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

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QY 325 GAGGATGCTATACCTAGTGTCTATAGAAATATCTAAATCCGAACCTAACCTGCC 384
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 437 GAAAGCTGTTTATATCTAATATGATGATTCAGACACTAAACC---AAAAATGCCACT 493
QY 385 GTTTTATACATACATACATGCTGTGTTTATATGCGTGAATAATCATCGTATATAT 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 494 GATATGATATGATTTATGCTGTGTTTCAACCTGGAACATCTTTACATGTTAT 553
QY 445 GGTCTGATATATTTCTTAAAGGA---TGTGCTGTGATTAACATACATATGCTTGG 501
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Db 554 GATGGCAAGTTTCTGCTGCGGTGGAAGAGTTATGTGATCAATGAACTATAGGGTG 613
QY 502 GGAGCTCTAGTGTCTTAAGTTTAAATTCAGAGAAGCTTAATGTGCGCGCTAATGCGGCG 561
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 614 GGTGCCCTAGATTTCTTACTTT---GCCAGCAAAATCTGAGGCTCCAGGGAACATGGGT 670
QY 562 GTTAAAGATCAAGTATGCGCTTGGCTTGGATTAATAATTAATTTGATGCTGCTG 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 671 TATATTGATCAACAGTGTGCTCTCAGTGTGTTCAAAAAAATAATAGACGCTTGTGTA 730
QY 622 AATCCGATATATTAACAGTCTTTGGTGAAGTGGCGGTGCTGCTC 668

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Db 721 AATCCTAAAGTGAATCTCTTTGGAGAAAGTGCAGAGACGCTTC 777

RESULT 4
US-09-880-107-2271

Sequence 2271, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

CURRENT APPLICATION NUMBER: US/09/880,107

PRIOR FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 2271

LENGTH: 2381

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474

US-09-880-107-2271

Query Match 3.6%; Score 62.2; DB 10; Length 2381;
Best Local Similarity 54.8%; Pred. No. 6.7e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

Qy 325 GAGAGTGTCTATACCTAGTGTCTATACGAATAATCCCGAAACTAAAGCTCC 384
Db 427 GAGAGCTGTATATCTAATGATGATGATGATGATGATGATGATGATGATG 483
Qy 385 GTTTAGTATACATACATGCTGCTTTTATATCGGTGAATCATCGATGTAT 444
Db 484 GTATTGATATGATTTAGTGTGCTGTTTCAAACTGAACATCTTTTACATGTTAT 543
Qy 445 GTCCTGATTTATTCATTAATAAAGA---TGTGCTGTGATTAACATCAATATGCTTG 501
Db 544 GATGCAAGTTTCTGCTCGGCTTAAGAAGTATTTAGTGTCAATGATATAGGCTG 603
Qy 502 GAGCTGTAGTTTCTAAGTTTAATTCAGAAAGCTTAATGTCCTGATGCTCCGC 561
Db 604 GGTGCTTGAAGTCTTCTAGCTTT---GCCAGAAATCTGAGGCTCCAGGAAATGGGT 660
Qy 562 CTTAAGATCAAGTATGCTGCTGCTGATTAATAAATATGCGCACTTTGCTGC 621
Db 661 TTATTGATCAACAGTGTGCTTCTAGTGTGCTTCAAAAAAATATATGACGCTTTG 720
Qy 622 AATCCGATTAATTAATACAGTCTTTGCTGAAGTCCGCTGCTGCTC 668
Db 721 AATCCTAAAGTGAATCTCTTTGGAGAAAGTGCAGAGACGCTTC 767

RESULT 5
US-09-748-739A-3

Sequence 3, Application US/09748739A

Patent No. US20020119489A1

GENERAL INFORMATION:

APPLICANT: Lockridge, Oksana

APPLICANT: Mackins, Jeffrey D.

TITLE OF INVENTION: Butyrylcholinesterase Variants and

TITLE OF INVENTION: Methods of Use

FILE REFERENCE: P-IX 4143

CURRENT APPLICATION NUMBER: US/09/748,739A

CURRENT FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2416
TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Human Butyrylcholinesterase variant

NAME/KEY: CDS

LOCATION: (214)...(1935)

US-09-748-739A-3

Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6.8e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

Qy 325 GAGAGTGTCTATACCTAGTGTCTATACGAATAATCCCGAAACTAAAGCTCC 384
Db 481 GAGAGCTGTATATCTAATGATGATGATGATGATGATGATGATGATGATG 537
Qy 385 GTTTAGTATACATACATGCTGCTTTTATATCGGTGAATCATCGATGTAT 444
Db 538 GTATTGATATGATTTAGTGTGCTGTTTCAAACTGAACATCTTTTACATGTTAT 597
Qy 445 GTCCTGATTTATTCATTAATAAAGA---TGTGCTGTGATTAACATCAATATGCTTG 501
Db 598 GATGCAAGTTTCTGCTCGGCTTAAGAAGTATTTAGTGTCAATGATATAGGCTG 657
Qy 502 GAGCTGTAGTTTCTAAGTTTAATTCAGAAAGCTTAATGTCCTGATGCTCCGC 561
Db 658 GGTGCTTGAAGTCTTCTAGCTTT---GCCAGAAATCTGAGGCTCCAGGAAATGGGT 714
Qy 562 CTTAAGATCAAGTATGCTGCTGCTGATTAATAAATATGCGCACTTTGCTGC 621
Db 715 TTATTGATCAACAGTGTGCTTCTAGTGTGCTTCAAAAAAATATATGACGCTTTG 774
Qy 622 AATCCGATTAATTAATACAGTCTTTGCTGAAGTCCGCTGCTGCTC 668
Db 775 AATCCTAAAGTGAATCTCTTTGGAGAAAGTGCAGAGACGCTTC 821

RESULT 6
US-09-748-739A-5

Sequence 5, Application US/09748739A

Patent No. US20020119489A1

GENERAL INFORMATION:

APPLICANT: Lockridge, Oksana

APPLICANT: Mackins, Jeffrey D.

TITLE OF INVENTION: Butyrylcholinesterase Variants and

TITLE OF INVENTION: Methods of Use

FILE REFERENCE: P-IX 4143

CURRENT APPLICATION NUMBER: US/09/748,739A

CURRENT FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 2416

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Human Butyrylcholinesterase variant

NAME/KEY: CDS

LOCATION: (214)...(1935)

US-09-748-739A-5

Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6.8e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

Qy 325 GAGAGTGTCTATACCTAGTGTCTATACGAATAATCCCGAAACTAAAGCTCC 384
Db 481 GAGAGCTGTATATCTAATGATGATGATGATGATGATGATGATGATGATG 537

Query Match	3.6%	Score 62.2	DB 10	Length 2416
Best Local Similarity	54.8%	Pred. No. 6.8e-06		
Matches 100	Conservative	0	Mismatches 148	Indels 9
			Gaps	3
QY	325	GAGCATTTCTATACCTAAGTGTATACGATAATCTAATATCCGGAACCTAAACGTCC	384	
Db	481	GAAAGACTGTTTATATCTAATATGTATGATCCAGCACTTAACG--AAAAATGCCACT	537	
QY	385	GTTTATGTTACATACATGCGTGTGGTTTATATACGGTGAATAATCATCTGTGATATAT	444	
Db	538	GTTATTTATATGCTATTTATGTGTGTGTTTCAAACTGSAACATCATCTTTACATGTTTAT	597	
QY	445	GGTCTGATTAATTTTCATTAATAAAGA---TGTGGTGTGATTAACTATACATATATCGTTG	501	
Db	598	GATGCGCAAGTTTCTGGCTGCGGTTGAAGAGATTATTTAGTGCATATGACATTAAGGCT	657	
QY	502	GAGGCTCTAGGTTTCTTAAGTTTAATTCACAAGACCTTAATGTGCCCCGTAATGCCGCG	561	
Db	658	GGGCGCCCTAGGATTTCTTGACTTT---GCCAAGGAATCCTGAGGCTCCAGGGAACATGGGT	714	
QY	562	CTTAAAGATCAAGTCATAGCGCTTGGCTTGAGTTAAATAATTTCCGCACTTGTGGCG	621	
Db	715	TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGACGCTTTGGTGA	774	
QY	622	AATCCGATATATTACAGTCTTTGGTGAAGTCCGCGTGTGCTTC	668	

RESULT 9
US-09-893-519A-112
; Sequence 112, Application US/09893519A
; Publication No. US20030027243A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS PHARMACEUTICALS, INC.
; APPLICANT: THOMPSON, Craig
; APPLICANT: MOORE, Jeffrey
; APPLICANT: BURMAN, Ed T.
; APPLICANT: BRADLEY, John
; APPLICANT: DESILVA, Thamara
; APPLICANT: HARRIS, Sandra
; APPLICANT: KOMARNITSKY, Svetlana
; APPLICANT: MENDILLO, Marc
; APPLICANT: MCCOY, Melissa
; APPLICANT: SANDERSON, Karen
; APPLICANT: HAO, Taiq
; APPLICANT: ZHU, Shuhao
; APPLICANT: LONG, Fan
; APPLICANT: DAVIDOV, Eugene


```

RESULT 10
US-09-974-300-1107
Sequence 1107, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ IDS NOS: 8481
SOFTWARE: FASTSQ for Windows Version 4.0.
SEQ ID NO 1107
LENGTH: 657
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-1107

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[illegible]

RESULT 12
US-09-934-323-1

Sequence 1, Application US/09934323
Patent No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: CURTIS, ROY A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYL ESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-081001
CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (420)...(2924)
US-09-934-323-1

Query Match 3.4%; Score 57.6; DB 10; Length 4667;
Best Local Similarity 54.2%; Pred. No. 0.00015;
Matches 117; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 530 CAGAAAGCCTTAAATGTCGGGTAATGCGGCTTAAGATCAAGTATGCGCTTGGCTT 589
DB 1090 CCGGGGACGAGCGCTGCAAAAGGCACTATGCGCTCTGAGCCAGATCAGGCGCTGCT 1149
QY 590 GATTAATAATTAATGCGCAACTTTGGTGCAATCCGATTAATTAATTAATGCTTTGGTG 649
DB 1150 GCGTCACTGAAGAACATGCGCACTTTGGGGGCGAGCCCGAGCATATCACCATTCTTGGT 1209
QY 650 AAGTGGCGGCTGCTGCTTACACCATCATGATGATTAACCGAACAACCTCGCGCTTTT 709
DB 1210 CCGGGGAGGCGGCTCTGCTGCTTACACCTTCTGATCTCTCCACCATTCAGAAAGGCTGT 1269
QY 710 TCCATCGTGATCTACTATGTCGGGTAATGCTATTT 745
DB 1270 TCCAGAAAGCCATGCGCCAGAGTGGCACCGCCATT 1305

RESULT 13

US-09-954-531-1038

Sequence 1038, Application US/09954531

Patent No. US20020165180A1

GENERAL INFORMATION:

APPLICANT: Weaver, Zoe

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand

FILE REFERENCE: 689290-77

CURRENT APPLICATION NUMBER: US/09/954,531

CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: US/60/233,133

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,009

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,034

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,509

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: US/60/234,567

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1038

LENGTH: 2191

TYPE: DNA

ORGANISM: Homo sapiens

US-09-954-531-1038

Query Match 3.3%; Score 56.8; DB 9; Length 2191;

Best Local Similarity 53.2%; Pred. No. 0.00016;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGGATGTCCTATACCTAAGTGTCTATACGAATATCTTAATCCGAA---ACTAA 378
DB 436 TCTGAGAGCTGCTGCTATCTACGACATCTACGCGGCCATAGCATGAGAGCTCTAAC 495
QY 379 CGTCCCGTTTGTATATACATATGATGCTGTTTATATATGCTGTAATCATGCTGAT 438
DB 496 CTGCGGCTATGCTGTGATTCACAGGTGCTGCGCTTCTTTTG--GCATGGCTTCTTGT 553
QY 439 ATGATAGTCTGATATTTTCAATTAAGAGATGCTGTGATTAATACATATGCT 498
DB 554 ATGATGTTCCATGCTGCTGCTCT--TGAGAAAGCTGTGTGATCATCTACGATACGCC 612
QY 499 TTGGAGCTCTAGCTTTTCTAGTTTAATTCAGAGACCTTAATGTCGGCTATGCC 558
DB 613 CTGGGCTCTCTGGGCTT-----CTTCACGACTGAGAGACAGCAACCGCAACTG 666
QY 559 GGCCTTAAGATCAAGTCAATGCGCTTGCCTGGATTAAATTAATTAATGCGCAACTTGT 618
DB 667 GCGTACCTGAGACCAAGTGGCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
QY 619 GCGAATCCGATATATTTACAGCTTTTGTGAAAGTCCGCGCTGCTGCTGCTGCTGCTG 678
DB 727 GCGAATCCGATATATTTACAGCTTTTGTGAAAGTCCGCGCTGCTGCTGCTGCTGCTG 786
QY 679 ATGATGTTAAAGCAACATGCGGCTTCTTCTCATGCTGCTAT 722
DB 787 CTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830

RESULT 14

US-09-880-107-3854

Sequence 3854, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3854

LENGTH: 2191

TYPE: DNA

ORGANISM: Homo sapiens

OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y09616

US-09-880-107-3854

Query Match 3.3%; Score 56.8; DB 10; Length 2191;
Best Local Similarity 53.2%; Pred. No. 0.00016;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGGATGTCCTATACCTAAGTGTCTATACGAATATCTTAATCCGAA---ACTAA 378
DB 436 TCTGAGAGCTGCTGCTATCTACGACATCTACGCGGCCATAGCATGAGAGCTCTAAC 495
QY 379 CGTCCCGTTTGTATATACATATGATGCTGTTTATATATGCTGTAATCATGCTGAT 438
DB 496 CTGCGGCTATGCTGTGATTCACAGGTGCTGCGCTTCTTTTG--GCATGGCTTCTTGT 553
QY 439 ATGATAGTCTGATATTTTCAATTAAGAGATGCTGTGATTAATACATATGCT 498

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Db 554 ATGATGTTCCATGCTGCTGCT-TGGAGAACGCTGCTGCTCATCATCAGTACCGC 612
QY 499 TTGGAGCTTACGTTTCTAAGTTTAATTCAGAACACTTAATGTGCCGGTATGCC 558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 613 CTGGGTGCTCTGGGCTT-----CTTCAGCACTGGAGCAAGCAAGCAAGCACTGG 666
QY 559 GGCCTTAAGATCAAGTACGCTTGGCTTGGATTAAATAATTTGGCCAACTTTGGT 618
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 667 GGTACCTGAGCAAGTGGCTGCACTACGCTGGGTCCAGCAAGAAATATGCCCACTTTGA 726
QY 619 GGCATATCCCGATTAATATATACAGTCTTTGGTGAAGTGGCGGCTGCTTACCACTAC 678
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 727 GGCACCTCTGACCGCTGCTACATTTTGGCGAGTCTGGCGGTGGCAGCAGTGTCTTGG 786
QY 679 ATGATGTTAACCGAACAACCTGGGCTTTTCCATCGTGAT 722
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 787 CTGTGTTGTCCTCCCATATCCCAAGAGACTCTTCCACGAGGCAT 830
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RESULT 15

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US-10-102-806-271
: Sequence 271, Application US/10102806
: Publication No. US20030054421A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA103P1c1
: CURRENT APPLICATION NUMBER: US/10/102,806
: CURRENT FILING DATE: 2002-03-22
: PRIOR APPLICATION NUMBER: 09/925,298
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05881
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 846
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 271
: LENGTH: 2484
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (194)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (623)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (2396)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (2484)
: OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-271
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Query Match 3.38; Score 56.8; DB 9; Length 2484;

Best Local Similarity 53.28; Pred. No. 0.00017; Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

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QY 322 TCAGAGATTTGCTATACCTAAGTCTATACGATTAATCTAAATCCGAA---ACTAAA 378
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Db 950 TCTGAGAGACTGCTTACTACATCTACACGCGGCCCATAGCCATGAAAGCTCTAAC 1009
QY 379 CGTCCGTTTAAATACATACAGTGGTGGTTTAAATATCGTGAATAATCATCGTAT 438
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1010 CTGCGGTGATGCTGTGATCCACGCTGTGGTTTGG--GCATGGCTCTCTGT 1067
QY 439 ATGTATGCTCTGATTAATTTCAATTAAGATGTGTGATTAACATACATATGCT 498
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1068 ATGATGTTCCATGCTGCTGCT-TGGAGAACGCTGCTGCTCATCATCAGTACCGC 1126
QY 499 TTGGAGCTTACGTTTCTAAGTTTAATTCAGAACACTTAATGTGCCGGTATGCC 558
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Db 1127 CTGGGTGCTCTGGGCTT-----CTTCAGCACTGGAGCAAGCAAGCAAGCAAGCACTGG 1180
QY 559 GGCCTTAAGATCAAGTACGCTTGGCTTGGATTAAATAATTTGGCCAACTTTGGT 618
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1181 GGTACCTGAGCAAGTGGCTGCACTACGCTGGGTCCAGCAAGAAATATGCCCACTTTGA 1240
QY 619 GGCATATCCCGATTAATATATACAGTCTTTGGTGAAGTGGCGGCTGCTTACCACTAC 678
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1241 GGCACCTCTGACCGTGTACCATTTTGGCGAGTCTGGGGTGGCAGAGTGTCTTGG 1300
QY 679 ATGATGTTAACCGAACAACCTGGGCTTTTCCATCGTGAT 722
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1301 CTGTGTTGTCCTCCCATATCCCAAGAGACTCTTCCACGAGGCAT 1344
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Job time : 106.528 secs

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GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

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Title: US-09-776-910-3

Perfect score: 1713

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Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1709.8	99.8	1713	6	ARI53438 Sequence
4	1706.6	99.6	1713	6	ARI53440 Sequence
5	1701.8	99.3	1713	6	ARI53437 Sequence
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7	1701.8	99.3	2240	3	LCU56636 Sequence
8	1676.6	97.9	1713	6	ARI53438 Sequence
9	985.6	57.5	2160	3	AF133341 Musca dom
10	959.4	56.0	2175	3	AF133082 Haematobi
11	955	55.8	1710	6	ARI53445 Sequence
12	680.4	39.7	2017	3	AY051473 Sequence
13	378.6	22.1	2660	3	AT121675 Drosophila
14	377	22.0	2820	3	DMU51050 Drosophila
15	372.2	21.7	5735	2	AC015272 Drosophila
16	372.2	21.7	18459	3	AC008312 Drosophila
17	372.2	21.7	197597	3	AC011253 Drosophila
18	372.2	21.7	309023	3	AE003671 Drosophila
19	365.4	21.3	1962	3	AY051497 Drosophila
20	323	18.9	2122	3	AY058637 Drosophila
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22	300.4	17.5	13044	2	AC014297 Drosophila
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24	300.4	17.5	173373	3	AC008349 Drosophila
25	300.4	17.5	307363	3	AE003457 Drosophila
26	289.8	16.9	2050	3	AF216210 Drosophila
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32	238.2	13.9	188459	3	AC008312 Drosophila
33	238.2	13.9	197597	3	AC011253 Drosophila
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35	229.6	13.4	1724	3	AY069743 Drosophila
36	227.6	13.3	2401	3	DMU51054 Drosophila
37	224.2	13.1	933	3	AF216216 Drosophila
38	224.2	13.1	1836	3	COESERES1 Drosophila
39	224	13.1	3447	3	DMU51052 Drosophila
40	219.2	12.8	1630	3	COESERES2 Drosophila
41	214	12.5	84252	2	AC009207 Drosophila
42	212	12.4	1401	3	CPU43544 Culex pipie
43	207.4	12.1	6028	3	AF177382 Culex tri
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ALIGNMENTS

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LOCUS      ARI53439
DEFINITION Sequence 3 from patent US 6235515.
ACCESSION  ARI53439
VERSION     ARI53439.1 GI:15120971
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 1713)
AUTHORS     Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
             Rubin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.A.,
             Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
TITLE       Malathion carboxylesterase
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JOURNAL	Patent: US 6255515-A 3 22-MAY-2001;
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SOURCE	1. 1713
	/organization="unknown"
BASE COUNT	515 a 506 c 370 g 522
ORIGIN	

BASE COUNT 515 a 305 c 370 g 523 t
ORIGIN

Query Match 99.9%; Score 1711.4; DB 6; Length 1713;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAAATTCACACCTTACTTGTGAGAGAAATTTAAATGGAAGATTAAATGATTTGAAAT 60
DB 1 ATGAAATTCACACCTTACTTGTGAGAGAAATTTAAATGGAAGATTAAATGATTTGAAAT 60
QY 61 AAGTTTTAAACATATCGTTTAACTACCAATGAACGGGTGATGCTGAACGATATGCG 120
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QY 121 AAAGTGAAGCGCTTAAACGTTTAACTGATGATGATTCCTACTACAGTTTGAAGGT 180
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QY 181 ATACCGTACGCGCCACCGCGAGGTGGAGCTGATTTAAAGACCCCGACCAACA 240
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QY 241 CCCTGGATGCTGCGCGATTTGCAATCATAAAGATAGTCAAGTGAATTTT 300
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QY 301 ATAAAGGCAAAAGTGTGTGCTCAGAGAGATTGCTATACCTAAGTGTATACGAATAT 360
DB 301 ATAAAGGCAAAAGTGTGTGCTCAGAGAGATTGCTATACCTAAGTGTATACGAATAT 360
QY 361 CTAAATCCCGAAATAAACGTCGGTTTATATACATACATGCTGGTGTATATATC 420
DB 361 CTAAATCCCGAAATAAACGTCGGTTTATATACATACATGCTGGTGTATATATC 420
QY 421 GGTGAATATCATCGTATATGATGTCCTGATATTTTCAATTAAGAGATGCTGTG 480
DB 421 GGTGAATATCATCGTATATGATGTCCTGATATTTTCAATTAAGAGATGCTGTG 480
QY 481 ATTAACATACAAATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAACCTT 540
DB 481 ATTAACATACAAATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAACCTT 540
QY 541 AATGTCGCGGTATGCGGCTTAAAGATCAATGATGCTGCGGTGATTAATAAT 600
DB 541 AATGTCGCGGTATGCGGCTTAAAGATCAATGATGCTGCGGTGATTAATAAT 600
QY 601 AATTGCGCCAACTTTGGTGGCAATCCGATTAATTTACAGTCTTTGGTGAAGTCCGCT 660
DB 601 AATTGCGCCAACTTTGGTGGCAATCCGATTAATTTACAGTCTTTGGTGAAGTCCGCT 660
QY 661 GTCGCTCTACCACTACATGATGTTAAACGACAAACCTGCGGTCTTTTCCATGCTGCT 720
DB 661 GTCGCTCTACCACTACATGATGTTAAACGACAAACCTGCGGTCTTTTCCATGCTGCT 720
QY 721 ATACTAATGCTGGTAAATGCTATTTGTCCTAATGCTAATACCAATGCAATCGTCC 780
DB 721 ATACTAATGCTGGTAAATGCTATTTGTCCTAATGCTAATACCAATGCAATCGTCC 780
QY 781 TTACACTTAGCCAAATTTGCGCGCTATTAAGGTGAGATTAATGATGATTTTGGAA 840
DB 781 TTACACTTAGCCAAATTTGCGCGCTATTAAGGTGAGATTAATGATGATTTTGGAA 840
QY 841 TTTCTTATGAAGCCCAAGCCACAGATTTTAAATTAACCTTGAGGAAAAAGTTTAACTCTA 900
DB 841 TTTCTTATGAAGCCCAAGCCACAGATTTTAAATTAACCTTGAGGAAAAAGTTTAACTCTA 900
QY 901 GAAAGGCTACAAATTAAGGCTATTTCTTTTGTCCCACTGTTTGAGCCATATCAAGCC 960
DB 901 GAAAGGCTACAAATTAAGGCTATTTCTTTTGTCCCACTGTTTGAGCCATATCAAGCC 960
QY 961 GCTGATTTGTCTTACCAAAACATCTCGGGAATGTTTAAACTGCTTGGGTAATTCG 1020

DB 961 GCTGATTTGTCTTACCAAAACATCTCGGGAATGTTTAAACTGCTTGGGTAATTCG 1020
QY 1021 ATACCACTATGATGGTAAACACTTCAATGAGGCTTATTTTCACTTCAATTCCTTAAG 1080
DB 1021 ATACCACTATGATGGTAAACACTTCAATGAGGCTTATTTTCACTTCAATTCCTTAAG 1080
QY 1081 CAATGCTATGCTTGTGAAGGATTTGAAACCTGTGCAATTTTGTGCCAAGGAATG 1140
DB 1081 CAATGCTATGCTTGTGAAGGATTTGAAACCTGTGCAATTTTGTGCCAAGGAATG 1140
QY 1141 GCTGATGCTGAACGCGCGCCCGAGACCTTGAATGAGGTGCTTAAATTAAGGCT 1200
DB 1141 GCTGATGCTGAACGCGCGCCCGAGACCTTGAATGAGGTGCTTAAATTAAGGCT 1200
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTTGTCTCACAATCTAT 1260
DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTTGTCTCACAATCTAT 1260
QY 1261 TTTGTTTCCCATGATCGCTTGTGCAATTAAGTTCATCAACCTCGGTAACACC 1320
DB 1261 TTTGTTTCCCATGATCGCTTGTGCAATTAAGTTCATCAACCTCGGTAACACC 1320
QY 1321 GTCTACTTGTATCGCTTGCATTCGATTTGAGAGATCTTATCAATCCCTATCGATATATG 1380
DB 1321 GTCTACTTGTATCGCTTGCATTCGATTTGAGAGATCTTATCAATCCCTATCGATATATG 1380
QY 1381 CGTAGTGACGCTGCTGTTAAAGGCTGTAGTCATGCTGATTAATTAACCTATTTCTTCG 1440
DB 1381 CGTAGTGACGCTGCTGTTAAAGGCTGTAGTCATGCTGATTAATTAACCTATTTCTTCG 1440
QY 1441 AATCAATTTGGCCAAACGATATGCTTAAAGATCGGCTGAATCAAAACATTAAGCTATG 1500
DB 1441 AATCAATTTGGCCAAACGATATGCTTAAAGATCGGCTGAATCAAAACATTAAGCTATG 1500
QY 1501 ACTGATATGATGATACATTTTGGCCACACCTGATCTTATAGCAATGAATTAAGAT 1560
DB 1501 ACTGATATGATGATACATTTTGGCCACACCTGATCTTATAGCAATGAATTAAGAT 1560
QY 1561 ATGGAATATGTTTCTGCGGATTCATTAAGAAATCCGATGAAGTATACAGTGTGTAAT 1620
DB 1561 ATGGAATATGTTTCTGCGGATTCATTAAGAAATCCGATGAAGTATACAGTGTGTAAT 1620
QY 1621 ATTAGTATGATTAAGAAATATGATGATGCTGCTGAATGATTAAGATTAACATGAGAG 1680
DB 1621 ATTAGTATGATTAAGAAATATGATGATGCTGCTGAATGATTAAGATTAACATGAGAG 1680
QY 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713

RESULT 3
ARI53438
LOCUS ARI53438 1713 bp DNA Linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6235515.
ACCESSION ARI53438
VERSION ARI53438.1 GI:15120970
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Robinson, G. Charlesde., Quetleville., Claudianos, C., Smyth, K. A.,
Boyce, T. Mark., Oakeshot, J. Graham. and Brownlie, J. Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 1 22-MAY-2001;
FEATURES Location/DnaIiflers
1. 1713
BASE COUNT 515 a 304 c 370 g 524 t
ORIGIN

Query Match 99.8%; Score 1709.8; DB 6; Length 1713;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTACTTGTGAGAGAAATTAATGAGATTAAATGCAATGAAAT 60
 DB 1 ATGAATTTCAACGTTACTTGTGAGAGAAATTAATGAGATTAAATGCAATGAAAT 60
 QY 61 AAGTTTAAACATGCTTAACTAACCAATGAACGGTGGAGTGAACCTGAATATGCG 120
 DB 61 AAGTTTAAACATGCTTAACTAACCAATGAACGGTGGAGTGAACCTGAATATGCG 120
 QY 121 AAAGTGAAGGCGTTAAACGTTAACTGTAGATGATTTCTACTACATTTTGAGAGT 180
 DB 121 AAAGTGAAGGCGTTAAACGTTAACTGTAGATGATTTCTACTACATTTTGAGAGT 180
 QY 181 ATACCGTACCGCCCAACCGCCAGTGGGAGCTGAGATTTAAAGCACCACCGACCA 240
 DB 181 ATACCGTACCGCCCAACCGCCAGTGGGAGCTGAGATTTAAAGCACCACCGACCA 240
 QY 241 CCGTGGAGTGTGGCGCATTTGTGCAATCAATGAATAGTCAAGTGAATGATTT 300
 DB 241 CCGTGGAGTGTGGCGCATTTGTGCAATCAATGAATAGTCAAGTGAATGATTT 300
 QY 301 ATACGGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGAATAT 360
 DB 301 ATACGGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGAATAT 360
 QY 361 CTAAATCCGCAAACTAAGCTCCGTTTAACTATACATACATGCTGCTTTATATATC 420
 DB 361 CTAAATCCGCAAACTAAGCTCCGTTTAACTATACATACATGCTGCTTTATATATC 420
 QY 421 GTGAAATATCATGTATATGTATGCTGCTGATTTATTTCAATTAAGATGCTGCTG 480
 DB 421 GTGAAATATCATGTATATGTATGCTGCTGATTTATTTCAATTAAGATGCTGCTG 480
 QY 481 ATTAACATACAAATATGTTGGAGCTTAAGTCTTAAGTTTAAATTCAGAGACCTT 540
 DB 481 ATTAACATACAAATATGTTGGAGCTTAAGTCTTAAGTTTAAATTCAGAGACCTT 540
 QY 541 AATGTCCCGGTAAATGCTGCTTAAAGATCAATGATGCTGCTGCTGCTGCTGCTG 600
 DB 541 AATGTCCCGGTAAATGCTGCTTAAAGATCAATGATGCTGCTGCTGCTGCTGCTG 600
 QY 601 AATGCGCCAACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 DB 601 AATGCGCCAACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 661 GCTGCTTACCCCACTACATGATGTTAAACGCAAACTGCGGCTTTTCCATGCTGCT 720
 DB 661 GCTGCTTACCCCACTACATGATGTTAAACGCAAACTGCGGCTTTTCCATGCTGCT 720
 QY 721 ATACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 DB 721 ATACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 781 TTACCTTATGCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB 781 TTACCTTATGCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 841 TTTCTTATGCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 DB 841 TTTCTTATGCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 901 GAAGAGCGTACAAATAGGTCATGTTTCTTTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 DB 901 GAAGAGCGTACAAATAGGTCATGTTTCTTTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 961 GCTGATTTGCTTACCCCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 DB 961 GCTGATTTGCTTACCCCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020

QY 1021 ATACCCATATGATGGGTAACTGCTATATGAGGCTATATTTTCACTTCAATTTTAAG 1080
 DB 1021 ATACCCATATGATGGGTAACTGCTATATGAGGCTATATTTTCACTTCAATTTTAAG 1080
 QY 1081 CAAATGCTATGCTTGTGTAAGAAATGGAACCTTGTCTCAATTTTGTGCCAATGTAATG 1140
 DB 1081 CAAATGCTATGCTTGTGTAAGAAATGGAACCTTGTCTCAATTTTGTGCCAATGTAATG 1140
 QY 1141 GCTGATGCTTAACGACCGCCCGCAGAGACCTTGGAAATGGGTCCTAAATTAAGAGCT 1200
 DB 1141 GCTGATGCTTAACGACCGCCCGCAGAGACCTTGGAAATGGGTCCTAAATTAAGAGCT 1200
 QY 1201 CATGTTACAGAGAAACACCAACAGCTGAATTAATGATGCTGCTGCTGCTGCTGCTG 1260
 DB 1201 CATGTTACAGAGAAACACCAACAGCTGAATTAATGATGCTGCTGCTGCTGCTGCTG 1260
 QY 1261 TTTCTGTTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 DB 1261 TTTCTGTTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 QY 1321 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 DB 1321 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 QY 1381 CGTAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 DB 1381 CGTAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 QY 1441 AATCAATTTGGCCAAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 DB 1441 AATCAATTTGGCCAAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 QY 1501 ACTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 DB 1501 ACTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 QY 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 DB 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 QY 1621 ATTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 DB 1621 ATTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 QY 1681 TCGATGCTTGAAGAAACATAGATTTATTTTAC 1713
 DB 1681 TCGATGCTTGAAGAAACATAGATTTATTTTAC 1713

RESULT 4
 ARI53440 1713 bp DNA linear PAT 08-AUG-2001
 LOCUS Sequence 5 from patent US 6235515.
 DEFINITION ARI53440
 ACCESSION ARI53440
 VERSION ARI53440.1 GI:15120972
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolm, Rodin, G. Charlesde, Quetleville, Claudianos, C., Smyth, K. A., Boyce, T. Mark, Oakshott, J. Graham, and Brownlie, J. Colin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 5 22-MAY-2001;
 FEATURES location/qualifiers
 source 1..1713
 BASE COUNT 516 a 305 c 369 g 523 t
 ORIGIN
 Query Match 99.8%; Score 1706.6; DB 6; Length 1713;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1709: Conservative 0; Mismatches 4; Indels 0; Gaps 0;				
QY	1	ATGATTTCAACGTTAGTTGATGAGAAATTAATGAGATTAATGATGAAAT	60	
Db	1	ATGATTTCAACGTTAGTTGATGAGAAATTAATGAGATTAATGATGAAAT	60	
QY	61	AAAGTTTAACTATCGTTTAACACCAATGAAACGGTGTAGCTGAACATGATATGCG	120	
Db	61	AAAGTTTAACTATCGTTTAACACCAATGAAACGGTGTAGCTGAACATGATATGCG	120	
QY	121	AAAGTGAAGCGCTTAAACGTTTAACTGTACGATGATTCCTACACGTTTGAGGGT	180	
Db	121	AAAGTGAAGCGCTTAAACGTTTAACTGTACGATGATTCCTACACGTTTGAGGGT	180	
QY	181	ATACCGTAGCGCCAAACCGCCAGTGGGTGAGTGAATTAAGACCCCAAGCCACACA	240	
Db	181	ATACCGTAGCGCCAAACCGCCAGTGGGTGAGTGAATTAAGACCCCAAGCCACACA	240	
QY	241	CCCTGGGATGGTGTGCGCGATTTGTGCAATCATTAAGATGATGATGATGATGATG	300	
Db	241	CCCTGGGATGGTGTGCGCGATTTGTGCAATCATTAAGATGATGATGATGATGATG	300	
QY	301	ATAACGGGCAAGTGTGTGCTCAGAGATTTGTCTATACCTAAGTGTCTATACGAATAT	360	
Db	301	ATAACGGGCAAGTGTGTGCTCAGAGATTTGTCTATACCTAAGTGTCTATACGAATAT	360	
QY	361	CTAAATCCCGAACTAAACGTCCTGTTTATATACATACATGATGATGATGATGATG	420	
Db	361	CTAAATCCCGAACTAAACGTCCTGTTTATATACATACATGATGATGATGATGATG	420	
QY	421	GGTGAAATCATCGTATATGATGCTGATTTTCAATTTAAAGATGTGTGTG	480	
Db	421	GGTGAAATCATCGTATATGATGCTGATTTTCAATTTAAAGATGTGTGTG	480	
QY	481	ATTAACATACATATCGTTTGGGAGCTTAGTCTTCTAAGTTTAAATTCAGAGACCTT	540	
Db	481	ATTAACATACATATCGTTTGGGAGCTTAGTCTTCTAAGTTTAAATTCAGAGACCTT	540	
QY	541	AATGCGCCGGTAAATGCGGCGCTTAAAGATCAAGTCAATGCGCTTGTGATTAATAT	600	
Db	541	AATGCGCCGGTAAATGCGGCGCTTAAAGATCAAGTCAATGCGCTTGTGATTAATAT	600	
QY	601	AATGCGCCAACTTGTGTGGCAATCCGATATATTTACAGTCTTGTGTGAAGTCCCGT	660	
Db	601	AATGCGCCAACTTGTGTGGCAATCCGATATATTTACAGTCTTGTGTGAAGTCCCGT	660	
QY	661	GCTGCTTACCCACTACATGATGTTAACCGAACAACTCGCGCTTTTCCATCTGCT	720	
Db	661	GCTGCTTACCCACTACATGATGTTAACCGAACAACTCGCGCTTTTCCATCTGCT	720	
QY	721	ATACGAATGTGGGTAAATGATGATTTGCTATGCTATACCAATGTCACATCTGCTCC	780	
Db	721	ATACGAATGTGGGTAAATGATGATTTGCTATGCTATACCAATGTCACATCTGCTCC	780	
QY	781	TTCACTTAGCCAAATTTGGCGGCTATTAAGGTGAGATTAATGATGATGATGATG	840	
Db	781	TTCACTTAGCCAAATTTGGCGGCTATTAAGGTGAGATTAATGATGATGATGATG	840	
QY	841	TTTCTTATGAAGCCACAGGATTTTAACTTGAAGAAAAGTTTAACTCTA	900	
Db	841	TTTCTTATGAAGCCACAGGATTTTAACTTGAAGAAAAGTTTAACTCTA	900	
QY	901	GAAAGCGGTACAAATTAAGTATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT	960	
Db	901	GAAAGCGGTACAAATTAAGTATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT	960	
QY	961	GCTGATTTGTCTTACCACCAATCTTGGGAAATGTTAAACGCTGCTGGGTATTCG	1020	
Db	961	GCTGATTTGTCTTACCACCAATCTTGGGAAATGTTAAACGCTGCTGGGTATTCG	1020	
QY	1021	ATACCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1080	
Db	1021	ATACCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1080	

QY	1081	CAATGCTTATGCTTGTAAAGAAATGGAACCTTGTCAATTTTGTGCAAGTAAATG	1140	
Db	1081	CAATGCTTATGCTTGTAAAGAAATGGAACCTTGTCAATTTTGTGCAAGTAAATG	1140	
QY	1141	GCTGATGCTGAACGCGCCGCCAGACAGCTTGAAGTGGTGTCTTAAATTAAGAGCT	1200	
Db	1141	GCTGATGCTGAACGCGCCGCCAGACAGCTTGAAGTGGTGTCTTAAATTAAGAGCT	1200	
QY	1201	CATGTTACAGGAGAACACCAACAGCTGATATTTTATGATCTTTGCTCTACATCTAT	1260	
Db	1201	CATGTTACAGGAGAACACCAACAGCTGATATTTTATGATCTTTGCTCTACATCTAT	1260	
QY	1261	TTCTGCTTCCCATGATCGTTTGTGGAATTAAGCTTCAATCACACCGGCTACACC	1320	
Db	1261	TTCTGCTTCCCATGATCGTTTGTGGAATTAAGCTTCAATCACACCGGCTACACC	1320	
QY	1321	GCTTACTTGTATCGCTTGACCTTGATTCGAAAGATCTTATCAATCCGATGATATG	1380	
Db	1321	GCTTACTTGTATCGCTTGACCTTGATTCGAAAGATCTTATCAATCCGATGATATG	1380	
QY	1381	CGTATGACGCTGCTTGAAGGCTGTGTCTATGCTGATGATTAACCTATTTCTTGG	1440	
Db	1381	CGTATGACGCTGCTTGAAGGCTGTGTCTATGCTGATGATTAACCTATTTCTTGG	1440	
QY	1441	AATCAATGGCCAAACGATGCTTAAAGATGCGTGAATACAAACATTAAGACGATG	1500	
Db	1441	AATCAATGGCCAAACGATGCTTAAAGATGCGTGAATACAAACATTAAGACGATG	1500	
QY	1501	ACTGATATGATGATCAATTTTGCACACAGCTGATTCCTTATGAGCAATGAATGAGT	1560	
Db	1501	ACTGATATGATGATCAATTTTGCACACAGCTGATTCCTTATGAGCAATGAATGAGT	1560	
QY	1561	ATGAAATGTTTCTGCGGATCCATTAAGAAATCCGATGAAGTATACAGCTTTGAT	1620	
Db	1561	ATGAAATGTTTCTGCGGATCCATTAAGAAATCCGATGAAGTATACAGCTTTGAT	1620	
QY	1621	ATTAGTATGAATTTGAATGATGATGCTTGAAGATGATTAACATTAAGTGGAG	1680	
Db	1621	ATTAGTATGAATTTGAATGATGATGCTTGAAGATGATTAACATTAAGTGGAG	1680	
QY	1681	TCGATGTTTGAAGAAACATAGAGATTTATTTAG	1713	
Db	1681	TCGATGTTTGAAGAAACATAGAGATTTATTTAG	1713	
RESULT 5				
LOCUS	AR062837	1713 bp	DNA	linear
DEFINITION	Sequence 1 from patent US 5843758.			
ACCESSION	AR062837			
VERSION	AR062837.1	GI:5990528		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 1713)			
AUTHORS	Russell, R. Joyce., Newcomb, R. David., Robin, G. Charlesde. Quetteville., Boyce, T. Mark., Campbell, P. Malcolm., Oakeshott, J. Graham. and Smyth, K. A.			
TITLE	Enzyme based bioremediation			
JOURNAL	Patent: US 5843758-A 1 01-DEC-1998;			
FEATURES	Location/Qualifiers			
Source	1..1713			
BASE COUNT	516 a 305 c 370 g 522 t			
ORIGIN	/organism="unknown"			
Query Match	99.3%; Score 1701.8; DB 6; Length 1713;			
Best Local Similarity	99.6%; Pred. No. 0;			
Matches 1706: Conservative 0; Mismatches 7; Indels 0; Gaps 0;				
QY	1	ATGATTTCAACGTTAGTTGATGAGAAATTAATGAGATTAATGATGAAAT	60	

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Db 1 ATGAATTTACAGTGTAGTTGATGAGAAATTAATAATGAAATTAATGCAATTTGAAAT 60
QY 61 AAGTTTAAACATCGTTAACTACCAATGAAGGCTGTGCTGAAACCTGAATATGCGC 120
Db 61 AAGTTTAAACATCGTTAACTACCAATGAAGGCTGTGCTGAAACCTGAATATGCGC 120
QY 121 AAGTGAAGGCGTTAAACGTTAACTGTGTGATGATTCCTACTACAGTTTAAAGGT 180
Db 121 AAGTGAAGGCGTTAAACGTTAACTGTGTGATGATTCCTACTACAGTTTAAAGGT 180
QY 181 ATACGTTAGGCCCAACCGCACTGGGTGACCTGACATTTAAAGCACCAGGACCAACA 240
Db 181 ATACGTTAGGCCCAACCGCACTGGGTGACCTGACATTTAAAGCACCAGGACCAACA 240
QY 241 CCCTGGATGTGTGCGGCGATTTGCAATCATAAAGATGATGCGTCAAGTTGATTTT 300
Db 241 CCCTGGATGTGTGCGGCGATTTGCAATCATAAAGATGATGCGTCAAGTTGATTTT 300
QY 301 ATACGGGCAAGGTGTGTGCTCAGAGGATTTGTCTATACCTAAGTGTCTATACGAATAT 360
Db 301 ATACGGGCAAGGTGTGTGCTCAGAGGATTTGTCTATACCTAAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCGAACTAAACGTCGCCGTTTACTATACATACATGATGATGATGATGATG 420
Db 361 CTAAATCCCGAACTAAACGTCGCCGTTTACTATACATACATGATGATGATGATGATG 420
QY 421 GGTGAAATATCATGTATATGTATGTGCTGATTAATTCATTAAGAGATGTGCTGTTG 480
Db 421 GGTGAAATATCATGTATATGTATGTGCTGATTAATTCATTAAGAGATGTGCTGTTG 480
QY 481 ATTAACATACATATGCTTTGGGAGCTGCTAGTTTCTAGTTTAAATTCAGAGACCTT 540
Db 481 ATTAACATACATATGCTTTGGGAGCTGCTAGTTTCTAGTTTAAATTCAGAGACCTT 540
QY 541 AATGTGCCCGGTAAATGCCGCGCTTAAAGATCAATCACTGCGCTGCTGATTAATAAT 600
Db 541 AATGTGCCCGGTAAATGCCGCGCTTAAAGATCAATCACTGCGCTGCTGATTAATAAT 600
QY 601 AATGGCCCAACTTGTGTGCAATCCGATTAATTAATTAATTAATTAATTAATTAAT 660
Db 601 AATGGCCCAACTTGTGTGCAATCCGATTAATTAATTAATTAATTAATTAATTAAT 660
QY 661 GCTGCTCTACCCACTACATGATTTAAACCAAACTGCGCTCTTTCATCGTGTG 720
Db 661 GCTGCTCTACCCACTACATGATTTAAACCAAACTGCGCTCTTTCATCGTGTG 720
QY 721 ATACTATGTGCGGTATGCTATTTGCTTCCATTTGCTAATACCAATGTCAACATGCTGCC 780
Db 721 ATACTATGTGCGGTATGCTATTTGCTTCCATTTGCTAATACCAATGTCAACATGCTGCC 780
QY 781 TTCACCTTACCCAAATTTGCGCGCTAATAGGCTGAGGATTAATGATGATGATGATG 840
Db 781 TTCACCTTACCCAAATTTGCGCGCTAATAGGCTGAGGATTAATGATGATGATGATG 840
QY 841 TTTCTTATGAAGCCCAAGCAGATTTAATAAACTTGAGAAAAAGTTTAACTCTA 900
Db 841 TTTCTTATGAAGCCCAAGCAGATTTAATAAACTTGAGAAAAAGTTTAACTCTA 900
QY 901 GAAGACGCTAGCAATTAAGGCTGCTTTGCTTTGCTCCACACTGTGAGCCATATCAGACC 960
Db 901 GAAGACGCTAGCAATTAAGGCTGCTTTGCTTTGCTCCACACTGTGAGCCATATCAGACC 960
QY 961 GGTGATGTGTCTTACCCAAACATCCTCGGAAATGTTAAAGCTTGGGGTAAATTCG 1020
Db 961 GGTGATGTGTCTTACCCAAACATCCTCGGAAATGTTAAAGCTTGGGGTAAATTCG 1020
QY 1021 ATACCCACATATGATGGTAAACCTTCAATATGAGGCTATTTTTCACCTCAATCTTAAAG 1080
Db 1021 ATACCCACATATGATGGTAAACCTTCAATATGAGGCTATTTTTCACCTCAATCTTAAAG 1080
QY 1081 CAATGCTATGCTTGTAAAGAACTGTGCAATTTTGTGCAAGTAAATG 1140
|||||

Db 1081 CAATGCTATGCTTGTAAAGAAATGGAACCTGTGCAATTTTGTGCCAAGTAAATG 1140
QY 1141 GGTGATGCTGAACGACCGCCCGAGAGCCCTTGAATGGGTGCTAAATTAAGAGCT 1200
Db 1141 GGTGATGCTGAACGACCGCCCGAGAGCCCTTGAATGGGTGCTAAATTAAGAGCT 1200
QY 1201 CATGTTCAGAGAGAACCAACACAGCTGATTAATTTATGATGCTTTCCTCAATCTAT 1260
Db 1201 CATGTTCAGAGAGAACCAACACAGCTGATTAATTTATGATGCTTTCCTCAATCTAT 1260
QY 1261 TTTGCTTCCCATGATGCTTGTGTCATTTAGTTTAAATGATGATGATGATGATGATG 1320
Db 1261 TTTGCTTCCCATGATGCTTGTGTCATTTAGTTTAAATGATGATGATGATGATGATG 1320
QY 1321 GTCTACTTGTATGCTTGTGATGCTTGTGATGCTGAGAGATCTTATATCCATGCTATATG 1380
Db 1321 GTCTACTTGTATGCTTGTGATGCTTGTGATGCTGAGAGATCTTATATCCATGCTATATG 1380
QY 1381 CGTAGTGAAGGCTGTTAAGGCTGTTAGTCAATGCTGATGATTAACCTATTTCTGCG 1440
Db 1381 CGTAGTGAAGGCTGTTAAGGCTGTTAGTCAATGCTGATGATTAACCTATTTCTGCG 1440
QY 1441 AATCAATTTGCGCAACGATATGCTTAAAGAAATCGCTGAATACAAACATTTGAAGTATG 1500
Db 1441 AATCAATTTGCGCAACGATATGCTTAAAGAAATCGCTGAATACAAACATTTGAAGTATG 1500
QY 1501 ACTGATATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db 1501 ACTGATATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 ATGGAATATGTTTCTGCGGATCCATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
Db 1561 ATGGAATATGTTTCTGCGGATCCATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
QY 1621 ATTAGTGAATGAATGAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 ATTAGTGAATGAATGAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 TCGATGTTGAAAAACATAGATTAATTTTAG 1713
Db 1681 TCGATGTTGAAAAACATAGATTAATTTTAG 1713

RESULT 6
AR153441 1713 bp DNA Linear PAT 08-Aug-2001
LOCUS AR153441
DEFINITION Sequence 7 from patent US 6235515.
ACCESSION AR153441
VERSION AR153441.1 GI:15120973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolm, Robin, G. Charlesde, Queteleville, Claudianos, C., Smyth, K. A., Boyce, F. Mark, Oakeshott, J. Graham, and Brownlie, J. Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 7 22-MAY-2001;
FEATURES Location/Qualifiers
source 1..1713
BASE COUNT 516 a 305 c 370 g 522 t
ORIGIN
Query Match 99.3%; Score 1701.8; DB 6; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATGAATTTCAAGCTTGTGATGAGAAATTAATAATGAAATGCAATTTGAAAT 60
Db 1 ATGAATTTCAAGCTTGTGATGAGAAATTAATAATGAAATGCAATTTGAAAT 60
|||||

QY 61 AAGTTTAACTATCGTTTAACTACCAATGAACGGGTGAGTGAAGTGAATATGCG 120
 |||||
 Db 61 AAGTTTAACTATCGTTTAACTACCAATGAACGGGTGAGTGAAGTGAATATGCG 120
 QY 121 AAAGTGAAGGCGTTTAAAGCTTTAACTGTCAGATGATTCCTACAGTTTGGAGGT 180
 |||||
 Db 121 AAAGTGAAGGCGTTTAAAGCTTTAACTGTCAGATGATTCCTACAGTTTGGAGGT 180
 QY 181 ATACCGTACGCGCCCAACCGCCGAGTGGGTGAGTGAATTAAGCACCACGACCAACA 240
 |||||
 Db 181 ATACCGTACGCGCCCAACCGCCGAGTGGGTGAGTGAATTAAGCACCACGACCAACA 240
 QY 241 CCTGGAGTGTGCGCGGATTTGTCATCATTAAGATGATGATGATGATGATGATGAT 300
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 Db 241 CCTGGAGTGTGCGCGGATTTGTCATCATTAAGATGATGATGATGATGATGATGAT 300
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 organophosphate resistance, complete cds.
 ACCESSION
 U56636
 VERSION
 U56636.1
 KEYWORDS
 GI:1336079
 ORGANISM
 Lucilia cuprina.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Oestroidea; Calliphoridae; Lucilia.
 TITLE
 Isolation of alpha cluster esterase genes associated with
 organophosphate resistance in *Lucilia cuprina*
 JOURNAL
 Insect Mol. Biol. 5 (3), 211-216 (1996)
 MEDLINE
 96392952
 PUBMED
 8799740
 REFERENCE
 2 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Russell,R.J. and Oakeshott,J.G.
 cDNA cloning, baculovirus-expression and kinetic properties of the
 esterase, E3, involved in organophosphorus resistance in *Lucilia*
 cuprina
 JOURNAL
 Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
 MEDLINE
 97215578
 PUBMED
 9061925
 REFERENCE
 3 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Ollis,D.L., Cheah,E., Russell,R.J. and
 Oakeshott,J.G.
 A single amino acid substitution converts a carboxylesterase to an
 organophosphorus hydrolase and confers insecticide resistance on a

JOURNAL blowfly
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
 PUBMED 97352821
 9207114
 4 (bases 1 to 2240)
 Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
 Two different amino acid substitutions in the *alpha*-esterase, E3,
 confer alternative types of organophosphorus insecticide resistance
 in the sheep blowfly
 JOURNAL Unpublished
 5 (bases 1 to 2240)
 Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
 Direct Submission
 Submitted (24-Apr-1996) Richard D. Newcomb, Molecular Genetics,
 HortResearch, Private Bag 92 169, Auckland, New Zealand
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DEFINITION	Sequence 2 from patent US 5843758.		
ACCESSION	AR062838		
VERSION	AR062838.1	GI:5990529	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1713)		
AUTHORS	Russell,R.Joyce., Newcomb,R.David., Robin,G.Charlesde. Quetteville.,		
	Boyce,T.Mark., Campbell,P.Malcolm., Parker,A.Gerard.,		
	Oakesholt,J.Graham. and Smyth,K.-A.		
TITLE	Enzyme based bioremediation		
JOURNAL	Patent: US 5843758-A 2 01-DEC-1998;		
FEATURES	Location/Qualifiers		
source	1..1713		
BASE COUNT	506 a 299 c 363 g 515 t	30 others	
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ACCESSION AF133341
VERSION AF133341.1 GI:4768932
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SOURCE Musca domestica.
ORGANISM Musca domestica.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidae; Muscidae; Musca.
REFERENCE 1 (bases 1 to 2160)
AUTHORS Claudianos,C., Russell,R.J. and Oakeshott,J.G.
TITLE The same amino acid substitution in orthologous esterases confers
JOURNAL organophosphate resistance on the house fly and a blowfly
MEDLINE Insect Biochem. Mol. Biol. 29 (8), 675-686 (1999)
PUBMED 99381228
AUTHORS 2 (bases 1 to 2160)
TITLE Claudianos,C., Russell,R.J. and Oakeshott,J.G.
JOURNAL Direct Submission
PUBMED 10451921
AUTHORS Submitted (07-MAR-1999) Entomology, CSIRO, Clunies Ross, Canberra,
JOURNAL ACT 2601, Australia
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polya_signal 2115..2120
BASE COUNT 661 a 440 c 466 g 593 t
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Best Local Similarity 73.5%; Pred. No. 8, 2e-211;
Matches 1258; Conservative 0; Mismatches 454; Indels 0; Gaps 0;
QY 1 ATGAATTTCAACGTTAGTTTGATGAGAAATTAATGAAGATTAATGATTAAT 60
Db 217 ATGAATTTCAAGTTAGTCAATGAGAGGCTCTCGTGAACCTCAATGATGTCAT 276
QY 61 AAGTTTAACTATACGTTTACTACCAATGAACGGTGTGACTGAACCTGAATATGGC 120
Db 277 AATACACAACTACCGCTGTGACCAATGAACCCAAATACGATACGAAATATGA 336
QY 121 AAAGTAAAGCGTTAAAGCTTTACTGTACGATGATTCCTACTAGTTTGAAGGT 180
Db 337 CAATTTAAGGGTGTAAAGCAATGACCGCTACGATGATTTTCTACTACGTTGAGAGT 396
QY 181 ATACCGTACGCCCAACGCCACAGTGGTGAAGCTGAGATTTAAAGCACCCACGACACA 240
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QY 241 CCGTGGATGGTGGCGGATGTTGCAATCATTAAGTATAGTCAAGTTCATTTT 300
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QY 301 ATTAAGGGCAAAAGTGTGCTCAGAGAGATGTTCTATACCTAAGTCTATACGAATAT 360
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Db 637 GCGCAAGCAATTCGTAATCTGTTTGGTCCGACTACTTTATGAAGAAACCCGAGGCTTTG 696
QY 481 ATTAACTATACATATGCTTTGGAGCTCTAGGTTTCTTAAGTTTAAATTCAGAGACCTT 540
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QY 541 AATGCGCGGTATAGCGCGCTTAAGATCAAGTCAATGCGCTTGGCTGATTAATAAT 600
Db 757 AATGTCGCCGCAAGCTGTGCTCAAGATCAAGTATGCTTGAAGTGGTCAAGAGT 816
QY 601 AATTGCCCAACTTGGTGGCAATCCGATATATTACAGTCTTGGTGAAGATGGCGGT 660
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QY	661	GTGCGCCCTACCCACATGATGATTAACGGAACAACGCGGGCTTTCATCGTGGT	720
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Db	937	ATCATGATGTCGGGTAAATTCATGATGCTCATGGGCGCTCAAGATGCGCAAGTGTGGCG	996
QY	781	TTTCACTTACCCAAATTTGGCCGGCTATTAAGGGTGGAGGATATGATTAAGATGTTTGGAA	840
Db	997	CTCACCACTGGCCAAACGCTGTGGCTTAAGGGAGAGACAAAGAAAAGATATCCTGGAA	1056
QY	841	TTTTCTATGAAACCCACAGCACAGATATTAATAAAAACTTGAGGAAAAGTTTTAACTCTA	900
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QY	901	GAAAGCGCTCAAAATTAAGTCATGTTCTTTTGGTCCCACGTGTGAGCCATATCAGACC	960
Db	1117	GAAAGAAATGCAAAATTAAGTCATGTTCTTTTGGACCCACCTGTGAACCATACAGACA	1176
QY	961	GCATATGCTCTTACCCAAACATCCTCGGAAATGGTTAAACATGCTGGGGTAAATTCG	1020
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QY	1021	ATACCCATATGATGGGTAAACACTTCATATAGAGGTCTATTTTTCATTTCAATCTTAAG	1080
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QY	1081	CAAAATGCTATGCTGTGTTAAGAAATTTGGAACCTGTGTCATTTTGTGCGCAAGGAATG	1140
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QY	1201	CATGTTACAGAAACACCAACAGCTGATTTTATGAGATCTTTGCTTCACATCTAT	1260
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QY	1621	ATTATGATGAATTAAGAAATGATGATGTGCTGAAATGATGAATTAACATGAGAG	1680
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Db	1897	AGTATATTCATTAAGAAAGGATATGTTTAA 1928	

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RESULT 10
LOCUS AF139082 2175 bp mRNA linear INV 20-OCT-2000
DEFINITION Haematobia irritans irritans alpha E7 esterase (ae7) mRNA, complete cds.
ACCESSION AF139082
VERSION AF139082.1 GI:6502938
KEYWORDS
ORGANISM
SOURCE
Haematobia irritans irritans.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Haematobia.
REFERENCE
AUTHORS Guerrero,F.D.
TITLE Cloning of a horn fly cDNA, HialphaE7, encoding an esterase whose transcript concentration is elevated in diazinon-resistant flies
JOURNAL Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)
MEDLINE 20445807
PubMed 10986298
FEATURES
source 2 (bases 1 to 2175)
Guerrero,F.D.
Direct Submission
Submitted (30-MAR-1999) USDA-ARS, Knippling-Bushland U.S. Livestock Insects Research Laboratory, 2700 Fredericksburg Rd., Kerrville, TX 78028, USA
Location/Qualifiers
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/strain="Camp Cooley 4/97"
/sub_species="irritans"
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/clone="HP41CC"
/note="pyrethroid and diazinon-resistant"
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BASE COUNT 690 a 365 c 435 g 605 t
ORIGIN
Query Match 56.0%; Score 959.4; DB 3; Length 2175;
Best Local Similarity 72.5%; Pred. No. 6.3e-205;
Matches 1242; Conservative 0; Mismatches 471; Indels 0; Gaps 0;

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OY 181 ATACCGTACCCCAACCGCCAGTGGAGCTGAGATTCTTAAGCACCAGCCAGCAGACA 240
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DB 462 ATACCATATGTCACCAACCTCTGCTGGGAGATTAAAGATTAGGCTCCACACAGCTCGTC 521
OY 241 CCTCGGATGCTGCGCGATGTTGCAATCAATAAAGATCAGTCAAGTGTGATTTT 300
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DB 522 CCTTGGATGAGTAAAGATGTTGTCATGCTGCCCTCCGTTGGTTCAACAGATTTCC 581
OY 301 ATACGGGCAAAAGTGTGGCTCAGAGGATTTCTATACCTAGTGTCTATACGAATAT 360
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DB 582 ATATCCGGCACTCAAGTGTGGAGATTGTTATATTGAATGCTAAACGAATAT 641
OY 361 CTAAATCCCGAACTAAACGTCCTTTTATATACATACATGCTGTGTTTATATAC 420
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DB 642 TTAATATGATACAAAGCTCCGTTTGTCTTCATGCTGTGTTGTTTCAATTTCT 701
OY 421 GGTGAATATCATGCTGATATGTTGCTCTGATTTATTTCAATTAAGATGCTGTG 480
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DB 702 GGGGAAGCTAATAGAAACATTAATGCGCGATTAATTTCAATAAGAGACGTTGCTTC 761
OY 481 ATTAACATACATATGTTTGGAGCTAGTCTTCTAAGTTTAATTCAGAAAGCTT 540
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DB 762 ATACATGCTCAATATGCTTGGGCTGTAGTTTCTAAGTTTAATTCGAAATCTC 821
OY 541 AATGTCCTCGGTAAATGCGGCTTAAAGATCAAGTATGCGCTTGGTGGATTAAAT 600
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DB 822 AATGATCTGCTAATGCTGGCTTAAAGATCAAGTATGCGCTTGGGATGATTAAAC 881
OY 601 AATGGGCCAATGTTGGTGGCAATCCCGATTAATATATACAGTCTTGGTGAAGTGGCG 660
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DB 882 AATGTGCGAGCTTGTGGCGATCCCGATGATTAATGCTAATTTGGCAGAGTGTGGA 941
OY 661 GCTGCTTACCACACTACATGATGTTAACCAGCAAACTCGGCTTGTTCATGCTGG 720
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DB 942 GCGGCTCCACGAGCTATATGATGATTAAGAGAAATTAATGACAGAGTGTATGAT 1001
OY 721 ATACTAATGCTGGGATATGCTATTTGCTCATTTGGCTAATACCAATGTCACATGCTGC 780
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DB 1002 GTTTGATGCTGGAACCTGATGCTATGCTATGAGGCCATACCAATGTCACATGCTGCT 1061
OY 781 TTACCTTACCCAAATTTGCGGCTTAAAGGATGAGATTAATGATGATTTTGGAA 840
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DB 1062 TATACATTTGCCAAAGATTTGTTTCAAGAGAAATTAATGACAGAGTGTATGAT 1121
OY 841 TTTTATTAAGAACCAAGCCACAGATTTAATAAATTGAGCAAAAGTTTAACTCTA 900
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OY 901 GAAGAGCGTACAATAAGGTCATGTTTCTTGGTCCCACTGTTGAGGCATATCAGACC 960
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DB 1182 GAGGAACCTTCTGATGATGATTTGCTTGGTCCACACAGAACCTTATGAAACA 1241
OY 961 GCTGATTTGCTTACCAACATCCTCGGAAATGCTTAAACTGCTTGGGCTAATTC 1020
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OY 1021 ATACCCACTATGATGGGTACACTTCAATGAGGCTATTTTACCTCAATCTTAAAG 1080
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DB 1302 ATACCCACTTATATAGGGAATCCTCGATATGAGGTTTATTTAATTCGCTTGGAAA 1361
OY 1081 CAAATGCGCTATGCTTAAAGATTTGAAACTTGTGCAATTTTGTGCAAGTAAATTTG 1140
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DB 1362 CAAATCTCTCATATTAATTAAGAGTTGGAACATTTGAATGTATGATCTGTGAGTTG 1421
OY 1141 GCTGATGCTGAACGACGCGCCAGAGACCTTGAATGGGTGCTTAAATTTAAAGGCT 1200
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DB 1422 GATGTTGAAGATCGAGTTCTCCAGAAATCTTGAATTTGATGATCTTAAAGAAATTTG 1481
OY 1201 CATGTTACAGGAAGACCAACACACTGATTAATTTATGATCTTGTCTTCACATCTAT 1260
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DB 1482 TATGATGCTGAGAGACACCAACATTTGAAGTTTACAGAAATTTGCTCAAGATTTTAC 1541

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OY 1261 TTCTGTTTCCCATGCAATGCTTTGTTGCAATTAATGCTTTCACACCTCCGTACACC 1320
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DB 1542 TTTTGGATATCAATGATGCTTTTCTGCAATTAATGATATATGCTGCGCTCGCCC 1601
OY 1321 GCTCACTTATGATGCTTCGACTTCGATTTGGAGATCTTATCAATCCCTATGATTATG 1380
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DB 1602 ATCTACCTATATGCTTTGATTTGATTCGAAAGATTTATTAATCCCTATGCAATTAAG 1661
OY 1381 GGTATGAGACGTGCTGTTAAGGCTGTTAGTCAATGCTGATGAATTAACCTATTTCTTGG 1440
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DB 1662 CGTTATGAGACGTGCTGTTAAGGCGCTAGTCAACACGATGAATTAATCTATCTTCTGG 1721
OY 1441 AATCAATTTGGCCAAAGCTATGCTTAAAGATGCGCGATATCAAAACATTAAGTACGTATG 1500
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OY 1501 ACTGATATATGATATGCAATTTGGCACCAGTGTATCTTATAGCAATGAATGAAGT 1560
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DB 1782 ATAGCATTTTGGACACAAATTTGCTACGCGCAATCAATATAGTCCGAAATTAATGGC 1841
OY 1561 ATGGAATATGTTTCTCGGATCCATTAAGAAATCCGATGAAGTATCAAGTGTGTAAT 1620
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DB 1842 ATGGAATATACACATGAGATTCATTGAAATAATCGATGAGGTCTCAAAATGATGAAC 1901
OY 1621 ATTAGTATGATGAATTAAGATGATGCTGCTGAATGATTAAGATTAACATGAAGGAG 1680
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DB 1902 ATAGGCGATGATGATGAAGTTATGATTTGATTTGCCAGAAATGGAATAATTTGAAGATGCGAG 1961
OY 1681 TCGATGTTGAAAACATAGAGATTTATTTTAG 1713
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DB 1962 AGTGTTCATTAAGAACGCGGAAATGTTTAG 1994
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RESULT 11
AR153445
LOCUS AR153445 1710 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 14 from patent US 6235515.
ACCESSION AR153445
VERSION AR153445.1 GI:15120977
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1710)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Roblin,G.Charlesde,Quetleville., Claudianos,C., Smyth,K.-A.,
Boyce,T.Mark., Oakeshort,J.Graham, and Brownlie,J.Colin.
Malariaion carboxylesterase
Patent: US 6235515-A 14 22-MAY-2001;
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BASE COUNT 498 a 369 c 394 g 449 t
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Query Match 55.8%; Score 955; DB 6; Length 1710;
Best Local Similarity 73.3%; Pred. No. 6.2e-204;
Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;
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OY 104 CTGAATGATTAATGCAAGATGAAGCGCTTAAACGTTTAATGCTGTACGATGATTCCT 163
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DB 104 TCGATATGATTAATGCAAAATTAAGGCTGTTAAACGAATGACGCTTACGATGATTCCT 163
OY 164 ACTACAGTTTGGAGGTATACCGTACGCCCAACGCCACGCTGAGTGAAGTGAATTAAG 223
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RESULT 12
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 DEFINITION
 Drosophila melanogaster GH13950 full length cDNA.
 AY051473
 VERSION
 AY051473.1 GI:15291256
 KEYWORDS
 P11.CDNA.
 SOURCE
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 2017)
 AUTHORS
 Stapleton,M., Broksstein,P., Hong,L., Abdayani,A., Carlson,J.,
 Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,
 Gonzalez,M., Guarin,H., Li,P., Liao,G., Miranda,A., Mungall,C.J.,
 Nunoo,J., Paclebo,J., Paragas,V., Park,S., Phoumanavong,S., Wan,K.,
 Yu,C., Lewis,S.E., Rubin,G.M. and Celisner,S.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 COMMENT
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720
 This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a polyA tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unsplined precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our web site
 (<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.
 location/Qualifiers
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Matches 1075; Conservative 0; Mismatches 636; Indels 3; Gaps 1;

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VERSION AY121675.1 GI:21464397
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SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2660)
Stapleton, M., Brokstein, P., Hong, L., Abmayyan, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
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Patel, S., Phouaneavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M.,
and Celisner, S.
REFERENCE
AUTHORS
TITLE Direct Submission
JOURNALS Submitted (13-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
COMMENT
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unsplined precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu.
FEATURES
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Best Local Similarity 53.9%; Pred. No. 1.4e-74;
Matches 877; Conservative 0; Mismatches 729; Indels 21; Gaps 4;
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RESULT 14
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DEFINITION Drosophila melanogaster alpha esterase (ae7); gene, partial cds.
ACCESSION U51050
VERSION U51050.1 GI:1272313
KEYWORDS
SOURCE
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 2820)
Robln,C., Medveczky,K.M., Russell,R.J. and Oakeshott,J.G.
Duplication and Divergence of the genes of the alpha-esterase
cluster of Drosophila melanogaster
J. Mol. Evol. (1996) In press
2 (bases 1 to 2820)
Robln,C.
Direct Submission
Submitted (11-MAR-1996) Charles Robln, Biotechnology, CSIRO div.
Entomology, Cluntes Ross Street, Canberra, ACT 2601, Australia
LOCATION/Qualifiers
1. 2820
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BASE COUNT 777 a 609 c 657 g 776 t 1 others
ORIGIN
Query Match 22.0%; Score 377; DB 3; Length 2820;
Best Local Similarity 54.7%; Pred. No. 3.2e-74;
Matches 1056; Conservative 0; Mismatches 610; Indels 263; Gaps 5;
QY 46 AATGCAATGAAATAAGTTTAACTATCTTTAACTACCAATGAAGGTTGAGCT 105
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QY 1343 TGTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1402
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QY 1403 GTGTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1462
Db 2510 GTGTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2569
QY 1463 CTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1522
Db 2570 CTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2629
QY 1523 CTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1582
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QY 1643 TTGATGTCCTGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1702
Db 2750 TGTATGTCCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2809
QY 1703 ATTTATTTT 1711
Db 2810 ATTTATTTT 2818

RESULT 15
AC015272/c 57335 bp DNA linear HTG 16-NOV-1999
LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
DEFINITION
AC015272
VERSION AC015272.1 GI:6436063
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidae; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 57335)
AUTHORS Adams,M. and Venter,J.C.
TITLES Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
JOURNAL Rockville, MD, USA
COMMENT This sequence was identified as CDL:10213452 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
source 1..57335
location/Qualifiers
BASE COUNT 17106 a 11816 c 11532 g 16881 t
ORIGIN
Query Match 21.7%; Score 372.2; DB 2; Length 57335;
Best Local Similarity 54.6%; Pred. No. 2.8e-73;
Matches 1053; Conservative 0; Mismatches 613; Indels 263; Gaps 5;

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QY 166 TACAGTTTGAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 225
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QY 361 -----CTAATCCGGAACATAAGC 380
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QY 510 -----AGTTTTCTTAATTAATTCAGAAAGACCTTAATGCGCGGAATGCGCGGC 562
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QY 920 TCAATGTTTCTTTGCTCCACTGTGACATATCAGACCGGTGATGCTTTACCCA 979
Db 35461 TAAATGTTTCTTTGCTCCACTGTGACATATCAGACCGGTGATGCTTTACCCA 35402
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QY 1040 ACATTTATATGAGGCTCT----- 1058
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QY 1059 -----ATTTTCACTTCAATTTCTTAAGCAATGCTATGCTGT 1097
Db 35281 TTTTCACTTCAATTAATTAATTTATTTTACAGAGGTAAGCTTAATGCGGAGTGTCT 35222
QY 1098 TTAGGAATTTGAAACTTGTGTAATTTTGTGCAAGTGAATGGCTGATGCTGAAGCCAC 1157
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QY 1158 CGCCCGACAGACTTGAAGAAATGCTGCTAAATTAAGAAAGGCTCATGTTACAGAGAAAC 1217
Db 35161 TAAAGAAAGAACTGATGCTGCTGACAGATTCGAGATGTTTCATGCTGCTGCTGCTGCT 35102
QY 1218 ACCAAGACTGATTAATTTTATGAT----- 1242
Db 35101 AAGCAAGCCGAGATTAATTAATGATGATGATGATGCTGCTCAATTAAGTCTTACATATCAT 35042
QY 1243 -----CTTGTCTCAGATCATTTTCTGTGTTCCCATGATGCTT 1282

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Db 35041 AACCTGTAATTTATTTCAAGCTCTGTTGCTGATTAATTAATTAATTAATTAATTAAT 1402
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Db 34981 TGTTCATTAAGCTTTCAATCAACACCTCCGCTACCGGCTACCTGATGCTGACT 13422
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QY 1403 GTGTGATGCTGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1462
Db 34861 GGTTCAGCCATGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14622
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Db 34621 TCGATGCTGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 17022
QY 1703 ATTTATTTT 1711
Db 34561 ATTTATTTT 34553

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Search completed: April 11, 2003, 06:03:00
 Job time : 3045.03 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model.

Run on: April 10, 2003, 22:58:21 ; Search time 246.905 Seconds

15624.094 Million cell updates/sec

Title: US-09-776-910-3

Sequence: 1 atgaattccaacgttagtt.....aacatagagatttatttag 1713

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370

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Minimum DB seq length: 0
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Maximum DB seq length: 20000000000

Pre-processing:	Minimum Match	0%
Post-processing:	Minimum Match	0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1701.8	99.3	1713	16	AA091561	Op-sensitive ester
2	1701.8	99.3	1713	18	AA068596	Lc-alpha-E7 malath
3	1681	98.1	1713	16	AA091566	Op-resistant ester
4	1677.8	97.9	1713	16	AA091564	Op-resistant ester
5	1677.8	97.9	1713	16	AA091563	Op-resistant ester
6	1676.2	97.9	1713	16	AA091565	Op-resistant ester
7	1674.6	97.8	1713	16	AA091562	Op-resistant ester
8	955	55.8	1710	18	AA068597	Op-alpha-E7 gene.
9	680.4	39.7	2001	23	AB102067	Drosophila melanog

10	381.8	22.3	1704	23	ABLO2081	Drosophila melanog
11	372.2	21.7	6175	23	ABLO2066	Drosophila melanog
12	368.2	21.5	1665	23	ABLO2039	Drosophila melanog
13	365.4	21.3	1792	23	ABLO4689	Drosophila melanog
14	323.6	18.9	1593	23	ABLO2103	Drosophila melanog
15	323	18.9	1863	23	ABLO1859	Drosophila melanog
16	311.4	18.2	1761	23	ABLO1033	Drosophila melanog
17	305.8	17.9	1719	23	ABLO2101	Drosophila melanog
18	304.6	17.8	1878	23	ABLO1947	Drosophila melanog
19	300.4	17.5	3856	23	ABLO10332	Drosophila melanog
20	300.4	17.5	67279	23	ABLO7668	Drosophila melanog
21	270	15.8	1809	24	ABAO90480	Drosophila cell cy
22	238.2	13.9	4320	23	ABLO4688	Drosophila melanog
23	229.6	13.4	1727	23	ABLO1943	Drosophila melanog
24	228.6	13.3	4242	23	ABLO2102	Drosophila melanog
25	224	13.1	5006	23	ABLO2080	Drosophila melanog
26	198.8	11.6	4294	23	ABLO2038	Drosophila melanog
27	198.8	11.4	4294	23	ABLO2100	Drosophila melanog
28	196	11.4	1987	19	AAV00762	C. fells esterase,
29	196	11.3	1987	19	AAV00763	C. fells esterase,
30	194.4	11.3	1652	23	ABLO1945	Drosophila melanog
31	193.2	11.3	2613	23	ABLO9064	Drosophila melanog
32	191.8	11.2	5130	23	ABLO1858	Drosophila melanog
33	185.8	10.8	1590	19	AAV00764	C. fells esterase,
34	185.8	10.8	1590	19	AAV00765	C. fells esterase,
35	178	10.4	1540	19	AAV00766	C. fells esterase,
36	178	10.4	1584	19	AAV00757	C. fells esterase,
37	178	10.4	2007	19	AAV00754	C. fells esterase,
38	178	10.4	2007	19	AAV00755	C. fells esterase,
39	178	10.4	2007	22	AAV00752	Ctenocephalides fel
40	167.6	9.8	4288	23	ABLO1942	Drosophila melanog
41	164.2	9.6	1783	23	ABLO2029	Drosophila melanog
42	148	8.6	4283	23	ABLO1946	Drosophila melanog
43	143.8	8.4	1488	19	AAV00767	C. fells esterase
44	143.8	8.4	1590	19	AAV00743	C. fells esterase,
45	143.8	8.4	1590	22	AAV02169	Ctenocephalides fel

ALIGNMENTS

RESULT 1	
AAQ91561	
ID	AAQ91561 standard; cDNA; 1713 BP.
XX	
AC	AAQ91561;
XX	
DT	22-DEC-1995 (first entry)
XX	
DE	OP-sensitive esterase E3 Lc743 clone.
XX	
KW	Esterase; E3; bioremediation; organophosphate; car
KW	insecticide; pesticide; water decontamination; mea
KW	ss.
XX	
OS	Lucilia cuprina.
XX	
FH	Key
FT	1.1713
CDS	
FT	/*tag= a
XX	
PN	W09519440-A1.
XX	
PD	20-JUL-1995.
XX	
PF	13-JAN-1995; 95MO-AU00016.
XX	
PR	13-JAN-1994; 94AU-0003347.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PI	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG,
PI	Parker AG, Robin GC, Russell RJ, Smyth K;

XX WP1: 1995-263870/34.
 DR P-PSDB: AAR78142.
 XX
 PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meal etc.
 XX
 PS Claim 5; Page 12-17; 38pp; English.
 CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA
 CC library was amplified using cluster-specific esterase primers.
 CC Isolated clone LC743, a probable full-length cDNA, was expressed
 CC using a baculovirus vector in insect cells and shown to encode
 CC an OP-susceptible E3 esterase, useful in bioremediation.
 XX
 SO Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other:
 Query Match 99.3%; Score 1701.8; DB 16; Length 1713;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 1 ATGAAATTCACGCTAGTTGATGAGAAATTAATGAAGATTAATGATGAAAT 60
 1 ATGAAATTCACGCTAGTTGATGAGAAATTAATGAAGATTAATGATGAAAT 60
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 1681 TCGATGTTGAAAAAATAGATGATTTATTTAG 1713
 1681 TCGATGTTGAAAAAATAGATGATTTATTTAG 1713
 RESULT 2
 ID AAT68596 standard; DNA: 1713 BP.
 XX AAT68596:
 AC AAT68596:
 XX
 DT 08-AUG-1997 (first entry)

XX LC-alpha-E7 malathion susceptible esterase clone LC743.
 XX Malathion carboxylesterase; organophosphate; insecticide;
 KW pesticide; remediation; bioremediation; decontamination; esterase;
 KW ss.
 XX Lucilia cuprina.
 XX
 FH Key Location/Qualifiers
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 FT primer_bind 1686..1713
 FT /*tag- b
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 FT mutation 1344
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 XX PD 29-MAY-1997.
 XX PE 22-NOV-1996; 96WO-AU00746.
 XX PR 23-NOV-1995; 95AU-0006751.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;
 PI Newcomb RD, Oakshott JG, Robin GC, Russell RJ, Smyth K;
 XX WPI: 1997-298113/27.
 DR P-PSDB; AAM17765.
 XX
 PT DNA encoding enzyme that degrades organophosphate pesticides-
 PT useful for decontamination of soil, water, food etc
 XX
 PS Claim 4; Fig 1; 52pp; English.
 XX
 CC DNA molecule LC743 (AAT68596) codes for an esterase (AAM17765) from
 CC a malathion susceptible strain of Lucilia cuprina. Comparison
 CC with a consensus sequence from derived from clones of the
 CC LC-alpha-E7 resistant allele (see also AAM17768) indicated only one
 CC replacement site difference, a Trp to Leu substitution at amino
 CC acid position 251 (nucleotide position 752). This mutation is an
 CC excellent candidate for the malathion resistance mutation. The
 CC resistant enzyme acts as a malathion carboxylesterase and can be
 CC formulated for use in degrading environmental carboxylester or
 CC dimethyl general organophosphates.
 XX
 SO Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;
 Query Match 99.3%; Score 1701.8; DB 18; Length 1713;
 Best Local Similarity 99.6%; Pred. No. 0;

Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ATGAATTCACACCTTACTGTTATGAGAAATTTAAATGCAATTAATTCATTAAT 60
 DB 1 ATGAATTCACACCTTACTGTTATGAGAAATTTAAATGCAATTAATTCATTAAT 60
 QY 61 AAGTTTAACTATACCTTAACTACCAATGAACCGGTGATGAGCAATGATATGAC 120
 DB 61 AAGTTTAACTATACCTTAACTACCAATGAACCGGTGATGAGCAATGATATGAC 120
 QY 121 AAGTGAAGCGCTTAAACGTTAACTGTAGATGATCTTACTACAGTTTGAAGGT 180
 DB 121 AAGTGAAGCGCTTAAACGTTAACTGTAGATGATCTTACTACAGTTTGAAGGT 180
 QY 181 ATACCGTACGCCCAACCGCCAGTGGGTAGCTGAATTTAAAGCACCAGGACCAACA 240
 DB 181 ATACCGTACGCCCAACCGCCAGTGGGTAGCTGAATTTAAAGCACCAGGACCAACA 240
 QY 241 CCTGGATGCTGTCGCGATTTGCAATCATATAAGATTAAGTCAAGTTGATTTT 300
 DB 241 CCTGGATGCTGTCGCGATTTGCAATCATATAAGATTAAGTCAAGTTGATTTT 300
 QY 301 ATACGGGCAAAAGTGTGCTCAGAGATGTCTATACCTAAGTGTCTATACGAATAT 360
 DB 301 ATACGGGCAAAAGTGTGCTCAGAGATGTCTATACCTAAGTGTCTATACGAATAT 360
 QY 361 CTAAATCCGGAACATTAACGTCGCTTATGATATCATACATGAGTGGTTTATATC 420
 DB 361 CTAAATCCGGAACATTAACGTCGCTTATGATATCATACATGAGTGGTTTATATC 420
 QY 421 GGTGAAATCATGCGATATGATATGCTGATATTTTCATTAAAGAGATGCTGTG 480
 DB 421 GGTGAAATCATGCGATATGATATGCTGATATTTTCATTAAAGAGATGCTGTG 480
 QY 481 ATTAACATACATATGCTTGGAGCTAGCTTTTCTAAGTTTAAATTCAGACACTT 540
 DB 481 ATTAACATACATATGCTTGGAGCTAGCTTTTCTAAGTTTAAATTCAGACACTT 540
 QY 541 AATGCCCCGGTAATGCCGCTTAAGATCAAGCATGCGTTCGTTGATTAATAT 600
 DB 541 AATGCCCCGGTAATGCCGCTTAAGATCAAGCATGCGTTCGTTGATTAATAT 600
 QY 601 AATTGCGCAACTTGTGTCGATCCGATATATATACAGTCTTGTGGAAGTCCGGT 660
 DB 601 AATTGCGCAACTTGTGTCGATCCGATATATATACAGTCTTGTGGAAGTCCGGT 660
 QY 661 GCTGCTCTACCCACTACATGATGTTAAACGAACCAACTCGCGTCTTCCATGCTGT 720
 DB 661 GCTGCTCTACCCACTACATGATGTTAAACGAACCAACTCGCGTCTTCCATGCTGT 720
 QY 721 ATACTAATGCTGGGTAATGCTATTTGCTCATTTGCTTAATACCATGTCACATGTCGC 780
 DB 721 ATACTAATGCTGGGTAATGCTATTTGCTCATTTGCTTAATACCATGTCACATGTCGC 780
 QY 781 TTCACCTTAGCCAAATTTGCGCGCTATTAAGGCTGAGATTAAGATATTTTGA 840
 DB 781 TTCACCTTAGCCAAATTTGCGCGCTATTAAGGCTGAGATTAAGATATTTTGA 840
 QY 841 TTTCTTATGAAGCCAGACACAGATTTAATTAACCTTGAGAAAAAGTTTAACTCTA 900
 DB 841 TTTCTTATGAAGCCAGACACAGATTTAATTAACCTTGAGAAAAAGTTTAACTCTA 900
 QY 901 GAAGAGCGTACAAATTAAGTCAATGTTTCTTTGCTCCACAGTGTGAGCCATATAGAC 960
 DB 901 GAAGAGCGTACAAATTAAGTCAATGTTTCTTTGCTCCACAGTGTGAGCCATATAGAC 960
 QY 961 GCTGATTTGCTTACCCAAACATCTCGGGAAGATTTAAACCTGTTGGGTAATTCG 1020
 DB 961 GCTGATTTGCTTACCCAAACATCTCGGGAAGATTTAAACCTGTTGGGTAATTCG 1020
 QY 1021 ATACCACTATGATGAGTGAACACTCATATGAGGCTATTTTCTACCTCAATCTTAAG 1080
 DB 1021 ATACCACTATGATGAGTGAACACTCATATGAGGCTATTTTCTACCTCAATCTTAAG 1080

OY 1081 CAATATCCCTATGCTTTGTAAGGAATTTGAAACCTTGTCAATTTTGTGCCAAGCAATTC 1140
 DB 1081 CAATATCCCTATGCTTTGTAAGGAATTTGAAACCTTGTCAATTTTGTGCCAAGCAATTC 1140
 OY 1141 GCTGATGCTGAACGCAACCGCCCAAGACCTTGAATGGGTCTAAATTTAAATTAAGGCT 1200
 DB 1141 GCTGATGCTGAACGCAACCGCCCAAGACCTTGAATGGGTCTAAATTTAAATTAAGGCT 1200
 OY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTTCACATCTAT 1260
 DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTTCACATCTAT 1260
 OY 1261 TTCTGCTTCCCATGATGCTTTGTTGCAATTCAGTTCAATCCACACCGCGGTACACC 1320
 DB 1261 TTCTGCTTCCCATGATGCTTTGTTGCAATTCAGTTCAATCCACACCGCGGTACACC 1320
 OY 1321 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 DB 1321 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 OY 1381 CGTAGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 DB 1381 CGTAGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 OY 1441 AATCAATTTGGCCAAACGCTATGCTTAAAGAAATCGGTAATACAAACAAATTTGAACGTATG 1500
 DB 1441 AATCAATTTGGCCAAACGCTATGCTTAAAGAAATCGGTAATACAAACAAATTTGAACGTATG 1500
 OY 1501 ACTGATATATGATACAAATTTGGCCACACCTGTAATCTTATAGCAATGAATTTGAAGT 1560
 DB 1501 ACTGATATATGATACAAATTTGGCCACACCTGTAATCTTATAGCAATGAATTTGAAGT 1560
 OY 1561 ATGGAATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 DB 1561 ATGGAATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 OY 1621 ATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 DB 1621 ATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 OY 1681 TCGATGCTTGAACAACTAGAGATTTATTTAG 1713
 DB 1681 TCGATGCTTGAACAACTAGAGATTTATTTAG 1713
 RESULT 3
 ID AA091566 standard; cDNA: 1713 BP.
 XX AA091566;
 AC AA091566;
 DT 22-DEC-1995 (first entry)
 XX OP-resistant esterase Lc7L103con.
 DE OP-resistant esterase Lc7L103con.
 XX Escerases; E3; bioremediation; organophosphate; carbamate;
 KM Insecticide; pesticide; water decontamination; meat decontamination;
 KM ss.
 XX Lucilia cuprina.
 OS Lucilia cuprina.
 FH Key Location/Qualifiers
 FT CDS 1..1713
 FT /*tag- a
 XX W09519440-A1.
 XX 20-JUL-1995.
 XX 13-JAN-1995; 95WO-AU00016.
 XX 13-JAN-1994; 94AU-0003347.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 DR WPI: 1995-263870/34.
 XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 PS Example 4; Page 12-17; 38pp; English.
 XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC Op-susceptible esterase E3 of L. cuprina) from a diazinon
 CC resistant strain, 1landllo 103. 4 isolated clones were
 CC sequenced (Lc7L103 A-D; AA091562-65) that encoded diazinon-resistant
 CC esterases; a consensus sequence is given in AA091566.
 CC
 SQ Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;
 Query Match 98.1%; Score 1681; DB 16; Length 1713;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1693; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGGAAGATTTAATGATTTGAAAT 60
 DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGGAAGATTTAATGATTTGAAAT 60
 OY 61 AAGTTTAACTATGCTTTTAACTACCAATGAACGCTGATGCTGATGCTGATGCTGATGCTG 120
 DB 61 AAGTTTAACTATGCTTTTAACTACCAATGAACGCTGATGCTGATGCTGATGCTGATGCTG 120
 OY 121 AAAGTAAAGGCGTTAAACGTTAACTGATGATGATGATGATGATGATGATGATGATGATG 180
 DB 121 AAAGTAAAGGCGTTAAACGTTAACTGATGATGATGATGATGATGATGATGATGATGATG 180
 OY 181 ATACGCTACGCCCAACCGCCAGTGGTGAGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 ATACGCTACGCCCAACCGCCAGTGGTGAGATGATGATGATGATGATGATGATGATGATGAT 240
 OY 241 CCCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 DB 241 CCCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 OY 301 ATACGCGCAAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 301 ATACGCGCAAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 OY 361 CTAAATCCCGAATCTAAAGCTCCGCTTAAATGATGATGATGATGATGATGATGATGATGAT 420
 DB 361 CTAAATCCCGAATCTAAAGCTCCGCTTAAATGATGATGATGATGATGATGATGATGATGAT 420
 OY 421 GGTGAATATCATGCTGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 DB 421 GGTGAATATCATGCTGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 OY 481 ATTAACATACAAATGCTTGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 DB 481 ATTAACATACAAATGCTTGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 OY 541 AATGCGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 541 AATGCGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 OY 601 AATGCGCGCAACTTTGCTGCAATCCGATATATTAACGCTTTTGGTGAAGTGGCGGT 660
 DB 601 AATGCGCGCAACTTTGCTGCAATCCGATATATTAACGCTTTTGGTGAAGTGGCGGT 660
 OY 661 GCTGCTCTACCACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 DB 661 GCTGCTCTACCACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720

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QY 721 ATACTAATGTGGGTAATAGCTATTGTCATTTGGCTAATACCAATGTCACATCGTCC 780
DB 721 ATACTAATGTGGGTAATAGCTATTGTCATTTGGCTAATACCAATGTCACATCGTCC 780
QY 781 TTCACTTACGCAAAATTTGGCGGCTATPAGGGTGAAGATATPAGATGTTTGGAA 840
DB 781 TTCACTTACGCAAAATTTGGCGGCTATPAGGGTGAAGATATPAGATGTTTGGAG 840
QY 841 TTCTTTTGAAGCCAGGCCAGAGATTATTAACCTTGAGGAAAAAGTTTAACTCTA 900
DB 841 TTCTTTTGAAGCCAGGCCAGAGATTATTAACCTTGAGGAAAAAGTTTAACTCTA 900
QY 901 GAAGAGGCTACAAATTAAGTATGTTTCTTTGTCCTTGTCCACTGTGAGCCATATCAGACC 960
DB 901 GAAGAGGCTACAAATTAAGTATGTTTCTTTGTCCTTGTCCACTGTGAGCCATATCAGACC 960
QY 961 GCTGATGTGCTTACCACCAACATCTCGGGAATGTTTAAACTGCTTGGGGTAATTG 1020
DB 961 GCTGATGTGCTTACCACCAACATCTCGGGAATGTTTAAACTGCTTGGGGTAATTG 1020
QY 1021 ATACCCACTATGATGGGTAAACACTTCAATPAGGGTCTATTGTCCTTCAATCTTAA 1080
DB 1021 ATACCCACTATGATGGGTAAACACTTCAATPAGGGTCTATTGTCCTTCAATCTTAA 1080
QY 1081 CAATGCTATGCTTGTTAAGGAATGGAACCTTGTCAATTTGTGCGCAAGTGAATG 1140
DB 1081 CAATGCTATGCTTGTTAAGGAATGGAACCTTGTCAATTTGTGCGCAAGTGAATG 1140
QY 1141 GCTGATGCTGAACGACCGCCCGGAGACCTTGGAAATGGGTGCTAAATTAAGAGCT 1200
DB 1141 GCTGATGCTGAACGACCGCCCGGAGACCTTGGAAATGGGTGCTAAATTAAGAGCT 1200
QY 1201 CATGTACAGAGAAACCAACAGCTGATATTTATGATCTTTGCTCTCACATCTAT 1260
DB 1201 CATGTACAGAGAAACCAACAGCTGATATTTATGATCTTTGCTCTCACATCTAT 1260
QY 1261 TTTGTTGTTCCCATGATGCTTGTGCAATTTAGCTTCAATCAACCTCGGTAACCC 1320
DB 1261 TTTGTTGTTCCCATGATGCTTGTGCAATTTAGCTTCAATCAACCTCGGTAACCC 1320
QY 1321 GTCTACTTGTATGCTTGCACCTTGCAGATCGAGAGATCTTATCAATCCCTATGATATG 1380
DB 1321 GTCTACTTGTATGCTTGCACCTTGCAGATCGAGAGATCTTATCAATCCCTATGATATG 1380
QY 1381 CGTAGTGGACCTGGTGTAAAGGGTGTAGTATGCTATGATGAATTAACCTATTCTTGG 1440
DB 1381 CGTAGTGGACCTGGTGTAAAGGGTGTAGTATGCTATGATGAATTAACCTATTCTTGG 1440
QY 1441 AATCAATTTGGCCAAACGATGCTTAAGAAATCGGCTGAATCAAAACAAATGAACGTATG 1500
DB 1441 AATCAATTTGGCCAAACGATGCTTAAGAAATCGGCTGAATCAAAACAAATGAACGTATG 1500
QY 1501 ACTGGTATATGATATCAATTTGCCACCACTGTATATCCTTATAGCAATGAATGAAGGT 1560
DB 1501 ACTGGTATATGATATCAATTTGCCACCACTGTATATCCTTATAGCAATGAATGAAGGT 1560
QY 1561 ATGGAATATGTTTCTCGGATCCCAATTAAGAAATCCGATGAAGTATCAAGTGTGAT 1620
DB 1561 ATGGAATATGTTTCTCGGATCCCAATTAAGAAATCCGATGAAGTATCAAGTGTGAT 1620
QY 1621 ATTAGTATGATTAAGAAATGATGATGCTGGAATGAATGAATGAATGAATGAAGGAG 1680
DB 1621 ATTAGTATGATTAAGAAATGATGATGCTGGAATGAATGAATGAATGAATGAAGGAG 1680
QY 1681 TCGATGTTTGAAGAAACATAGAGATTATTTAG 1713
DB 1681 TCGATGTTTGAAGAAACATAGAGATTATTTAG 1713

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RESULT 4
AA091564
ID AA091564 standard; cDNA; 1713 BP.

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XX AC AA091564;
XX DT 22-DEC-1995 (first entry)
XX DE OP-resistant esterase Lc7L103C allele.
XX KW Esterase; E3; bioremediation; organophosphate; carbamate;
XX KW insecticide; pesticide; water decontamination; meat decontamination;
XX OS Lucilia cuprina.
XX FT Key 1.1713
XX FT CDS /tag- a
XX PN W09519440-A1.
XX PD 20-JUL-1995.
XX PF 13-JAN-1995; 95WO-AU00016.
XX PR 13-JAN-1994; 94AU-0003347.
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX DR WPI, 1995-263870/34.
XX PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX PT eliminate residues of organo:phosphate and carbamate pesticides from
XX PS water, meat etc.
XX PS Example 4; Page 12-17; 38pp; English.
XX CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX CC resistant strain, Ilandillo 103. 4 isolated clones were
XX CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
XX CC esterases. The esterases, or cells expressing them, are used
XX CC in bioremediation.
XX SO Sequence 1713 BP; 512 A; 308 C; 368 G; 525 T; 0 other;
Query Match 97.9%; Score 1677.8; DB 16; Length 1713;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1691; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 ATGAATTTCAACGTTAGTTTGTGATGAGAGAAATTAATGAGATTAATGCAATTAAT 60
DB 1 ATGAATTTCAACGTTAGTTTGTGATGAGAGAAATTAATGAGATTAATGCAATTAAT 60
QY 61 AAGTTTAACTATCGTTTAACTACCAATGAAGCGGTGATGCAAGCAATGATATGCG 120
DB 61 AAGTTTAACTATCGTTTAACTACCAATGAAGCGGTGATGCAAGCAATGATATGCG 120
QY 121 AAAGTGAAGCGGTTAAAGCTTTAACTGTATGATGATATTCCTTACAGTTTGAAGGT 180
DB 121 AAAGTGAAGCGGTTAAAGCTTTAACTGTATGATGATATTCCTTACAGTTTGAAGGT 180
QY 181 AAAGTGAAGCGGTTAAAGCTTTAACTGTATGATGATATTCCTTACAGTTTGAAGGT 240
DB 181 AAAGTGAAGCGGTTAAAGCTTTAACTGTATGATGATATTCCTTACAGTTTGAAGGT 240
QY 241 CCCTGGATGATGATGCGGATTTGTCATATGAATGAATGAATGAATGAATGAATGAAT 300
DB 241 CCCTGGATGATGATGCGGATTTGTCATATGAATGAATGAATGAATGAATGAATGAAT 300
QY 301 ATACGGGCAAAAGTGTGCTGACAGAGATGCTATATCTTAAGTGTCTATACGAATAT 360
DB 301 ATACGGGCAAAAGTGTGCTGACAGAGATGCTATATCTTAAGTGTCTATACGAATAT 360

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Db 301 ATTACAGCAAGTGTGGCTCAGAGATTGCTATACCTAAGCGCTATACGAATAT 360
 QY 361 CTAATCCGAAACTAAAGTCCGTTTGTATATACATAGTGTGTATATATC 420
 Db 361 CTAATCCGAAACTAAAGTCCGTTTGTATATACATAGTGTGTATATATC 420
 QY 421 GGTGAATATCATCGTATATGATGTCTCTATATTTTCATTAAGAGATGTGCTTG 480
 Db 421 GGTGAATATCATCGTATATGATGTCTCTATATTTTCATTAAGAGATGTGCTTG 480
 QY 481 ATTAACATACATATCGTTGGAGCTAGTGTCTTCTAAGTCTTAAATTCAGAGACTT 540
 Db 481 ATTAACATACATATCGTTGGAGCTAGTGTCTTCTAAGTCTTAAATTCAGAGACTT 540
 QY 541 AATGTCGCGGTAATGCGGCTTAAGATCAAGTCATGCGCTTGCCTGGATTAAAAAT 600
 Db 541 AATGTCGCGGTAATGCGGCTTAAGATCAAGTCATGCGCTTGCCTGGATTAAAAAT 600
 QY 601 AATGTCGCGCACTTGGTGGCAATCCGATATATATACAGTCTTGGTGAAGTCCGCT 660
 Db 601 AATGTCGCGCACTTGGTGGCAATCCGATATATATACAGTCTTGGTGAAGTCCGCT 660
 QY 661 GCTGCTCTACCACTACATGATGTAAACGACAACTGCGGCTTTTCCATCGTGT 720
 Db 661 GCTGCTCTACCACTACATGATGTAAACGACAACTGCGGCTTTTCCATCGTGT 720
 QY 721 ATACTAATGCGGTATGCTATTTGCTTCCATGCTATACCAATGCTCAACATCGTGC 780
 Db 721 ATACTAATGCGGTATGCTATTTGCTTCCATGCTATACCAATGCTCAACATCGTGC 780
 QY 781 TTCACCTTAAGCAAAATGCGCGCTATAGGATGATGATGATGATGATGATGATGATG 840
 Db 781 TTCACCTTAAGCAAAATGCGCGCTATAGGATGATGATGATGATGATGATGATGATG 840
 QY 841 TTTCTTTTGAAGCAAGCCACAGATTTAATAAAGTTAAAGTTAAAGTTAAAGTTAA 900
 Db 841 TTTCTTTTGAAGCAAGCCACAGATTTAATAAAGTTAAAGTTAAAGTTAAAGTTAA 900
 QY 901 GAAGAGCGTCAAAATAGTGTATGTTCTTTGCTTCCGCTGTAGCCATATCAGACC 960
 Db 901 GAAGAGCGTCAAAATAGTGTATGTTCTTTGCTTCCGCTGTAGCCATATCAGACC 960
 QY 961 GCTGATGTGTCTTACCAAAATCCTCGGGAATGTTAAACTGCTGGGCTAATTCG 1020
 Db 961 GCTGATGTGTCTTACCAAAATCCTCGGGAATGTTAAACTGCTGGGCTAATTCG 1020
 QY 1021 ATACCACTATGATGGGTAACTTCAATGAGGCTATTTTCACTTCAATTCCTTAAG 1080
 Db 1021 ATACCACTATGATGGGTAACTTCAATGAGGCTATTTTCACTTCAATTCCTTAAG 1080
 QY 1081 CAAATGCTATGCTTGTAAAGAAATGGAACCTGTGCAATTTGTGGCAAGTGAATG 1140
 Db 1081 CAAATGCTATGCTTGTAAAGAAATGGAACCTGTGCAATTTGTGGCAAGTGAATG 1140
 QY 1141 GCTGATGTGTAAGCAAGCCGCTGAGACCTTGAAGATGGTGTAAATTAAGAGCT 1200
 Db 1141 GCTGATGTGTAAGCAAGCCGCTGAGACCTTGAAGATGGTGTAAATTAAGAGCT 1200
 QY 1201 CATGTATACGAGAAACACCAACCGCGATTAATTAATGATCTTGTCTACATCTAT 1260
 Db 1201 CATGTATACGAGAAACACCAACCGCGATTAATTAATGATCTTGTCTACATCTAT 1260
 QY 1261 TTTCTGTTCCCATGATGATGCTTGTGCAATTAAGTTCAATCAGACCTCGGTACACC 1320
 Db 1261 TTTCTGTTCCCATGATGATGCTTGTGCAATTAAGTTCAATCAGACCTCGGTACACC 1320
 QY 1321 GCTCTACTGTATCGCTTGCATCTGATTCGAGATCTTAATCAATCCATGCTATATG 1380
 Db 1321 GCTCTACTGTATCGCTTGCATCTGATTCGAGATCTTAATCAATCCATGCTATATG 1380
 QY 1381 CGTACTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 Db 1381 CGTACTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440

QY 1441 AATCAATTTGGCCAAACGATATGCTTAAGAAATCGCGTGAATACAAAACAAATGAACGTATG 1500
 Db 1441 AATCAATTTGGCCAAACGATATGCTTAAGAAATCGCGTGAATACAAAACAAATGAACGTATG 1500
 QY 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 Db 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 QY 1561 ATGGAATATGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
 Db 1561 ATGGAATATGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
 QY 1621 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Db 1621 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 QY 1681 TCGATGTTGAAAAACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
 Db 1681 TCGATGTTGAAAAACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
 RESULT 5
 ID AA091565 standard; cDNA; 1713 BP.
 AC AA091565;
 XX
 DT 22-DEC-1995 (first entry)
 DE
 XX
 KW Op-resistant esterase Lc7L103D allele.
 KW Esterase; E3; bioremediation; organophosphate; carbamate;
 KW insecticide; pesticide; water decontamination; meat decontamination;
 SS.
 XX
 OS Lucilia cuprina.
 XX
 FH Key
 FT CDS 1..1713
 FT /*tag= a
 XX
 PN W09519440-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 13-JAN-1995; 95MO-AU00016.
 XX
 PR 13-JAN-1994; 94AU-0003347.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Roblin GC, Russell RJ, Smyth K;
 XX
 DR WPI: 1995-263870/34.
 XX
 PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Example 4; Page 12-17; 38pp; English.
 XX
 CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC Op-susceptible esterase E3 of *L. cuprina*) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (Lc7L103 A-D; AA091562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used
 CC in bioremediation.
 XX
 SQ Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other;
 Query Match 97.9%; Score 1677.8; DB 16; Length 1713;

Best Local Similarity 98.7%; Pred. No. 0;
Matches 1691; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```

QY 1 ATGAATTTCAACGTTAGTTGATGAGAGAAATTAATGAGATTAAATCATTCATTGAAAT 60
Db 1 ATGAATTTCAACGTTAGTTGATGAGAGAAATTAATGAGATTAAATCATTCATTGAAAT 60
QY 61 AAGTTTAACTATGCTTAACCTAACCAATGAACCGGTGAGTGAATGATATAGGC 120
Db 61 AAGTTTAACTATGCTTAACCTAACCAATGAACCGGTGAGTGAATGATATAGGC 120
QY 121 AAGTGAAGGCGTTAAAGCTTTAACTGTAGATGATTCCTACTACATTTTGAGGCT 180
Db 121 AAGTGAAGGCGTTAAAGCTTTAACTGTAGATGATTCCTACTACATTTTGAGGCT 180
QY 181 ATACCGTACGCCCAACGCCAGTGGGTGAGCTGAGATTTAAAGCACCACGACCAACA 240
Db 181 ATACCGTACGCCCAACGCCAGTGGGTGAGCTGAGATTTAAAGCACCACGACCAACA 240
QY 241 CCGTGGATGCTGCGCGCATTTGTCATCATTAAGTAAAGTAAAGTAAAGTAAAGT 300
Db 241 CCGTGGATGCTGCGCGCATTTGTCATCATTAAGTAAAGTAAAGTAAAGTAAAGT 300
QY 301 ATACGCGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAAGTCTATACGAATAAT 360
Db 301 ATACGCGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAAGTCTATACGAATAAT 360
QY 361 CTAAATCCCAAACTAAAGCTCCGTTTGTATACATACATGCTGATTTTATATATC 420
Db 361 CTAAATCCCAAACTAAAGCTCCGTTTGTATACATACATGCTGATTTTATATATC 420
QY 421 GGTGAATAATGCTGATGATGATGCTGATTTCTATTAAGTAAAGTAAAGTAAAGT 480
Db 421 GGTGAATAATGCTGATGATGATGCTGATTTCTATTAAGTAAAGTAAAGTAAAGT 480
QY 481 ATTAACATACATATCTTTGGGAGCTCTAGGTTTCTAAGTTTAAATGAGAAGACCTT 540
Db 481 ATTAACATACATATCTTTGGGAGCTCTAGGTTTCTAAGTTTAAATGAGAAGACCTT 540
QY 541 AATGTGCGCGGTAATGCGGCTTAAGATCAAGTCAATGCGCTTGGATTAAAT 600
Db 541 AATGTGCGCGGTAATGCGGCTTAAGATCAAGTCAATGCGCTTGGATTAAAT 600
QY 601 AATTGCGCAACTTTGGTGCAATCCGATTAATTTACAGCTTTGGTGAAGCGCGGT 660
Db 601 AATTGCGCAACTTTGGTGCAATCCGATTAATTTACAGCTTTGGTGAAGCGCGGT 660
QY 661 GCTGCCCTACCCACTACATGATGTTAAACCAACAACTGCGGCTTTTCCATCGTGT 720
Db 661 GCTGCCCTACCCACTACATGATGTTAAACCAACAACTGCGGCTTTTCCATCGTGT 720
QY 721 ATACTAATGTCGGGTATGCTATTTGTCATTTGCTAATACCATGTCATCGTGC 780
Db 721 ATACTAATGTCGGGTATGCTATTTGTCATTTGCTAATACCATGTCATCGTGC 780
QY 781 TTACCTTAGCCAAATTTGGCGGCTATTAAGGTGAGATGATTAAGATGTTTGAA 840
Db 781 TTACCTTAGCCAAATTTGGCGGCTATTAAGGTGAGATGATTAAGATGTTTGAA 840
QY 841 TTTCTTGAAGCCAGCCACAGATTTAATAAACTTGAGAAAAAGTTTAACTCTA 900
Db 841 TTTCTTGAAGCCAGCCACAGATTTAATAAACTTGAGAAAAAGTTTAACTCTA 900
QY 901 GAAGAGGCTCAAAATTAAGTATGATTTCTTTTGGTCCCACTGTTGAGCCATACAGAC 960
Db 901 GAAGAGGCTCAAAATTAAGTATGATTTCTTTTGGTCCCACTGTTGAGCCATACAGAC 960
QY 961 GCTGATTTGCTTACCAACAATCCTCGGAAATGTTAAATGCTGTTGGGTAATTCG 1020
Db 961 GCTGATTTGCTTACCAACAATCCTCGGAAATGTTAAATGCTGTTGGGTAATTCG 1020
QY 1021 ATACCACTATGATGGTAACTTCAATATGAGGCTATTTTTCACCTCAATTTCTTAAG 1080
Db 1021 ATACCACTATGATGGTAACTTCAATATGAGGCTATTTTTCACCTCAATTTCTTAAG 1080

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Db 1021 ATACCACTATGATGGTAACTTCAATATGAGGCTATTTTTCACCTCAATTTCTTAAG 1080
QY 1081 CAAATGCCCTATGCTGTTGAAGAAATTTGAAACTTGTGCAATTTTGGCCAGGAAATG 1140
Db 1081 CAAATGCCCTATGCTGTTGAAGAAATTTGAAACTTGTGCAATTTTGGCCAGGAAATG 1140
QY 1141 GCTGATGCTGAGCAGCCGCCGCCAGAGACCTTGGAATGGGTGCTAAATTAAGAAAGCT 1200
Db 1141 GCTGATGCTGAGCAGCCGCCGCCAGAGACCTTGGAATGGGTGCTAAATTAAGAAAGCT 1200
QY 1201 CATGTTACAGAGAAACCAACACAGCTGATTAATTTATGATCTTTGCTGCACATCAT 1260
Db 1201 CATGTTACAGAGAAACCAACACAGCTGATTAATTTATGATCTTTGCTGCACATCAT 1260
QY 1261 TTCTGTTCCCATGATCGTTTGTGCAATTTACGTTCAATACACACCTCCGTAACACC 1320
Db 1261 TTCTGTTCCCATGATCGTTTGTGCAATTTACGTTCAATACACACCTCCGTAACACC 1320
QY 1321 GTCCTACTTGTATGCTGCTGCACTTCGATTCGAAAGATCTTATCATCCCTATCGTATATG 1380
Db 1321 GTCCTACTTGTATGCTGCTGCACTTCGATTCGAAAGATCTTATCATCCCTATCGTATATG 1380
QY 1381 CGTAGTGAGCTGCTGTTAAGGCTGTTAGTATGATGATGATTAATTAACCTATTTCTGCG 1440
Db 1381 CGTAGTGAGCTGCTGTTAAGGCTGTTAGTATGATGATGATTAATTAACCTATTTCTGCG 1440
QY 1441 AATCAATTTGGCCAAACGTAATGCTTAAGAAATCGCGTGAATTAACAACAAATGAACGTATG 1500
Db 1441 AATCAATTTGGCCAAACGTAATGCTTAAGAAATCGCGTGAATTAACAACAAATGAACGTATG 1500
QY 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Db 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
QY 1561 ATGGAATAATGTTTCTGCGATCAATTAAGAAATCCGATGAAGATTAACAAGTGTGTAAT 1620
Db 1561 ATGGAATAATGTTTCTGCGATCAATTAAGAAATCCGATGAAGATTAACAAGTGTGTAAT 1620
QY 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Db 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 TCGATGTTTGAATAACATAGAGATTTTATTTAG 1713
Db 1681 TCGATGTTTGAATAACATAGAGATTTTATTTAG 1713

```

RESULT 6
AA091563
ID AA091563 standard; cDNA; 1713 BP.

XX AA091563;

DT 22-DEC-1995 (first entry)

XX OP-resistant esterase Lc7L103B allele.

XX Esterase; E3; bioremediation; organophosphate; carbamate;

KW insecticide; pesticide; water decontamination; meat decontamination;

OS ss.

XX Lucilia cuprina.

XX Key location/Qualifiers

FT CDS 1..1713

PD 20-JUL-1995.

PF 13-JAN-1995; 95MO-AU00016.

PR 13-JAN-1994; 94AU-0003347.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Roblin GC, Russell RJ, Smyth K;
 XX WPI: 1995-263870/34.
 XX
 PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Example 4: Page 12-17; 38pp; English.
 XX
 CC RT-PCR was used to clone a cDNA allele of *Lc-alpha-E7* (encoding
 CC O₂-susceptible esterase E3 of *L. cuprina*) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used
 CC in bioremediation.
 XX
 SQ Sequence 1713 BP; 513 A; 308 C; 368 G; 524 T; 0 other;
 Query Match 97.9%; Score 1676.2; DB 16; Length 1713;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 1690; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 1 ATGATATTCACGTTAGTGTGAGAGAAATTAAGAGATTAATGATGAAAT 60
 1 ATGATATTCACGTTAGTGTGAGAGAAATTAAGAGATTAATGATGAAAT 60
 61 AAGTTTTTAACATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAAT 120
 61 AAGTTTTTAACATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAAT 120
 121 AAGTGAAGAGCGTTAAAGCTTAATGCTTAATGCTTAATGCTTAATG 180
 121 AAGTGAAGAGCGTTAAAGCTTAATGCTTAATGCTTAATGCTTAATG 180
 181 ATACCGTACGCGCCCAACCGCCAGTGGGTGAGTGAATTAAGACCCG 240
 181 ATACCGTACGCGCCCAACCGCCAGTGGGTGAGTGAATTAAGACCCG 240
 181 ATACCGTACGCGCCCAACCGCCAGTGGGTGAGTGAATTAAGACCCG 240
 241 CCTGGGATGCTGTGCGCATGCTGCTTAATGCTTAATGCTTAATGCT 300
 241 CCTGGGATGCTGTGCGCATGCTGCTTAATGCTTAATGCTTAATGCT 300
 301 ATACCGGCGCAAGAGTGTGCTCAGAGATTTGCTAATGCTTAATGCT 360
 301 ATACCGGCGCAAGAGTGTGCTCAGAGATTTGCTAATGCTTAATGCT 360
 301 ATACCGGCGCAAGAGTGTGCTCAGAGATTTGCTAATGCTTAATGCT 360
 361 CTAAATCCCGAAGCTTAAGCTCCCTTTAGTATACATACATGCTGCT 420
 361 CTAAATCCCGAAGCTTAAGCTCCCTTTAGTATACATACATGCTGCT 420
 361 CTAAATCCCGAAGCTTAAGCTCCCTTTAGTATACATACATGCTGCT 420
 421 GGTGAAGATTCATGCTGCTATGCTGCTGCTTAATGCTTAATGCT 480
 421 GGTGAAGATTCATGCTGCTATGCTGCTGCTTAATGCTTAATGCT 480
 481 ATTAACATACATATGCTTTGGAGCTCTAGCTTTTCAATTAATTAAT 540
 481 ATTAACATACATATGCTTTGGAGCTCTAGCTTTTCAATTAATTAAT 540
 481 ATTAACATACATATGCTTTGGAGCTCTAGCTTTTCAATTAATTAAT 540
 541 AATGTCGCCGCTTAATGCTGCTTAAGATCAATGCTGCTGCTGCT 600
 541 AATGTCGCCGCTTAATGCTGCTTAAGATCAATGCTGCTGCTGCT 600
 541 AATGTCGCCGCTTAATGCTGCTTAAGATCAATGCTGCTGCTGCT 600
 601 AATTGCGCGCAATCTTGGTGGCAATCCGATTAATTAACAGCTTTGG 660
 601 AATTGCGCGCAATCTTGGTGGCAATCCGATTAATTAACAGCTTTGG 660
 601 AATTGCGCGCAATCTTGGTGGCAATCCGATTAATTAACAGCTTTGG 660
 661 GCTGCTCTACCCATACATGATGTAAACGCAACAACTGCGGCTTTTC 720

Db 661 GCTGCTCTACCCATACATGATGTAAACGCAACAACTGCGGCTTTTC 720
 QY 721 ATACTAATGTGGGTAATGCTATTTGCCATTTGGCTAATACCAATGTA 780
 QY 721 ATACTAATGTGGGTAATGCTATTTGCCATTTGGCTAATACCAATGTA 780
 QY 781 TTACCTTACCCAAATTTGGCGGCTTAAGGTGAGGATTAATGATG 840
 QY 781 TTACCTTACCCAAATTTGGCGGCTTAAGGTGAGGATTAATGATG 840
 QY 781 TTACCTTACCCAAATTTGGCGGCTTAAGGTGAGGATTAATGATG 840
 QY 841 TTCTATGTAAGCCCAAGGCGGCTTAATTAATTAATGAGGAAAGTT 900
 QY 841 TTCTATGTAAGCCCAAGGCGGCTTAATTAATTAATGAGGAAAGTT 900
 QY 841 TTCTATGTAAGCCCAAGGCGGCTTAATTAATTAATGAGGAAAGTT 900
 QY 901 GAAGACGCTAACAATTAAGTCTATGTTCTTTGGTCCACCTGAGCAT 960
 QY 901 GAAGACGCTAACAATTAAGTCTATGTTCTTTGGTCCACCTGAGCAT 960
 QY 901 GAAGACGCTAACAATTAAGTCTATGTTCTTTGGTCCACCTGAGCAT 960
 QY 961 GCTGATGCTGCTTACCCCAACATCTCGGGAATGTTAAACTGCTT 1020
 QY 961 GCTGATGCTGCTTACCCCAACATCTCGGGAATGTTAAACTGCTT 1020
 QY 961 GCTGATGCTGCTTACCCCAACATCTCGGGAATGTTAAACTGCTT 1020
 QY 1021 ATACCCATATGATGGGTAACTTCAATATGAGGCTATTTTCACTTCA 1080
 QY 1021 ATACCCATATGATGGGTAACTTCAATATGAGGCTATTTTCACTTCA 1080
 QY 1021 ATACCCATATGATGGGTAACTTCAATATGAGGCTATTTTCACTTCA 1080
 QY 1081 CAATGCTGCTGCTTAAAGATTTGAATTTGCAATTTTGTGCCAAG 1140
 QY 1081 CAATGCTGCTGCTTAAAGATTTGAATTTGCAATTTTGTGCCAAG 1140
 QY 1081 CAATGCTGCTGCTTAAAGATTTGAATTTGCAATTTTGTGCCAAG 1140
 QY 1141 GCTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1200
 QY 1141 GCTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1200
 QY 1141 GCTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1200
 QY 1201 CATGTTACAGAGAAACCAACACCTGATTAATTTTGAATCTTTGCT 1260
 QY 1201 CATGTTACAGAGAAACCAACACCTGATTAATTTTGAATCTTTGCT 1260
 QY 1201 CATGTTACAGAGAAACCAACACCTGATTAATTTTGAATCTTTGCT 1260
 QY 1261 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 QY 1261 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 QY 1261 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 QY 1321 GCTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1380
 QY 1321 GCTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1380
 QY 1321 GCTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1380
 QY 1381 GCTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1440
 QY 1381 GCTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1440
 QY 1381 GCTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1440
 QY 1441 AATGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1500
 QY 1441 AATGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1500
 QY 1441 AATGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1500
 QY 1501 ACTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1560
 QY 1501 ACTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1560
 QY 1501 ACTGATGCTGAAGCGGCGGCGGAGAGCTTGAATTTGGTCTTAAT 1560
 QY 1561 ATGGAAGATTTTCTGCGGAGTTCATTAAGAAATCCGATGAGTAT 1620
 QY 1561 ATGGAAGATTTTCTGCGGAGTTCATTAAGAAATCCGATGAGTAT 1620
 QY 1561 ATGGAAGATTTTCTGCGGAGTTCATTAAGAAATCCGATGAGTAT 1620
 QY 1621 ATTAAGTGAATTTGAAGAAATGATTTGCTGGAATGATTAAGTAA 1680
 QY 1621 ATTAAGTGAATTTGAAGAAATGATTTGCTGGAATGATTAAGTAA 1680
 QY 1621 ATTAAGTGAATTTGAAGAAATGATTTGCTGGAATGATTAAGTAA 1680
 QY 1681 TCGATGTTGGAAGAAACATAGAGATTTATTTAG 1713
 QY 1681 TCGATGTTGGAAGAAACATAGAGATTTATTTAG 1713
 QY 1681 TCGATGTTGGAAGAAACATAGAGATTTATTTAG 1713
 RESULT 7


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Db 1381 COTATGACCGTGTCTTAAGGCTGTAGTCACTGTGATGATTAACCATTTCTTCGG 1440
QY 1441 AATCAATTGGCCAAACGATAGCTTAAGAACGCTGATACAAAACATTTACCGTATG 1500
Db 1441 AATCAATTGGCCAAACGATAGCTTAAGAACGCTGATACAAAACATTTACCGTATG 1500
QY 1501 ACTGATATATGATACATTTTCCCACTGCTATCCCTATAGCAATTAAGTAAAGT 1560
Db 1501 ACTGATATATGATACATTTTCCCACTGCTATCCCTATAGCAATTAAGTAAAGT 1560
QY 1561 ATGGAATAATGTTCTCGGATCTAATTAAGAAATCCGATGAAGTGTGAAAT 1620
Db 1561 ATGGAATAATGTTCTCGGATCTAATTAAGAAATCCGATGAAGTGTGAAAT 1620
QY 1621 ATTACTGATGAATTAATGATTTGCTGCTGAATGATTAAGATTAACAAATGGGAG 1680
Db 1621 ATTACTGATGAATTAATGATTTGCTGCTGAATGATTAAGATTAACAAATGGGAG 1680
QY 1681 TCGATGTTTGAATAACATAGATTTATTTAG 1713
Db 1681 TCGATGTTTGAATAACATAGATTTATTTAG 1713

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RESULT 8

AAT68597
ID AAT68597 standard: DNA: 1710 BP.

AC AAT68597:

DT 08-AUG-1997 (first entry)

DE Md-alpha-E7 gene.

XX Malathion carboxylesterase: organophosphate; insecticide;

KW pesticide; remediation; bioremediation; decontamination; ds.

OS Musca domestica Rutgers strain.

FT key location/Qualifiers

FT mutation 752

FT /*tag= a

FT /note= "Trp-251 TGC codon is altered to a Ser

PN codon in resistant mutants"

XX MO9719176-AL.

PD 29-MAY-1997.

XX 22-NOV-1996; 96WO-AU00746.

PR 23-NOV-1995; 95AU-0006751.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

PI Boyce T, Brownlie JC, Campbell PM, Claudianos C;

PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

DR WPI: 1997-298113/27.

XX P-PSDB; AAW17767.

XX DNA encoding enzyme that degrades organophosphate pesticides -

PT useful for decontamination of soil, water, food etc

XX Claim 6; Fig 3; 52pp; English.

XX A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7

CC coding sequence of the Musca domestica Rutgers strain. It was

CC isolated by amplification of genomic DNA using alpha-esterase

CC consensus primers (see also AAT68598-99) and use of a 534 bp

CC amplicon to screen a genomic library of M. domestica. A

CC mutation of the gene, resulting in substn. of serine for tryptophan

CC at amino acid position 251 (see also AAW17767), confers malathion

CC resistance. The resistant enzyme acts as a malathion

CC carboxylesterase and can be formulated for use in degrading

CC environmental carboxylester or dimethyl general organophosphates.

XX Sequence 1710 BP; 498 A; 369 C; 394 G; 449 T; 0 other;

SO Query Match 55.8%; Score 955; DB 18; Length 1710;

Best Local Similarity 73.3%; Pred. No. 1.6e-252;

Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

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QY 44 TTAATGATTAAGATTTTAACTATCGTTTAACTACCAATGAAGCGGTGAG 103
Db 44 TTAATGATTAAGATTTTAACTATCGTTTAACTACCAATGAAGCGGTGAG 103
QY 104 CTGAATGATTAAGATTTTAACTATCGTTTAACTACCAATGAAGCGGTGAG 163
Db 104 CTGAATGATTAAGATTTTAACTATCGTTTAACTACCAATGAAGCGGTGAG 163
QY 164 ACTAGAGTTTGAAGGTTATACCGTACCGCAACCGCAGTGGTGAGCTGATTAAG 223
Db 164 ACTAGAGTTTGAAGGTTATACCGTACCGCAACCGCAGTGGTGAGCTGATTAAG 223
QY 224 CACCCAGGAGCAACACCCGCGATGGTGGCGGATTTGCAATGAAGTAAAGT 283
Db 224 CACCCAGGAGCAACACCCGCGATGGTGGCGGATTTGCAATGAAGTAAAGT 283
QY 284 CAGTCAAGTTGATTTTAACTACCGCAACAGTGTGCTCAGAGGATTTGCTATACCTAA 343
Db 284 CAGTCAAGTTGATTTTAACTACCGCAACAGTGTGCTCAGAGGATTTGCTATACCTAA 343
QY 344 GTGCTATACGAATATCTAAATCCCACTAAACGTCCTTTTACTATACATACATG 403
Db 344 GTGCTATACGAATATCTAAATCCCACTAAACGTCCTTTTACTATACATACATG 403
QY 404 GTGCTATACGAATATCTAAATCCCACTAAACGTCCTTTTACTATACATACATG 463
Db 404 GTGCTATACGAATATCTAAATCCCACTAAACGTCCTTTTACTATACATACATG 463
QY 464 AAAAGATGTGTGATTAACATACATATCGTTGGAGCTCTAGGTTTCTAGCT 523
Db 464 AAAAGATGTGTGATTAACATACATATCGTTGGAGCTCTAGGTTTCTAGCT 523
QY 524 TTAATTCAGAACCTTATATGCGCGTAATGCGCGCTTAAATGAATGATGAGGCT 583
Db 524 TTAATTCAGAACCTTATATGCGCGTAATGCGCGCTTAAATGAATGATGAGGCT 583
QY 584 TCGGCGAAAGTCTGTGTGGGCTCAACCATTAATGATGATGATGATGATGATGATG 703
Db 584 TCGGCGAAAGTCTGTGTGGGCTCAACCATTAATGATGATGATGATGATGATGATG 703
QY 704 GTCTTTCCATGCTGTGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 763
Db 704 GTCTTTCCATGCTGTGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 763
QY 764 AATGTCACATGCTGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 823
Db 764 AATGTCACATGCTGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 823
QY 824 ATTAAGGATGTTTGAATTTTATGTAAGAACCAAGCAGATGATTAATTAATTAAT 883
Db 824 ATTAAGGATGTTTGAATTTTATGTAAGAACCAAGCAGATGATTAATTAATTAAT 883
QY 884 AAAAAGTATCCGGAATTCCTATGTAAGAACCAAGTAAAGTAAAGTAAAGTAAAGT 943
Db 884 AAAAAGTATCCGGAATTCCTATGTAAGAACCAAGTAAAGTAAAGTAAAGTAAAGT 943
QY 944 TTGAGCATATACAGCCGCTGATTTGTCTTACCAACATCTCGGGAATGTTTAA 1003
Db 944 TTGAGCATATACAGCCGCTGATTTGTCTTACCAACATCTCGGGAATGTTTAA 1003
QY 944 TAGAACCATACAGCAGCCGCTGATTTGTCTTACCAACATCTCGGGAATGTTTAA 1003
Db 944 TAGAACCATACAGCAGCCGCTGATTTGTCTTACCAACATCTCGGGAATGTTTAA 1003

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QY 1004 CTGCTGGGGGAATTGATCCCATATGATGGTAACCTTCATATGAGGCTATTTT 1063
DB 1004 GCGCTGGGGGAATTGATCCCATATGATGGTAACCTTCATATGAGGCTATTTT 1063
QY 1064 TCACCTGATATTCCTTAAGCAATGCTTGTGTTAAGAACTTGCTCAAT 1123
DB 1064 CCAATGATATTCCTTAAGCAATGCTTGTGTTAAGAACTTGCTCAAT 1123
QY 1124 TTGTCGCAAGTGAATGGCTGATGCTGACGACCCGCCAGAGACCTTGAATG 1183
DB 1124 ATGTCCTGGGAGTGGCTGACGACGACGACGACGACGACGACGACGACG 1183
QY 1184 CTAATATTTAAAGGCTCATGTTTACAGAGAACCAACCAAGCTGATATTTTATG 1243
DB 1184 CCAATGATATTCCTTAAGCAATGCTTGTGTTAAGAACTTGCTCAAT 1243
QY 1244 TTGTCGCTCAATGATATTCCTTGTGTTGCTTGTGTTGCTTGTGTTGCT 1303
DB 1244 TTGTCGCTCAATGATATTCCTTGTGTTGCTTGTGTTGCTTGTGTTGCT 1303
QY 1304 ACACCTGCTGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1363
DB 1304 ACACGCTGCTGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1363
QY 1364 ATCCCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
DB 1364 ACCCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
QY 1424 TAACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
DB 1424 TAACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
QY 1484 AAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1543
DB 1484 AAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1543
QY 1544 GCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1603
DB 1544 GCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1603
QY 1604 TATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1663
DB 1604 TATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1663
QY 1664 AGATTAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1710
DB 1664 AAATTAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1710

RESULT 9
ABLO2067
ID ABL02067 standard; cDNA; 2001 BP.
XX
AC ABL02067;
XX
XX 26-MAR-2002 (first entry)
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 683;
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
PF 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
PR

XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
XX P-P.SDB; ABB57964.
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
PS Claim 1; SEQ ID NO 683; 21bp + Sequence Listing; English.
CC
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WPI
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 2001 BP; 502 A; 488 C; 521 G; 490 T; 0 other:
Query Match 39.7%; Score 680.4; DB 23; Length 2001;
Best Local Similarity 62.7%; Pred. No. 6.9e-177;
Matches 1075; Conservative 0; Mismatches 636; Indels 3; Gaps 1;
QY 1 ATGATTTTCAACGCTTATGTTGATGAGAAATTAATGAAGATTAATGATGAAT 60
DB 95 ATGATTTTCAACGCTTATGTTGATGAGAAATTAATGAAGATTAATGATGAAT 154
QY 61 AAGTTTAACTATGCTTAACTAATGAAGAAAGGCTGAGGCTGAAGCTGAATGAGC 120
DB 155 AAGTCCAGCAGTATGCTTAACTAATGAAGAAAGGCTGAGGCTGAAGCTGAATGAGC 214
QY 121 AAGTGAAGGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 180
DB 215 CAAGTGAAGGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 274
QY 181 ATACCTGACGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 240
DB 275 ATCCCTGACGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 334
QY 241 CCTGCTGAGGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 300
DB 335 CCTGCTGAGGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 394
QY 301 ATAAAGGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 360
DB 395 GTCTTGAATGAGGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 454
QY 361 CTAAATCCGAACTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 420
DB 455 GTGAAGGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 514
QY 421 GGTAAATATCATGCTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 480
DB 515 GGTAAATATCATGCTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 574
QY 481 ATTAACATACATATGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 540
DB 575 GTCAAGATACATATGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 634
QY 541 AATGCTCCGCTAATGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 600
DB 635 AATGCTCCGCTAATGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 694
QY 601 AATGCTCCGCTAATGCTTAACTAATGCTTAACTAATGAAGAAAGGCTGAGGCTGAATGAGC 660

Db	1775	GAGAGCCTGTATGACGACACAAAGATTATATGCT	1808
		RESULT 10	
XX	ABL02081		
ID	ABL02081	standard; cDNA; 1704 BP.	
XX	ABL02081;		
XX	26-MAR-2002	(first entry)	
XX	Drosophila melanogaster	expressed polynucleotide SEQ ID NO 725.	
XX	Drosophila	developmental biology; cell signalling; insecticide;	
XX	pharmaceutical; gene; ss.		
XX	Drosophila melanogaster.		
XX	WO200171042-A2.		
XX	27-SEP-2001.		
XX	23-MAR-2001; 2001WO-US09231.		
XX	23-MAR-2000; 2000US-191637P.		
XX	11-JUL-2000; 2000US-0614150.		
XX	(PEKE) PE CORP NY.		
XX	Venter JC, Adams M, Li PWD, Myers EW;		
XX	WPI: 2001-656860/75.		
XX	P-PsDB; ABB57978.		
XX	New isolated nucleic acid detection reagent for detecting 1000 or more		
XX	genes from Drosophila and for elucidating cell signalling and cell-cell		
XX	interactions -		
XX	Claim 1; SEQ ID NO 725; 21pp + Sequence Listing; English.		
XX	The invention relates to an isolated nucleic acid detection reagent		
XX	capable of detecting 1000 or more genes from drosophila. The invention is		
XX	useful in developmental biology and in elucidating cell signalling and		
XX	cell-cell interactions in higher eukaryotes for the development of		
XX	insecticides, therapeutics and pharmaceutical drugs. The invention		
XX	discloses genomic DNA sequences (AB116176-AB130511), expressed DNA		
XX	sequences (AB157737-AB172072).		
XX	(ABB57737-ABB72072).		
XX	The sequence data for this patent did not form part of the printed		
XX	specification, but was obtained in electronic format directly from WIP0		
XX	at ftp.wip0.int/pub/published_pct_sequences.		
XX	Sequence 1704 BP; 417 A; 445 C; 460 G; 382 T; 0 other;		
XX	Query Match	22.3%; Score 381.8; DB 23; Length 1704;	
XX	Best Local Similarity	54.0%; Pred. No. 1.1e-94;	
XX	Matches 879; Conservative	0; Mismatches 727; Indels	21; Gaps
QY	85	ACCAATGAACGGGTGCTAGCTGAACCTATGCAATGCAAGGAAAGGGCTTAACGTTTA	144
DB	64	ACCAATGACAAAGCTATCGCCGACACGGTCTACGGAAAGTGAAGGGGTGAATGGCAG	123
QY	145	ACTGTGACAGTGAATGCTCTACCTACAGTTTGAAGGGTATACGCTGACGCCAACCCGAGTG	183
DB	124	TCCATCTACGGCAACACTACTACCTTCGAGGGCATCCCTTGCCCAACCGCCGGTG	204
QY	205	GGTGAGCTGAGATTTAAAGCACCACGACCAACACCCTGGGATGATGCGCATGTG	264
DB	184	GCGAGGCTCCGCTTCAAGGCGCCCGTGGAGCCAGACACTGGTCAGATGTCAAGGGTGC	243
QY	265	TGCATCTATAAGATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA	324
DB	244	ACACATGTTTGGCGGCCGACCCCTGCGAGGTCAACATGTTTCAAGAGCTGCAAGGAC	303

OY	335	GAGGATGCTCTAATACCTAAAGGCTCTATACGAATAATCTAAATCCCGAAACTAAAGCTCC	384
Db	304	GAGAGCTCTCTGTACCTCAATGTCTACACCAGGAGTTACATCTCCACACAGACTTTGCCG	363
OY	385	GTTTATAGTATACATACATGGTGGTGGTTTATATNTCGTGAAATAATCATGTAATGAT	444
Db	364	GTTCTGGTTTGGATCTATGGCGGGGATTCCTCAATGGGAGAAAGCATCGGGGATCTGAC	423
OY	445	GCTCTGATTATTTTCATTAATAAAGATGTGGTGTGATTAACTACATATATCGTTTGGG	504
Db	424	AGCCGGACTCATTTATGATGAAACATGTCTACTGGTGAATATCCATATGGTTAGG	483
OY	505	GCTCTAGTTTTCTAACTTAATTAATTCAGAAAGACTTAATGTGCCGGTAATGCCGCTT	564
Db	484	GCCCTGGGATTCCTTACTCTTGGAGACAGAAACCTGGATCTCTGGAAACCCGGACTA	543
OY	565	AAAGATCAAGCATGAGGCTTGCCTGGATTAATAAATAATTTGGCGCACTTTGGTGGCAT	624
Db	544	AAGATCAAGTTATGCTCTTGGCTGGGTGCACAAAGAAATGGCCAGTCTTTGGTGGCAT	603
OY	625	CCCGATATATTAACAGTCTTTGGTGAAGTCCGGGTGCTCTACCCAGCATACATGAG	684
Db	604	CCCGATATATTAACCGTTTGGTGAAGTCTGGAGGTGCATCCACATATATGATG	663
OY	685	TTAACCGAACAACCTCGCGCTCTTTTCATCGTGATACTAATGTGGGTAATGTAAT	744
Db	664	CTGACGATCAGGCGCAAGGGCTATTTCACAAAGCATATTAATATGGGATCCGACTG	723
OY	745	TGTCCATTTGGTATACCCAATGCA--ACATCGTCCCTTACCTTACCCAAATGGCC	801
Db	724	GCACCTCTGGGGCAGACCCCAACCATTAATTTGGCCCTATCGCTGGCACAGGCCACT	783
OY	802	GCGTATAAGGCTGAGATTAATGATTAAGAGATGTTTGGATTTCTTATGAAGCCAAAGCA	861
Db	784	GCGTACACAGAGATGCTTAACGATCCGAGACTTTTGGCCATCTCAAGAAATGTAAGCC	843
OY	862	CAGGATTTAATAAACTTGAGGAAAAATTTTACTCTAAGAGACGTACAAATAGGT	920
Db	844	AGTAGCATGCTGAAGGTGGCCGAGATATCATCCATGAGAGAGACACAGCGGTTG	903
OY	921	--CATGTTCTCTTTGGTCCACTGTGTGAGCCATATCACCGCGATTTGTCTTACC	978
Db	904	ACCATGTTCACTTTGGACCCACCATCGAGCCCTATTTACGTCATATTTGTGTGATGCC	963
OY	979	AAACATCTCGGAGAAAGGTTTAAACATCGCTGGGGTAATTCATGCCCACTATGCGGT	1038
Db	964	AAGTCGCCACTGGAAATGATGCGGAGCTGTGGGGCAACAGCATTTCCATGTCTTCGGA	1023
OY	1039	AACACTTCATATGAGGGCTATATTTTCACTTCATTTCTTAAGCAAAATGCTATGCTGTT	1098
Db	1024	GGAATCTCTTCGAAGGTCTCTCATGTTTCCGGAAGTGAACAAAGTGGCCGGAATCGTT	1083
OY	1099	AAGGAATTCGAACCTGTGTCAATTTTGTGCCAAGTAATTTGGCTGATGTGAACGCACC	1158
Db	1084	TGCCAGTGGGTGACTCGAGAACTCGGCCCTCAAGATGCCACAGTGAATGACAGCA	1143
OY	1159	GCCCAGAGACCTTGGAAATGGGTGCTAAATTAATAAAGCATATGTTACAGAGAAACA	1218
Db	1144	AGAAAAGCGTTTGGAAAGAAAGTACAGAGACTATTTTGGCGATAGGACTCTGGCAGG	1203
OY	1219	CCAACAGCTGATATTTTATGATCTTTGTGCTCAACATATTTCTGTGCCATGAT	1278
Db	1204	AAGACCATATTTGGAGTACAGCATCTCTCTGTACAAATATTTCTGGCATGCAATTCAT	1263
OY	1279	CGTTTGTGCAATTAGCTTTCAATCAACCTCCGGTACACCCGCTTACTGTATCGCTTC	1338
Db	1264	AGGACTTTGCTCGCTGCTCTACACAGGCCCATTTGGCCCCCAACATTTCTGTACGATTC	1323
OY	1339	GACTTTCGATTCGGAAGATCTTATCANCCCTATACGATTAATCGATAGAGACGTGTGTT	1398
Db	1324	GATTTTCAGCTC---AAGCACTTCATATATACGATTAATACCTGTGGCCGCAAGGTG	1380

CC	XX	1399	AAGCGTTGTAGCATGCTGATGAATTAACCTATTCTCTCGAATTCATTTGGCCAAAGCT	1458
CC	XX	1399		
Db	1381	CGCGGACACCTGTACGCGGATGATCTGTCTATTGTTCTACAAATCGCGCTGCCAAAG	1440	
QY	1459	ATGCCCTAAGAATGCGCGTAATACAAAACATTTGAACGTATGATGATACAA	1518	
Db	1441	CTGAAGCGCCGACCGGAGTCTCAAGACCAATAAGCTTTGGTATGCATGGTGTTCAC	1500	
QY	1519	TTTGGCACCACTGGTATCTTTA-----GCAATGAATTAAGGATATGAA	1566	
Dc	1501	TTTGGCATTTTCGGGGATCCCAACATACCGATGCTCCGAGATGAGAAAGAACGCCG	1560	
QY	1567	AATGTTTCCTGGGAATTCATTAAGAAATCCATGATAGATATCAAGTCTTTGAATTTAGT	1626	
Db	1561	CGTGCGCGCTGGCTGCCATTTTCGAAGGACCATTAAGCTTCCATGCTGAATATATCG	1620	
QY	1627	GATGATTTGAATAATGATGATGTGCTGCTGAATGATTAAGATTAACAATGGAGTCATG	1686	
Db	1621	CACGATGTGCAATGTGATGATTGTTGCCCGAACCCGAAAGCTTGAGACTTGACATC	1680	
QY	1687	TTTGGAAA 1693		
Dc	1681	TACGACA 1687		
RESULT 11				
ABE02066				
ID	ABE02066	standard; cDNA; 6175 BP.		
XX	ABE02066;			
XX	26-MAR-2002 (first entry)			
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 680.			
XX				
KW	Drosophila; developmental biology; cell signalling; insecticide;			
KW	pharmaceutical; gene; ss.			
XX				
OS	Drosophila melanogaster.			
PN	WO200171042-A2.			
XX	27-SEP-2001.			
PD				
XX	23-MAR-2001; 2001WO-US09231.			
XX				
PR	23-MAR-2000; 2000US-191637P.			
PR	11-JUL-2000; 2000US-0614150.			
XX				
PA	(PEKE) PE CORP NY.			
XX				
PI	Venter JC, Adams M, Li PMD, Myers EW;			
XX				
DR	WPI: 2001-656860/75.			
DR	P-PSDB: ABB57963.			
PT				
PT	New isolated nucleic acid detection reagent for detecting 1000 or more			
PT	genes from Drosophila and for elucidating cell signalling and cell-cell			
PT	interactions -			
XX				
PS	Claim 1; SEQ ID NO 680; 21bp + Sequence Listing; English.			
XX				
XX	The invention relates to an isolated nucleic acid detection reagent			
CC	capable of detecting 1000 or more genes from Drosophila. The invention is			
CC	useful in developmental biology and in elucidating cell signalling and			
CC	cell-cell interactions in higher eukaryotes for the development of			
CC	insecticides, therapeutics and pharmaceutical drugs. The invention			
CC	discloses genomic DNA sequences (ABE01840-ABE16175), expressed DNA			
CC	sequences (ABE01840-ABE16175) and the encoded proteins			
CC	(ABB57737-ABB72072).			
CC	The sequence data for this patent did not form part of the printed			
CC	specification, but was obtained in electronic format directly from WIPO			
CC	at ftp.wipo.int/pub/published_pct_sequences.			

DT	26-MAR-2002	(first entry)
XX		
DE	Drosophila melanogaster	expressed polynucleotide SEQ ID NO 779.
XX		
XX	Drosophila; developmental biology; cell signalling; insecticide;	
KW	pharmaceutical; gene; ss.	
XX		
OS	Drosophila melanogaster.	
XX		
PN	WO200171042-A2.	
XX		
PD	27-SEP-2001.	
XX		
PF	23-MAR-2001; 2001WO-US09231.	
XX		
PR	23-MAR-2000; 2000US-191637P.	
PR	11-JUL-2000; 2000US-0614150.	
XX		
FA	(PEKE) PE CORP NY.	
XX		
PI	Venter JC, Adams M, Li PMD, Myers EW;	
XX		
XX	WPI: 2001-656860/75.	
DR	P-PSDB; ABB57996.	
XX		
PT	New isolated nucleic acid detection reagent for detecting 1000 or more	
PT	genes from Drosophila and for elucidating cell signalling and cell-cell	
XX	interactions -	
XX		
PS	Claim 1; SEQ ID NO 779; 21pp + Sequence Listing; English.	
XX		
CC	The invention relates to an isolated nucleic acid detection reagent	
CC	capable of detecting 1000 or more genes from Drosophila. The invention is	
CC	useful in developmental biology and in elucidating cell signalling and	
CC	cell-cell interactions in higher eukaryotes for the development of	
CC	insecticides, therapeutics and pharmaceutical drugs. The invention	
CC	discloses genomic DNA sequences (ABL01840-ABL16175-ABL30511), expressed DNA	
CC	sequences (ABB57737-ABB72072), and the encoded proteins	
CC	(ABB57737-ABB72072).	
CC	The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX		
XX	Sequence 1665 BP; 397 A; 446 C; 468 G; 354 T; 0 other;	

QY 1190 TTAAGAGCTATGTTACAGAGAAACACACAGCTGATATTTATGATCTTCT 1249
D 1291 TCTACTTCAACACAGAGATGCAAGATGATGAGATGTTGAGGCCCTGATATATTT 1340
QY 1250 CTCACATCTATTTGTTGCCCATGATGCTTTGTTGCAATTAAGTTCAATCACCT 1309
D 1341 CGCATGCGCATTTGGCAGATAGCATGCTTTATCTGCGCCGTCATCTTATGCC 1400
QY 1310 CCGGTACACCGCTCTACTTGTATGCTTCCGACTTCGATTCGAGAGATCTTATCCCT 1369
D 1401 CCAAAACGCCCATCTATCTATATGCTTTGACTTGCAGCTC---CCCGACTTCAATCAAT 1457
QY 1370 ATCGTATATGCTAGTACGATGCTGTTAAGGCTGATGATGATGATGATGATGAT 1429
D 1458 TTCGCCGACTGCTGCGGCGCATGCGATTCGCGAGTACGCCATGCGATGATGATGAT 1517
QY 1430 ATTTCTTCTGATCAATTTGGCAAGCATGCTTAAGAAATGCGGTAATACAAACAA 1489
D 1518 ACCTGTTCTACACATCATATACCTCCCAAACTGATTAAGTATGATGATGATGATGAT 1577
QY 1490 TTGAACGATACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1549
D 1578 TTGAGAGATGCTTGGCATGAGAGCTGTTGCTCCAGTGGGATCAAAATGCTCCAG 1637
QY 1550 AAATTGAAGTATGATAAATGTTCCCTGGATCCATTAAGAAATCCGATGATGATGAT 1609
D 1638 AACGAGGATGCTGCAAAATGAGGAGCGCTCCAGC-----TTAAAGAAATGCTCCG 1691
QY 1610 AGTCTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662
D 1692 AGTCTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1744

RESULT 14

ABL02103
ID ABL02103 standard; cDNA; 1593 BP.
AC ABL02103:
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 791.
XX Drosophila: developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI: 2001-656860/75.
XX P-PSDB: ABB58000.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX Claim 1; SEQ ID NO 791; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB16175), expressed DNA
CC sequences (AB16176-AB16175) and the encoded proteins
CC (AB57737-AB57737).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://ipo.int/pub/published_pct_sequences.

Sequence 1593 BP; 417 A; 394 C; 405 G; 377 T; 0 other;

Query Match 18.9%; Score 323.6; DB 23; Length 1593;

Best Local Similarity 52.9%; Pred. No. 1,1e-78; Matches 831; Conservative 0; Mismatches 709; Indels 32; Gaps 5;

QY 111 TGAATATGCAAGTAAAGCGTTAAAGCTTTAAGTATGATGATGATGATGATGATGAT 170
D 6 TGACTGCGCTCTGCGGAGTGAAGAAACAAATCTGGGAGGAGCTACTTACG 65
QY 171 TTTGAGGCTATACCGTACCGCAACCGCAGTGGTGAAGTATTAAGCAACCA 230
D 66 TTTGAGGAGATACCTTCCGAAAGCTCCGCTGGAGATGCTTCAAGCCCGCA 125
QY 231 GCGAACCAACCGCTGGATGCTGCGGATTTGCAATCAATTAAGATTAAGTACGTA 290
D 126 AGCAGTGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 185
QY 291 AGTGAATTTTAAAGGCAAGTGTGCTGAGAGATGCTTCAATGATGATGATGATGAT 350
D 186 GACACACATGTTTCAAGAAATACCGGCTCAGAGAGCTCCCTCAATTAATGATGAT 245
QY 351 TACGATATATCTAATCCCGAAACATCAAGCTCCCTTTAGTATCAATACATGATGAT 410
D 246 TGTCAAGATCTGACGCGGATTAACCTGCTCCCTGATGATGATGATGATGATGATGAT 305
QY 411 TTTTATATGCTGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 470
D 306 CTATCAATTTGGCGAAGCTTCTCGGATATGATGATGATGATGATGATGATGATGATGAT 365
QY 471 TGTGCTGATTAACATCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 530
D 366 TGTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
QY 531 AGAATCTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
D 426 TCCCACTAAAGCTTCCCGGAAATGCAAGTCTCAAGATCAATATGATGATGATGATGAT 485
QY 591 GATTAAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
D 486 GGTGCAACAAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
QY 651 AAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
D 546 AAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
QY 711 CCATGCTGATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770
D 606 CCACAAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 665
QY 771 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
D 666 TAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
QY 831 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
D 726 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785
QY 891 TTTAAGCTAGAGAGCTGATCAATATGATGATGATGATGATGATGATGATGATGATGAT 950
D 786 TCTGAGCAAGCATGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 845
QY 951 ATATGAGACCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1010

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1663.49 Seconds
(without alignments)
16677.553 Million cell updates/sec

Title: US-09-776-910-3
Perfect score: 1713
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066-segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
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7: em_estro:*
8: em_hlc:*
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14: gb_est5:*
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17: gb_gss:*
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24: em_gss_mus:*
25: em_gss_other:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315.2	18.4	778	9	AI062034 GH01076.5
2	282.4	16.5	649	9	AI388926 GH19977.5
3	266.8	15.6	688	9	AI403569 GH23036.5
4	258.2	15.1	671	9	AI517692 GH28740.5
5	256	14.9	569	13	BI609541 RH14337.5
6	251.6	14.7	674	13	BI628316 RH56682.5

7	251	14.7	676	13	BI635372
8	250	14.6	673	13	BI614181
9	248.6	14.5	660	13	BI639486
10	248.4	14.5	672	13	BI614443
11	248	14.5	670	13	BI233202
12	246.6	14.4	648	9	AI113763
13	246.6	14.4	648	9	AI403098
14	245	14.3	646	9	AI109901
15	245	14.3	646	9	AI293416
16	242.6	14.2	526	9	AI108080
17	241.4	14.1	516	9	AI108156
18	240.8	14.1	658	13	BI564586
19	240	14.0	656	13	BI619037
20	238.4	13.9	656	13	BI614821
21	238.2	13.9	669	13	BI588370
22	237.8	13.9	656	13	BI621302
23	234.8	13.7	628	9	AI109573
24	233	13.6	619	9	AI516869
25	232.6	13.6	638	13	BI564361
26	232.4	13.6	628	9	AI513346
27	232.2	13.6	630	9	AI403830
28	231.6	13.5	614	12	B6641228
29	231.6	13.5	647	13	BI575862
30	231.2	13.5	614	9	AI107729
31	231.2	13.5	614	9	AI134360
32	230.8	13.5	622	9	AI134524
33	229.6	13.4	633	13	BI370683
34	222.6	13.0	670	9	AI389766
35	221.4	12.9	614	13	BI617897
36	220.8	12.9	615	13	BI588504
37	220.2	12.9	587	9	AI517539
38	220.2	12.9	588	13	BI638519
39	220.2	12.9	607	13	BI624437
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ALIGNMENTS

RESULT 1
AI062034 LOCUS 778 bp mRNA linear EST 19-APR-2001
DEFINITION GH01076.5prine GH Drosophila melanogaster head pot2 Drosophila melanogaster cDNA clone GH01076.5prine similar to U51050:
Drosophila melanogaster alpha esterase (ae7) gene, partial cds,
mRNA sequence.

ACCESSION AI062034
VERSION AI062034.1 GI:3337873
KEYWORDS EST.
SOURCE Drosophila melanogaster
ORGANISM fruit fly.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 778)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HMT Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: 10 row: G column: 4
High quality sequence stop: 363.
Location/Qualifiers

FEATURES

0Y	908	GTACCAATTAAGTCATCTTTCTTTGGTCCACTGTTGAGCCATATAGACCGCTGATT	967
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0Y	968	GTGCTTTCACCAATATCCTCGGAGAAAGGTTAAACCTGGTGGGTAAATCGATGACCA	1027
Db	544	GTGTATATATCCAGCGCTCCAAAGAGATGATGAGACCGCCTGGAGTACTCATCCCA	603
0Y	1028	CTATGATGGGTAACTTCATGATGAGGGTCTAATTTT	1063
Db	604	TGTTATATAGAAACACTTCGTACGAGGCGTGGCTGT	639
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DEFINITION	AI403569 688 bp mRNA linear EST 19-Apr-2001		
ACCESSION	GH23036.5	prlme GH Drosophila melanogaster head pot2 Drosophila	
VERSION	AI403569	melanogaster cDNA clone GH23036 5prime similar to U51050:	
KEYWORDS	AI403569	Drosophila melanogaster alpha esterase (ae7) gene, partial cds,	
SOURCE	EST.	mRNA sequence.	
ORGANISM	fruit fly.		
REFERENCE	Drosophila melanogaster		
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
TITLE	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
JOURNAL	Ephydroidea; Drosophilidae; Drosophila.		
COMMENT	1 (bases 1 to 688)		
	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,		
	Lewis, S. and Rubin, G.M.		
	BDGP/HMT Drosophila EST Project		
	Unpublished (2001)		
	Contact: stapleton, M.		
	BDGP		
	Lawrence Berkeley National Lab		
	One Cyclotron Rd, Berkeley, CA 94720, USA		
	Fax: 510 486 6798		
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu		
	Plate: 230 row: C column: 12		
	High quality sequence stop: 648.		
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	/dev_stage="adult"		
	/lab_host="DHS - alpha"		
	/note="Organ: head; Vector: pot2; Site_1: EcoRI; Site_2:		
	XhoI; Sized fractionated cDNAs were directly ligated into		
	pot2. Plasmid cDNA library."		
BASE COUNT	161 a 174 c 197 g 156 t		
ORIGIN			
Query Match	15.6%; Score 266.8; DB 9; Length 688;		
Best Local Similarity	65.4%; Pred. No. 5.7e-62;		
Matches 391; Conservative 0; Mismatches 207; Indels 0; Gaps 0;			
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Db	91	ATGAATTAAGAACCTTGCGCTTTGTGAGAGCGCTTCGCGTGCCTCAAAACCATCGAGCAT	150
0Y	61	AAAGTTTAACTATCGTTTAAGTACCAATGAAGAGGAGTGTGCGTGAAGAACTAATATGGC	120
Db	151	AAAGTCCAGCACTATTCGCCAGTCGACCAATGAAGAGTTGTGCGGACACGGAGTACGCGC	210
0Y	121	AAAGTGAAGAGCGTTAAAGCTTAACTGATGATGATGATCTTACTACAGTTTGAGGAT	180
Db	211	CAAGTGAAGGAGTATCAAGGCTATCTCTCTTCATGATGTGCGCTACTTCAAGTTCAGAGGT	270
0Y	181	ATACCGTACGCCCAACCGCCACTGGGTGATGATGATTTAAAGCAACCCAGCGACCAACA	240

Db	Accession	Version	Keywords	Source	Organism	Title	Journal	Comment
Db	271	ATCCCGTACGCCACCCCTCCGGTGGGGGGGATGGCTTTAAAGCCCTCAGAGGCCATT						
Qy	241	CCCTGGGATGATGTCGCGGATGTTTGCAATCATFAAAGATTAAGTCAGTCGCAATGATTTT						
Db	331	CCCTGGGAGCGAGTTTCGCGACACGACCCAGGATTAAGCCCTCAGTCGACATTC						
Qy	301	ATMACGGCCAAAGTGTGTGGCTCAGAGGATTTGTCTATACCTAAGTGTCTATACGATAT						
Db	391	GCTTCGATTAAGTATAGAGGGCTCCGAGGACCTCTCTATCTCATATGTGTACCAACAT						
Qy	361	CTAATTCGCCGAACATAAGCTCCGCTTTAGTATACATATCATATGATGTGTATATATC						
Db	451	GTGAAGCCCGCAAGAGCTCGCCCGTTATGCTTTGGATTCACAGGAGAGGCTTCATTATC						
Qy	421	GGTGAAGATCATGATATGATATGATGTCCTGATATTTATTCATTAAGATGATGTGGTGG						
Db	511	GCGGAGGCGCAATCGGGAATGATATGATGCGCGGATTAATATTAAGAGATGTTGTCTC						
Qy	481	ATTAACTATACATATATCGTTTGGAGCTCTAGGCTTTTCATGATTAATTCAGAGACCTT						
Db	571	GTCAGATATACATACCTACGACTTGGGGCTTTGGGATTTATGATGATTAAGTCCCGAGCTA						
Qy	541	AATGTCGCCGATATATCGGCGCTTAAGATCATGATCATGCTTGGCTTGGATTAATA						
Db	631	AATGTCACGCAAAATGCTGGCTCTCAAGATCATGCTGGCCCTCAAGTGATCAGA						
RESULT 4								
LOCUS	A1517692	671 bp	mRNA					
DEFINITION	GH28740.5prlme GH Drosophila melanogaster head por2 Drosophila melanogaster CDNA clone GH28740 5prime similar to U51050:							
ACCESSION	A1517692							
VERSION	A1517692.1	GI:4420792						
KEYWORDS	EST.							
SOURCE	fruit fly.							
ORGANISM	Drosophila melanogaster							
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.							
AUTHORS	1 (bases 1 to 671) Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.							
TITLE	BDGP/HIMI Drosophila EST project							
JOURNAL	Unpublished (2001)							
COMMENT	Contact: Stapleton, M. BDGP Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST , estefruitfly@berkeley.edu Plate: 287 row: D column: 4 High quality sequence stop: 538. Location/Qualifiers 1..671 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="GH28740" /clone_lib="GH Drosophila melanogaster head por2" /sex="male and female" /dev_stage="adult" /lab_host="DHS - alpha" /note="Organ: head; Vector: por2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library." 155 a 170 c 193 g 153 t							
FEATURES	source							
BASE COUNT	155 a	170 c	193 g	153 t				
ORIGIN								
Query Match	15.1%	Score 258.2	DB 9	Length 671				
Best Local Similarity	65.6%	Pred.No. 1.3e-59						

	Plate:	RH_143	row:	D	column:	1
		High quality sequence stop: 447.				
		Location/Qualifiers				
		1..569				
/organism=	"Drosophila melanogaster"					
/db_xref="taxon:"	7227					
/clone="RH14337"						
/clone_lib="RH Drosophila melanogaster normalized Head pPic-1"						
/sex="male and female"						
/dev_stage="Adult"						
/lab_host="DH5-alpha Tona"						
/note="Organ: head; Vector: pfic1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN The library was normalized and excised using Cre recombinase. Plasmid cDNA Library."						
BASE COUNT	126 a	147 c	167 g	129 t		
ORIGIN						
Query Match	14.9%	Score 256;	DB 13;	Length 569;		
Best Local Similarity	65.7%;	Pred. No. 4.8e-59;				
Matches 373;	Conservative 0;	Mismatches 195;	Indels 0;	Gaps 0		
QY	17	GTTTGATGAGAAATTAAATGAAGAATAAATCATGTGAAAATACGTTTTTAACAATC	76			
Db	1	GCCTTGGGAGCGCTTCGCCGCTCCCAAAACCATCGACATTAAGTCOCAGAGATC	60			
QY	77	GTTAACACTACCAATGAAGCGSTGTACTCCAATCGATAATGCGAAGTAGAGGCCTTA	136			
Db	61	GCCAGTCGACCANTGAACAGTTGTCGCGCACACGGAGTACGGCCAAATGAGGGATCA	120			
QY	137	AACGTTTAACTGTGTCAGATGATTCCTACTACAGATTGAGGGTATACCGTAGCCCAC	196			
Db	121	AGCGTATATCTCTCTACGATGTGCCCTTCACTTCAGCTTCGAGGGATCCCTACGCCAGC	180			
QY	197	CGCCAGTGGGTGAGCTGAGATTAAAGCACCCGAGGACCAACACACCCTGGATGCTGTC	256			
Db	181	CTCCGGTGGGGAGATGGTCGGTTTAAAGCCCCCTCAGAGGCCCATTTCCCTGGACGATTC	240			
QY	257	GCGATTGTGCACATCAAAGATACTCACTAGTCAGTGTGATTTTAAACGGCCAAAGTGT	316			
Db	241	GCGACATGCAAGCCGCAAGAGATAAAGGCCGTCCAGGNGCAGTTGCTTGATGATAAGTAG	300			
QY	317	GTTGGCTCAGAGGATTCCTCAATCCATAAGTGTCTATACGATTAATCTCAATCCGAAACTA	376			
Db	301	AAGGCTCCGAGACATCCCTCTATCTCAATGATGTACACCAACAATGTGAAGCCGACAAAG	360			
QY	377	AACGTCGCTTTAGTATACATACATAGTGTGGTTTATTATCGGTGAATAATCATCGTG	436			
Db	361	CTCGCCCGGTTTATGTGTGGATTACAGGAGGAGGCTTCAATTCGGCGAGGCCAANTCGG	420			
QY	437	ATATGATGATGGTCCTGATTTTCATTAAAGAGANGTGGTGTGGATTAAACATACATATC	496			
Db	421	AATGATATGAGCCCGCATTTACTTATGAAGAAAGATGTTGTTCTCGACAGATACAGTACC	480			
QY	497	GTTTGGGAGCTCTAGGTTTCTPAGTTTAAATTCAGAAACCTPATATGTCGCCGGAATG	556			
Db	481	GACTTGGGGGCTTTGGGATTTATGAGCTTAAATTCGCCGAGCTAAATGTACAGGAANAG	540			
QY	557	CCGGCCTTAAGATCAAGCATGCGCTT	584			
Db	541	CTGGCTTCAGAGATCAGGTGCTGGCCTT	568			
RESULT 6						
LOCUS	Bi628316	674 bp	mRNA	linear	EST 10-SEP-2001	
DEFINITION	BH56682 Sprime RH Drosophila melanogaster normalized Head pfic-1 Drosophila melanogaster cDNA clone BH56682 5 similar to alpha-Est: Fban000112 GO: carboxyesterase (GO:0004091); carboxyesterase (GO:0004091) located on: 3R 84D5-84D5.; 08/22/2001, mRNA sequence. Accession Bi628316 GI:15530524					

KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 674)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champs, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Mungall, C.J., Nuno, J., Pacleb, J., Paragas, V., Park, S., Phouanevong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S. and Rubin, G.M.
TITLE BDGP/HMI RH Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, estfruitfly.berkeley.edu
Plate: RH.566 row: G column: 10
High quality sequence stop: 558.
Location/Qualifiers
1..674
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH56682"
/clone_lib="RH Drosophila melanogaster normalized Head p1C-1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: p1C1. Site.1: XhoI. Site.2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
BASE COUNT 153 a 170 c 195 g 155 t 1 others
ORIGIN
Query Match 14.7%; Score 251.6; DB 13; Length 674;
Best Local Similarity 65.4%; Pred. No. 8.2e-58;
Matches 368; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
FEATURES
source
1 ATGATTTCAACGCTAGTTGATGAGAAATTAATGAATTAATGAATTAATGAAT 60
111 ATGATTAAGAACCTCGCTTGTGGAGCGCTTGGCGCGCTCAAAACCATGCGCAT 170
61 AAGTTTAACTATGTTTAACTACCAATGAACGGTGTAGTGAACATAATATGCGC 120
111 AAGTCAGCACTATCGCCAGTCGACCAATGAACAGTTGTGCGCCGACGAGTACGCGC 230
121 AAAGTGAAGCGCTTAACGTTTAACTGTAGATGATGATCTCTACTAGATTGAGGGT 180
111 AAGTGAAGCGCTTAACGTTTAACTGTAGATGATGATCTCTACTAGATTGAGGGT 180
231 CAAGTGAGGGGTATCAACGCTATCTCTACGATGAGCCCTACTTACGCTTCAGAGGT 290
161 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCAACCCGACGACACACA 240
291 ATCCCGTACGCCCAACCGCTGGGTGGGAGTGGCGGTTTAAAGCCCGCCAGAGGCCCAT 350
241 CCGTGGAGTGTGCGCATGTTGATGATCAATCAATGAAGATTAATGATGATGATTTT 300
111 CCGTGGAGTGTGCGCATGTTGATGATCAATCAATGAAGATTAATGATGATGATTTT 300
351 CCGTGGAGTGTGCGCATGTTGATGATCAATCAATGAAGATTAATGATGATGATTTT 300
411 GCTTCGATTAAGTAGAGGGCTCCGAGGACTGCTCTATCTCAATGTGATGACCAACAT 470
301 ATACGGGCAAAAGTGTGCGCATGTTGATGATCAATCAATGAAGATTAATGATGATTT 360
411 GCTTCGATTAAGTAGAGGGCTCCGAGGACTGCTCTATCTCAATGTGATGACCAACAT 470
361 CTAAATCCCGAACTAAAGCTCCCTTTAGTATACATACATGAGTGTGTTTATTATC 420
471 GTGAAGCCCGACAAAGCTGCGCGGTTTGTGATTCACGAGGAGGCTTCATTTATC 530
421 GGTGAATATCATCGATATGATGATGATGATTTTCAATTAAGAGATGTGTTG 480

Db 531 GGCGAGGCCAATCGGGAGATGATGCGCCGGATTACTTATGAAGAGATTTGTTC 590
OY 481 ATTAACATACATATATGCTTTGGAGCTCTAGCTTTTCTTAATTAATCAGAACCTT 540
Db 591 GTACAGATACATATGCTTTGGAGCTCTAGCTTTTCTTAATTAATCAGAACCTT 540
OY 541 AATGCCCCGATATGCGCGCT 563
Db 651 AATGATCAGAGAAATGCTGCGCT 673
RESULT 7
B1635372
LOCUS B1635372 676 bp mRNA linear EST 10-SEP-2001
DEFINITION SD16705.5prine SD Drosophila melanogaster Schneider L2 cell culture
port2 Drosophila melanogaster cDNA clone SD16705 5 similar to
alpha-Est7: FBan0001112 GO: [carboxyesterase (GO:0004091);
carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5; 05/18/2001
cDNA sequence.
ACCESSION B1635372
VERSION B1635372.1 GI:15537582
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 676)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, estfruitfly.berkeley.edu
Plate: SD.167 row: A column: 5
High quality sequence stop: 641.
Location/Qualifiers
1..676
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD16705"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell culture port2"
/lab_host="DH5-alpha"
/note="Vector: pOT2; Site.1: EcoRI; Site.2: XhoI. Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
BASE COUNT 155 a 173 c 194 g 154 t
ORIGIN
Query Match 14.7%; Score 251; DB 13; Length 676;
Best Local Similarity 65.4%; Pred. No. 1.2e-57;
Matches 368; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
FEATURES
source
1 ATGATTTCAACGCTAGTTGATGAGAAATTAATGAATTAATGAATTAATGAAT 60
111 ATGATTAAGAACCTCGCTTGTGGAGCGCTTGGCGCGCTCAAAACCATGCGCAT 173
114 ATGATTAAGAACCTCGCTTGTGGAGCGCTTGGCGCGCTCAAAACCATGCGCAT 173
61 AAGTTTAACTATGTTTAACTACCAATGAACGGTGTAGTGAACATAATATGCGC 120
111 AAGTTTAACTATGTTTAACTACCAATGAACGGTGTAGTGAACATAATATGCGC 120
174 AAAGTTCAGCACTATCGCCAGTCGACCAATGAACAGTTGTGCGCCGACGAGTACGCGC 233
121 AAAGTGAAGCGCTTAACGTTTAACTGTAGATGATGATCTCTACTAGATTGAGGGT 180
234 CAAGTGAGGGGTATCAACGCTATCTCTACGATGAGTGCCTACTTACGCTTCAGAGGT 293
181 ATACCGTACGCCCAACCGCCAGTGGGTGAGATTTAAAGCAACCCGACGACACACA 240
111 ATACCGTACGCCCAACCGCCAGTGGGTGAGATTTAAAGCAACCCGACGACACACA 240

Db 294 ATCCGTCACGCCACCTCCGCTGGGGAGTTGCCGTTAAGCCCTCAGAGGCCCAT 353
Qy 241 CCTGGGATGATGTGCGGATGTTGCAATCATTAAGATAGTCAGTCAAGTATTT 300
Db 354 CCTGGGAGCGATTCGGCACTGCAGCCAGCGAGATAGCGCTCCAGTGCAGTTC 413
Qy 301 ATAAACGGCAAGTGTGTGCTCAGACGATTTGCTATACCTAGTGTCTATACGATAT 360
Db 414 GTCTTCGATTAAGGTAGAGGCTCCGAGGACTGCTCTATCTCATATGTACCAACAAT 473
Qy 361 CTAAATCCGGAACCTAAAGCTCCGCTTTTATATACATATAGTGTGTGTTTATTC 420
Db 474 GTAAAGCCCAACAGCTCGCCGCTTATGTTGATTCAGGAGAGGCTTCATATTC 533
Qy 421 GGTGAATATCATGCTATATGTTGCTGCTGATTTATTTAAAGGATGTGTTG 480
Db 534 GCGGAGCCCAATCGGAAATGTGTGGCCGATTTACTTTATGAAGACATGTGTTC 593
Qy 481 ATTAACATACATATGCTTTGGAGCTAGTCTTTCTAAGTTAAATTCAGACACTT 540
Db 594 GTACGATTAAGTACGACTTGGGGCTTTGGATTTATGATCTTAAGTCCCGAGCTA 653
Qy 541 AATGTCGCCGTAATGCCGCT 563
Db 654 AATGACAGGAATGCTGCT 676

RESULT 8
Bi614181 673 bp mRNA linear EST 07-SEP-2001
LOCUS RH43493.5prime RH Drosophila melanogaster normalized head pFIC-1
DEFINITION Drosophila melanogaster cDNA clone RH43493.5 similar to alpha-Est7:
Fban0001112 GO: [carboxylesterase (GO:0004091)] carboxylesterase
(GO:0004091) located on: 3R 84D5-84D5:: 08/18/2001, mRNA sequence.
Bi614181
ACCESSION Bi614181.1 GI:15509706
VERSION EST.
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 673)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
, J., Chame, M., Chavez, C., Dorsett, V., Farfan, D., Fritse, E., George
, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miera, S.,
Mungall, C.J., Nunco, J., Pacle, J., Paragas, V., Park, S.,
Phuanaenavong, S., Wan, K., Yu, C., Lewis, S.E., Celinker, S. and Rubin
, G.M.
TITLE BDGP/HMI RH Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estfruitfly.berkeley.edu
Plate: RH 434 row: H column: 9
High quality sequence stop: 553.
Location/Qualifiers
1. 673
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH43493"
/clone_1lb="RH Drosophila melanogaster normalized head
pFIC-1"
/sex="male and female"
/dev_stage="adult"
/lab_host="DHS-alpha Tona"
/note="Organ: head; Vector: pFIC1; Site:1; XhoI; Site:2;
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

BASE COUNT 153 a 169 c 195 g 155 t 1 others
ORIGIN
Query Match 14.6%; Score 250; DB 13; Length 673;
Best Local Similarity 65.2%; Pred. No. 2,2e-57;
Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
Qy 1 ATGAATTTCAAGCTTGGTTGATGAGAAATTAATGAGATTAATGATTAAT 60
Db 111 ATGAATTAAGATCTCGGCTTTGTGAGCCCTTGCGCTCAACATCGAGCAT 170
Qy 61 AAGTTTAAATATGCTTTAACTACCATGAACGCTGTGCTGAATCATATATGC 120
Db 171 AAATCCAGAGATATCCGAGTACCAATGAAGAGTGTGCTGACACGAGATAC 230
Qy 121 AAATGAAGGCGTTAAAGCTTTAACTGTGATGATATCTTACTACTACATTTG 180
Db 221 CAAGTGAGGATATCAAGCTCTATCTCTAGATGTGCTTACTACTACATTTG 290
Qy 181 ATACCGTACGCCCAACGCCAGTGGTACCTGAGATTTAAACACCCGAGCACA 240
Db 291 ATCCGTCAGCCCAAGCCCTCCGCTGGGAGTGGGTTTAAAGCCCTCAGAGCC 350
Qy 241 CCTGGATGCTGCGGATTTGTCATCATTAAGATAGTCAAGTTGATTT 300
Db 351 CCTGGAGCGAGTTCGCGACTGCAGCCAGCCGAAGATTAAGCCCTCAGTGCAG 410
Qy 301 ATACGGCCAAAGTGTGCTCAGAGATTTGCTATACCTAAGTCTTATAGAAAT 360
Db 411 GTCTTCGATTAAGTACGAGGCTCCGAGGAGCTCTATCTCAATGTGTACCAACA 470
Qy 361 CTAAATCCGGAACCTAAAGCTCCGCTTTATATACATATAGTGTGTTTATATC 420
Db 471 GTGAAGCCCGAAGAGCTGCGCGTTATGTTGATTCAGGAGAGCGCTTATATC 530
Qy 421 GGTGAATATCATGCTATATGATGCTGCTGATTTTATTAATAAAGAGTGTG 480
Db 531 GCGGAGCCCAATCGGAAATGTATGCGCGATTTCTTATGAAGAAGATGTGTC 590
Qy 481 ATTAACATACATATGCTTTGGAGCTAGTCTTTCTAAGTTAAATTCAGAAC 540
Db 591 GTACGATTAAGTACGACTTGGGGCTTTGGATTTATGAGCTTAAGTCCCGAG 650
Qy 541 AATGTCGCCGTAATGCCGCT 563
Db 651 AATGACAGGAATGCTGCT 673

RESULT 9
Bi639486 660 bp mRNA linear EST 10-SEP-2001
LOCUS SD22067.5prime SD Drosophila melanogaster Schneider I2 cell culture
DEFINITION POT2 Drosophila melanogaster cDNA clone SD22067.5 similar to
alpha-Est7: Fban0001112 GO: [carboxylesterase (GO:0004091)]
carboxylesterase (GO:0004091) located on: 3R 84D5-84D5:: 05/19/2001
, mRNA sequence.
Bi639486
VERSION Bi639486.1 GI:15541696
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 660)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA

Db 471 GTGAAGCCGACAGAGGCTGCGCCGGTTAGTTGGATTCCAGGAGAGGCTTCAATATC 530

QY 421 GGTAATAATCATGTCGTATGTATGTCCTGATTTATTTAAAGATGCGTGTG 480

Db 531 GCGAGAGCCCAATCGGAATGATGATGCGCGGATTTATGATAAAGATGTTGTTTC 590

QY 481 ATTACATACAAATATGCTTTGGAGCTAGCTTTTCTAAGTTTAAATTGAGAGACTT 540

Db 591 GTACAGATACAGTACGACTTGGCGCTTTGGATTATAGCTTAAGTCCCGGAGCTA 650

QY 541 AATGTCCCGGTAAATGCCGCC 562

Db 651 AATGTACCAAGAAATGCTGCC 672

RESULT 11

Bi233202 670 bp mRNA linear EST 11-JUL-2001

LOCUS RE29491.5prlme RE Drosophila melanogaster normalized Embryo pflc-1

DEFINITION Drosophila melanogaster cDNA clone RE29491 5 similar to alpha-Est7: FBan0001112 located on: 3R 84D5-84D5; 04/12/2001, mRNA sequence.

ACCESSION Bi233202

VERSION Bi233202.1 GI:14700784

KEYWORDS EST

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 670)

Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Bertman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouaneavong, S., Wan, K., Yu, C., Lewis, S. E., Celnikier, S. and Rubin, G. M.

TITLE BDGP/HMI RE Drosophila EST Project

JOURNAL Unpublished (2001)

COMMENT Contact: Stapleton, M.

BDGP Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu Plate: RE 294 row: H column: 7 High quality sequence stop: 534.

FEATURES

source

1..670

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="RE29491"

/clone_lib="RE Drosophila melanogaster normalized Embryo pflc-1"

/sex="male and female"

/dev_stage="0-24 hours mixed stage embryonic"

/lab_host="DHS-alpha Tona"

/note="Organ: embryo; Vector: pflc1, Site_1: XhoI, Site_2: BamHI. Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

BASE COUNT 152 a 168 c 194 g 155 t 1 others

ORIGIN

Query Match 14.5%, Score 248, DB 13, Length 670;

Best Local Similarity 65.1%, Pred. No. 7.9e-57;

Matches 365; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 1 ATGATTTCAAGCTAGTTGATGAGAAATTAATGAAGATTAATGCTTAAT 60

Db 110 ATGATTAAGAACCTTCGCTGTGTGGAGCGCTTGCGCGCTCAAAACCATTCGAGCAT 169

QY 61 AAGTTTAACTATCGTTTAACTACCAATGAAGCGTGTAGCTGAAGACTGAATATGCC 120

Db 170 AAAGTCACAGATATGCGCCAGTCCACCAATGAAGACAGTTGTGCGGACAGAGATAGCGC 229

QY 121 AAAGTAAGAGCGCTTAACGTTTAATCTGTCAGATGATTCCTACTAGACTTTAGAGGT 180

Db 230 CAAGTAGAGGGATCAAGGCTATCTCTCTAGAGATGCCCTACTACGCTTCAGAGGT 289

QY 181 ATACCTAGGCCCAACCCGACAGTGTGAGCTGAGATTAAAGCAACCCAGACCAACA 240

Db 290 ATCCGTACGCCACAGCTCCGGTGGGGAGTTGCGGTTTAAAGCCCTCAGAGGCCATT 349

QY 241 CCCTGGATGTGTGCGCGCATTTTGCATATCAATGAATAGTCAGTCAAGTGAATTT 300

Db 350 CCTGGGAGCGAGTTCCGACAGCTCCAGCCAGCAAGAGATGAAGCCGTCAGGTGAGCTT 409

QY 301 ATAAGCGCAAGTGTGTCAGAGATGTCATACCTAAGTGTATACGAATAT 360

Db 410 GTCTTCGATTAAGGTAGAGGCTCCAGAGACTGCTCTATCTCAATGTGACCAACAT 469

QY 361 CTAATCCCGAAACATAAGCGTCCGCTTTAGTATACATACATGCTGTTTATATTC 420

Db 470 GTGAAGCCCGACAAGGCTCGCCCGGTTATGTTGATTCACAGAGAGAGGCTTCATATTC 529

QY 421 GGTAATAATCATGTCGTATGTATGTCCTGATTTATTTATTTAAAAAGATGTGTGTTG 480

Db 530 GCGAGAGCCCAATCGGAATGTATGCGCCGATTTACTTATGANAAGATGTTTCTTC 589

QY 481 ATTACATACAAATATGCTTTGGAGCTAGCTTTTCTAAGTTTAAATTCAGAACACTT 540

Db 590 GTACAGATACATACGACTTGGCGCTTTGGAGTTTATGAGCTTATAGTCCCGGAGCTA 649

QY 541 AATGTCCCGGTAAATGCCGCC 561

Db 650 AATGTACCAAGAAATGCTGCC 670

RESULT 12

At113763 648 bp mRNA linear EST 19-APR-2001

LOCUS GH10213.5prlme GH Drosophila melanogaster head pot2 Drosophila

DEFINITION melanogaster cDNA clone GH10213 5prlme similar to U51050: Drosophila melanogaster alpha esterase (aef) gene, partial cds, mRNA sequence.

ACCESSION At113763

VERSION At113763.1 GI:3514566

KEYWORDS EST

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 648)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G. M.

TITLE BDGP/HMI Drosophila EST Project

JOURNAL Unpublished (2001)

COMMENT Contact: Stapleton, M.

BDGP Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu Plate: 102 row: B column: 1 High quality sequence stop: 435.

FEATURES

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 1 (bases 1 to 646)
 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G.M.
 BDGP/HHMI Drosophila EST Project
 Unpublished (2001)
 CONTACT: Stapleton, M.
 COMMENT BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
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 A1293416
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 1 (bases 1 to 646)
 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G.M.
 BDGP/HHMI Drosophila EST Project
 Unpublished (2001)
 CONTACT: Stapleton, M.
 COMMENT BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
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 Best Local Similarity 65.0%; Pred. No. 5.2e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
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; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
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; EARLIER FILING DATE: 1995-11-23
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; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
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Db 1381 CGTAGTGAGCTGTGTTAAGGGTGTAGTCATGCTATGATTAACCTAATTTCTCTGG 1440
OY 1441 AATGAATTTGGCAAGCTATGCTTAAAGATCGGCTGATTAACAAATTTGAACGTATG 1500
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Db 1441 AATGAATTTGGCAAGCTATGCTTAAAGATCGGCTGATTAACAAATTTGAACGTATG 1500
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OY 1501 ACTGTAATATGATACATTTGCCACCACTGTAATCCTTATGACAAATTAAGAGT 1560
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Db 1501 ACTGTAATATGATACATTTGCCACCACTGTAATCCTTATGACAAATTAAGAGT 1560
OY 1561 ATGGAATAATGTTTCTGGGATCCATTAAGAAATCCGATGAAGATACAACTGTTGAT 1620
    |||||||
Db 1561 ATGGAATAATGTTTCTGGGATCCATTAAGAAATCCGATGAAGATACAACTGTTGAT 1620
OY 1621 ATTAGATGATGAATTAAGAAATGATGTCCTGAATGATTAAGATTAACATGGAG 1680
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Db 1621 ATTAGATGATGAATTAAGAAATGATGTCCTGAATGATTAAGATTAACATGGAG 1680
OY 1681 TCGATGTTGAAAACATAGAGATTTATTTAG 1713
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Db 1681 TCGATGTTGAAAACATAGAGATTTATTTAG 1713

RESULT 3
US-09-68-960-1
; Sequence 1, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/A096/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ. ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-1

Query Match 99.8%; Score 1709.8; DB 4; Length 1713;
Best Local Similarly 99.9%; Pred. No. 0;
Matches 1711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ATGAATTTCAAGCTTAGTTGATGAGAAATTAAGAGATTAATGATTAATGAAAT 60
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Db 1 ATGAATTTCAAGCTTAGTTGATGAGAAATTAAGAGATTAATGATTAATGAAAT 60
OY 61 AAGTTTTAACTATCGTTTAACCTACCAATGAACGGGTGATAGCTGAACATGAATATGC 120
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Db 61 AAGTTTTAACTATCGTTTAACCTACCAATGAACGGGTGATAGCTGAACATGAATATGC 120
OY 121 AAGGTGAAGCGCTTAACGTTTAACCTGTGTACGATGATTCCTACTACAGTTTGAAGGT 180
    |||||||
Db 121 AAGGTGAAGCGCTTAACGTTTAACCTGTGTACGATGATTCCTACTACAGTTTGAAGGT 180
OY 181 ATACCGTAGCGCCAAACGCGGAGTGGTGAAGTGAATTAAGCAACCCAGCGACCAACA 240
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Db 181 ATACCGTAGCGCCAAACGCGGAGTGGTGAAGTGAATTAAGCAACCCAGCGACCAACA 240
OY 241 CCGTGGAGTGTGCGGATGTTGCAATCATTAAGATTAAGTCAAGTCAAGTTGATTTT 300
    |||||||
Db 241 CCGTGGAGTGTGCGGATGTTGCAATCATTAAGATTAAGTCAAGTCAAGTTGATTTT 300
OY 301 ATAAAGGCAAGTGTGTGCTCAGAGAGATGTCTATACCTAAGTGTCTATACGAATAT 360
    |||||||
Db 301 ATAAAGGCAAGTGTGTGCTCAGAGAGATGTCTATACCTAAGTGTCTATACGAATAT 360
OY 361 CTAATATCCGAACATAAAGCGTCCGTTTATGATATACATACATAGGAGTTTATATTC 420
    |||||||
Db 361 CTAATATCCGAACATAAAGCGTCCGTTTATGATATACATACATAGGAGTTTATATTC 420
OY 421 GGTGAATATCATGATATGATGTCCTGATTATTCAATTAAAGAGATGCTGTG 480
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Db 421 GGTGAAATCATCGTATATGATATGCTGATTTATTTCAATTAAGAGATGGTGTG 480
Qy 481 ATTAACATACATAATCTTTGGAGCTCTAGCTTTCTAAGTTAAATCAGAACCTT 540
Db 481 ATTAACATACATAATCTTTGGAGCTCTAGCTTTCTAAGTTAAATCAGAACCTT 540
Qy 541 AATGTCGGCGGTAATGCGCGGCTTAAAGATCAGTACGCTTGGTGGATTTAAAT 600
Db 541 AATGTCGGCGGTAATGCGCGGCTTAAAGATCAGTACGCTTGGTGGATTTAAAT 600
Qy 601 AATGTCGGCGGTAATGCGCGGCTTAAAGATCAGTACGCTTGGTGGATTTAAAT 600
Db 601 AATGTCGGCGGTAATGCGCGGCTTAAAGATCAGTACGCTTGGTGGATTTAAAT 600
Qy 661 GCTGCTCTACCCACTACATGATGTTAAACCGAACAACTCGCGCTTTTCATGCTG 720
Db 661 GCTGCTCTACCCACTACATGATGTTAAACCGAACAACTCGCGCTTTTCATGCTG 720
Qy 721 ATACTAATGTCGGGTATGCTATTTGCTCATTTGGCTAATACCAATGTCACATGCTGC 780
Db 721 ATACTAATGTCGGGTATGCTATTTGCTCATTTGGCTAATACCAATGTCACATGCTGC 780
Qy 781 TTGACCTTACCAATTTGGCGGCTTAAAGGTGAGATTAATGATPAGATGTTTGA 840
Db 781 TTGACCTTACCAATTTGGCGGCTTAAAGGTGAGATTAATGATPAGATGTTTGA 840
Qy 841 TTTCTTTGAAAGCAAGCAGATTTAAATTAATTAATTAATTAATTAATTAATTA 900
Db 841 TTTCTTTGAAAGCAAGCAGATTTAAATTAATTAATTAATTAATTAATTAATTA 900
Qy 901 GAAGAGGCTACAAATTAAGTATGTTTCTTTGGTCCCTGTCAGCATATCAGACC 960
Db 901 GAAGAGGCTACAAATTAAGTATGTTTCTTTGGTCCCTGTCAGCATATCAGACC 960
Qy 961 GCTGATGTCCTTACCAAAATCTCTGGGAAATGTTAAACTGCTGGGTAATTCG 1020
Db 961 GCTGATGTCCTTACCAAAATCTCTGGGAAATGTTAAACTGCTGGGTAATTCG 1020
Qy 1021 ATACCCATATGATGCTTACACTTCAATGAGGCTATTTTCACTTCAATTTCTTA 1080
Db 1021 ATACCCATATGATGCTTACACTTCAATGAGGCTATTTTCACTTCAATTTCTTA 1080
Qy 1081 CAAATGCTATGCTTAAAGAAATGGAATGTTGTCATTTTGTGCCAAGTGAATG 1140
Db 1081 CAAATGCTATGCTTAAAGAAATGGAATGTTGTCATTTTGTGCCAAGTGAATG 1140
Qy 1141 GCTGATGTCGAAGCAGCGCCGAGACCTTGAATGCTGCTAAATTAATAAGGCT 1200
Db 1141 GCTGATGTCGAAGCAGCGCCGAGACCTTGAATGCTGCTAAATTAATAAGGCT 1200
Qy 1201 CATGTTACAGGAAGAACCAACAGCTGATTTATGATGCTTGTCTCAGATCTAT 1260
Db 1201 CATGTTACAGGAAGAACCAACAGCTGATTTATGATGCTTGTCTCAGATCTAT 1260
Qy 1261 TTCTGGTCCCATGCTGCTTGTGCAATTAAGTTCACTACACTCCGGTACACC 1320
Db 1261 TTCTGGTCCCATGCTGCTTGTGCAATTAAGTTCACTACACTCCGGTACACC 1320
Qy 1321 GTCTACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1321 GTCTACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Qy 1381 CGTAGTGAAGTGTGTAAAGGTGTAGTCACTGATGATTAACCTATTTCTTGG 1440
Db 1381 CGTAGTGAAGTGTGTAAAGGTGTAGTCACTGATGATTAACCTATTTCTTGG 1440
Qy 1441 AATCAATGCGCAAGCTATGCTTAAAGATGCTGATTAACCAAAATTAAGCTAG 1500
Db 1441 AATCAATGCGCAAGCTATGCTTAAAGATGCTGATTAACCAAAATTAAGCTAG 1500
Qy 1501 ACTGCTATGATACAAATTTGCCACACTGTGATTCCTTAATGCAATGAAGGT 1560
Db 1501 ACTGCTATGATACAAATTTGCCACACTGTGATTCCTTAATGCAATGAAGGT 1560

Qy 1561 ATGGAATATGTTCTGGGATCATTAAAGATCCGATGAGTATACAGTGTGAT 1620
Db 1561 ATGGAATATGTTCTGGGATCATTAAAGATCCGATGAGTATACAGTGTGAT 1620
Qy 1621 ATTAGTATGATTAAGATGATGATGCTGCTGAATGATTAAGTAAATGAGG 1680
Db 1621 ATTAGTATGATTAAGATGATGATGCTGCTGAATGATTAAGTAAATGAGG 1680
Qy 1681 TCGATGTTGAAATACATAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAATACATAGATTTATTTAG 1713

RESULT 4
US-09-068-960-5
; Sequence 5, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-5

Query Match 99.6%; Score 1706.6; DB 4; Length 1713;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAAGGAATTAATGATTAAT 60
Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAAGGAATTAATGATTAAT 60
Qy 61 AAGTTTAACTATGCTTAACTACCAATGAACGCTGAGTGAATATGCT 120
Db 61 AAGTTTAACTATGCTTAACTACCAATGAACGCTGAGTGAATATGCT 120
Qy 121 AAAGTAAAGCGGTTAAACGTTAACTGTTACGATGATTTCTTACAGTTGAGGT 180
Db 121 AAAGTAAAGCGGTTAAACGTTAACTGTTACGATGATTTCTTACAGTTGAGGT 180
Qy 181 ATACCTAGCGCCACCGCAGTGGTGAATGATTTAAAGCACCACCGACCAACA 240
Db 181 ATACCTAGCGCCACCGCAGTGGTGAATGATTTAAAGCACCACCGACCAACA 240
Qy 241 CCCTGGATGTTGCGGATGTTGCAATCATTAAGATTAAGTCAAGTGAATTT 300
Db 241 CCCTGGATGTTGCGGATGTTGCAATCATTAAGATTAAGTCAAGTGAATTT 300
Qy 301 ATACGGGCAAGGTTGCTCAGAGATGCTTACCTAAGTGTATACGAATAT 360
Db 301 ATACGGGCAAGGTTGCTCAGAGATGCTTACCTAAGTGTATACGAATAT 360
Qy 361 CTAATCCGAAACTAAGCTCCGTTTATGATTAATACATGATGCTGTTTATATC 420
Db 361 CTAATCCGAAACTAAGCTCCGTTTATGATTAATACATGATGCTGTTTATATC 420
Qy 421 GGTGAAATATCGTATGATGATGCTGATTAATTAAGATGATGCTGTTG 480
Db 421 GGTGAAATATCGTATGATGATGCTGATTAATTAAGATGATGCTGTTG 480
Qy 481 ATTAACATACATATGTTGGAGCTAGGTTTCTAAGTTAAATTCAGAAAGCTT 540

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Db 481 AATTACATACATATCGTTGGAGCTCTAGTTTCTTAAGTTTAAATTGAGAGACCTT 540
Qy 541 AATGTCGGCGGTATATGCCGCTTAAAGATCAAGTCATGCGCTTGGATTAAAT 600
Db 541 AATGTCGGCGGTATATGCCGCTTAAAGATCAAGTCATGCGCTTGGATTAAAT 600
Qy 601 AATGTCGGCGGTATATGCCGCTTAAAGATCAAGTCATGCGCTTGGATTAAAT 600
Db 601 AATGTCGGCGGTATATGCCGCTTAAAGATCAAGTCATGCGCTTGGATTAAAT 600
Qy 661 GCTGCTCTACCACTACATGATGTTAAACCAACAACTCCGCGCTTTCCATCGTGT 720
Db 661 GCTGCTCTACCACTACATGATGTTAAACCAACAACTCCGCGCTTTCCATCGTGT 720
Qy 721 AATGTCGGCGGTATATGCCGCTTAAAGATCAAGTCATGCGCTTGGATTAAAT 780
Db 721 AATGTCGGCGGTATATGCCGCTTAAAGATCAAGTCATGCGCTTGGATTAAAT 780
Qy 781 TTTACCTTAGCCAAATTTGGCGGCTATAAGGCTAGATTAAGATGTTTGGAA 840
Db 781 TTTACCTTAGCCAAATTTGGCGGCTATAAGGCTAGATTAAGATGTTTGGAA 840
Qy 841 TTTCTTATGAAAGCCACAGCAGATTTAAACTTGAAGAAAAGTTTAACTCTA 900
Db 841 TTTCTTATGAAAGCCACAGCAGATTTAAACTTGAAGAAAAGTTTAACTCTA 900
Qy 901 GAAAGCGCTACAAATTAAGTCATGTTTCTTTCCTCCACTGTTGACCATATAGACC 960
Db 901 GAAAGCGCTACAAATTAAGTCATGTTTCTTTCCTCCACTGTTGACCATATAGACC 960
Qy 961 GCTGATTTGTTCTTACCCAAATCTCTGGGAAATGTTTAAACTGTTGGGTAATTCG 1020
Db 961 GCTGATTTGTTCTTACCCAAATCTCTGGGAAATGTTTAAACTGTTGGGTAATTCG 1020
Qy 1021 AATCCACTATGATGTTGTTAACTCATATGAGGCTATATTTTCACTCAATTCCTAG 1080
Db 1021 AATCCACTATGATGTTGTTAACTCATATGAGGCTATATTTTCACTCAATTCCTAG 1080
Qy 1081 CAAATGCTTATGCTTGAAGAACTTGTGCAATTTTGTGCGCAAGTGAATTTG 1140
Db 1081 CAAATGCTTATGCTTGAAGAACTTGTGCAATTTTGTGCGCAAGTGAATTTG 1140
Qy 1141 GCTGATGCTGAAGCAGCAGCCCAAGACCTTGAAGGCTTAAATTTAAAGGCT 1200
Db 1141 GCTGATGCTGAAGCAGCAGCCCAAGACCTTGAAGGCTTAAATTTAAAGGCT 1200
Qy 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTGTCTCACAATCTAT 1260
Db 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTGTCTCACAATCTAT 1260
Qy 1261 TTTCTGCTTCCCATCATGCTTGTGCAATTTCAATCAACACCTCCGCTGACCC 1320
Db 1261 TTTCTGCTTCCCATCATGCTTGTGCAATTTCAATCAACACCTCCGCTGACCC 1320
Qy 1321 GCTGCTTATGCTTGTGCAATTTCAATCAACCTTATCAATCCCTATGCTATATG 1380
Db 1321 GCTGCTTATGCTTGTGCAATTTCAATCAACCTTATCAATCCCTATGCTATATG 1380
Qy 1381 CGTAGTGAAGCTGTTAAAGGCTTATGCTATGCTGATTAACCTATTTCTTCTG 1440
Db 1381 CGTAGTGAAGCTGTTAAAGGCTTATGCTATGCTGATTAACCTATTTCTTCTG 1440
Qy 1441 AATCAATTTGCGCAACGATGCTTAAAGATCGCTGAATCAACAAATGACGATG 1500
Db 1441 AATCAATTTGCGCAACGATGCTTAAAGATCGCTGAATCAACAAATGACGATG 1500
Qy 1501 ACTGATATGATGATCAATTTGCGCAACGCTGATCTTATGCAATGAATGAAGT 1560
Db 1501 ACTGATATGATGATCAATTTGCGCAACGCTGATCTTATGCAATGAATGAAGT 1560
Qy 1561 ATGGAATATGTTCTCTGGATCAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
Db 1561 ATGGAATATGTTCTCTGGATCAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620

Db 1561 ATGGAATATGTTCTCTGGATCAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
Qy 1621 AATGTCATGATTAATGAAATGATGATGCTGTAATGATTAACATATGGAG 1680
Db 1621 AATGTCATGATTAATGAAATGATGATGCTGTAATGATTAACATATGGAG 1680
Qy 1681 TCGATGTTGAAATACATAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAATACATAGATTTATTTAG 1713

RESULT 5
US-08-669-524-1
; Sequence 1, Application US/08669524
; Patent No. 5843758
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, Robyn J.
; APPLICANT: NEWCOMB, Richard D.
; APPLICANT: ROBIN, Geoffrey C.
; APPLICANT: BOYCE, Thomas M.
; APPLICANT: CAMPBELL, Peter M.
; APPLICANT: PARKER, Anthony G.
; APPLICANT: OAKESHOT, John G.
; APPLICANT: SMYTH, Kerrie A.
; TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe Price Leblanc & Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 1451-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-669-524-1

Query Match 99.3%; Score 1701.8; DB 2; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAGATTAATGATGATAAAT 60
Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAGATTAATGATGATAAAT 60
Qy 61 AAGTTTAACTATCGTTTAACTACCAATGAAACGGTGTAGCTGAAACTGAATATG 120
Db 61 AAGTTTAACTATCGTTTAACTACCAATGAAACGGTGTAGCTGAAACTGAATATG 120
Qy 121 AAGTGAAGGCGTTAAACGTTTAACTGTGATGATGATTCCTACTACAGTTTGA 180
Db 121 AAGTGAAGGCGTTAAACGTTTAACTGTGATGATGATTCCTACTACAGTTTGA 180

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OY 181 ATACCGTACGCCCAACCCGAGTGGGTGAGTATTTAAAGCACCCAGGACCAACA 240
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Db 181 ATACCGTACGCCCAACCCGAGTGGGTGAGTATTTAAAGCACCCAGGACCAACA 240
OY 241 CCCTGGGATGGTGGCGGATTTGCAATCATAAAGATAGTCAGCAGTTGATTTT 300
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Db 241 CCCTGGGATGGTGGCGGATTTGCAATCATAAAGATAGTCAGCAGTTGATTTT 300
OY 301 ATAAAGGCAAGTGTGGCTCAGAGATGTCTATACCTAAAGTGTATACCAATAT 360
    |||||
Db 301 ATAAAGGCAAGTGTGGCTCAGAGATGTCTATACCTAAAGTGTATACCAATAT 360
OY 361 CTAAATCCCGAAAGCTAACGTCCTGTTTACTATACATACATGCTGGTGTATATC 420
    |||||
Db 361 CTAAATCCCGAAAGCTAACGTCCTGTTTACTATACATACATGCTGGTGTATATC 420
OY 421 GGTGAAATCATGATGATATGATGCTCTATATTTCAATTAAGAGATGTGTTG 480
    |||||
Db 421 GGTGAAATCATGATGATATGATGCTCTATATTTCAATTAAGAGATGTGTTG 480
OY 481 ATTAACATACATATCGTTTGGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAGACCT 540
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Db 481 ATTAACATACATATCGTTTGGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAGACCT 540
OY 541 AATGTGCGCGGTAAATGCCGCTTAAAGATCAAGTCATGGCCTTGCGTGGATTTAAAT 600
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Db 541 AATGTGCGCGGTAAATGCCGCTTAAAGATCAAGTCATGGCCTTGCGTGGATTTAAAT 600
OY 601 AATGCGCCCAACTTGGTGGCAATCCGCTAATATTTACACTTGGTGAAGGCCGT 660
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Db 601 AATGCGCCCAACTTGGTGGCAATCCGCTAATATTTACACTTGGTGAAGGCCGT 660
OY 661 GCTGCTCTACCCACTACATGATGTATTAACGCAAACTGCGGTCTTTTCCATCGTGT 720
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Db 661 GCTGCTCTACCCACTACATGATGTATTAACGCAAACTGCGGTCTTTTCCATCGTGT 720
OY 721 ATACTATATGCGGGTATGCTATTTGTCATTTGGCTAATCCCAATGTCAACATCGTGC 780
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Db 721 ATACTATATGCGGGTATGCTATTTGTCATTTGGCTAATCCCAATGTCAACATCGTGC 780
OY 781 TTACCTTTAGCCAAATTTGCCGCTAATAGGCTAGAGATATGATTAAGATGTTTGGAA 840
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Db 781 TTACCTTTAGCCAAATTTGCCGCTAATAGGCTAGAGATATGATTAAGATGTTTGGAA 840
OY 841 TTTCTTATGAAGCAAGCAGACAGATTTATTAATAAAGTTTGAAGAAAGTTTAACTCTA 900
    |||||
Db 841 TTTCTTATGAAGCAAGCAGACAGATTTATTAATAAAGTTTGAAGAAAGTTTAACTCTA 900
OY 901 GAAGAGCGTACAATAAGTGCATGTTCTTTGTCCTCCACTGTGAGCATATCAGACC 960
    |||||
Db 901 GAAGAGCGTACAATAAGTGCATGTTCTTTGTCCTCCACTGTGAGCATATCAGACC 960
OY 961 GGTGATTTGCTTTACCCAAACATCTCGGGAATGTTAAACTCTGGGGTAAATTCG 1020
    |||||
Db 961 GGTGATTTGCTTTACCCAAACATCTCGGGAATGTTAAACTCTGGGGTAAATTCG 1020
OY 1021 ATACCCATATGATGGTAAACATTTATGAGGCTCTATTTTCTCACTCAATTTCTAAG 1080
    |||||
Db 1021 ATACCCATATGATGGTAAACATTTATGAGGCTCTATTTTCTCACTCAATTTCTAAG 1080
OY 1081 CAAATGCCATATGATGGTAAACATTTGTCATATTTTGTGCAAGTGAATTCG 1140
    |||||
Db 1081 CAAATGCCATATGATGGTAAACATTTGTCATATTTTGTGCAAGTGAATTCG 1140
OY 1141 GGTGATTTGCTTTACCCAAACATCTCGGGAATGTTAAACTCTGGGGTAAATTCG 1200
    |||||
Db 1141 GGTGATTTGCTTTACCCAAACATCTCGGGAATGTTAAACTCTGGGGTAAATTCG 1200
OY 1201 CATGTTACGAGAAACACCAACAGCTGATTTTATGAGATCTTGTCTCACAATCTAT 1260
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Db 1201 CATGTTACGAGAAACACCAACAGCTGATTTTATGAGATCTTGTCTCACAATCTAT 1260

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OY 1261 TTTGTTTCCCATGCAATCGTTTGTTCGAATTTACGTTTCAATCAGACCTCGGTACACC 1320
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OY 1321 GTCTACTTGTATGCTTGCAGCTTGAGTGGGAAGATCTTTCATCCCTTCTATTAAG 1380
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Db 1321 GTCTACTTGTATGCTTGCAGCTTGAGTGGGAAGATCTTTCATCCCTTCTATTAAG 1380
OY 1381 CTTAGTGGAGCTGGTGTAAAGGGTGTAGTCAATGATGATGAATTAACCTATTTCTTGG 1440
    |||||
Db 1381 CTTAGTGGAGCTGGTGTAAAGGGTGTAGTCAATGATGATGAATTAACCTATTTCTTGG 1440
OY 1441 AATCAATTTGCCCAACCTATGCTTAAGAAATCGCGTGAATACAAACATTTGACCTATG 1500
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Db 1441 AATCAATTTGCCCAACCTATGCTTAAGAAATCGCGTGAATACAAACATTTGACCTATG 1500
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Db 1501 ACTGATATGATGATACAAATTTGCCACACCTGTAATCCTATATGCAATGAATTTGAAGT 1560
OY 1561 ATGGAATAATGTTTCTGGGATCCAAATTAAGAAATCCGATGAAGTATACAAAGTGTGAAT 1620
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Db 1561 ATGGAATAATGTTTCTGGGATCCAAATTAAGAAATCCGATGAAGTATACAAAGTGTGAAT 1620
OY 1621 ATTAGTATGATGATTAAGAAATGATGATGCTGCGTAAGTGAATTAACATGGGAG 1680
    |||||
Db 1621 ATTAGTATGATGATTAAGAAATGATGATGCTGCGTAAGTGAATTAACATGGGAG 1680
OY 1681 TCGATGTTTGAATAACATAGAGATTTATTTAG 1713
    |||||
Db 1681 TCGATGTTTGAATAACATAGAGATTTATTTAG 1713

RESULT 6
US-09-068-960-7
? Sequence 7, Application US/09068960A
? Patent No. 6235515
? GENERAL INFORMATION:
? APPLICANT: Commonwealth Scientific and Industrial Rarch. Org.
? TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
? FILE REFERENCE: Attorney Docket No. 6235515 50179-051
? CURRENT APPLICATION NUMBER: PCT/AU96/00746
? EARLIER FILING DATE: 1998-05-20
? EARLIER FILING DATE: 1996-11-22
? EARLIER APPLICATION NUMBER: AU 6751
? NUMBER OF SEQ ID NOS: 43
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 7
? LENGTH: 1713
? TYPE: DNA
? ORGANISM: Lucilia cuprina
US-09-068-960-7

Query Match 99.3%, Score 1701.8; DB 4; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGCAAGTTAAATGCATGAAAT 60
    |||||
Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGCAAGTTAAATGCATGAAAT 60
OY 61 AAGTTTAACTATCGTTTAACTACCAATGAACGGGTGAGTGAACATGAATATGCG 120
    |||||
Db 61 AAGTTTAACTATCGTTTAACTACCAATGAACGGGTGAGTGAACATGAATATGCG 120
OY 121 AAAGTGAAGGCGTTAAACGTTTAACTGTGTAGCATGATTTCTACTACAGTTTGAAGGT 180
    |||||
Db 121 AAAGTGAAGGCGTTAAACGTTTAACTGTGTAGCATGATTTCTACTACAGTTTGAAGGT 180
OY 181 ATACCGTACGCCCAACCCGAGTGGGTGAGTATTTAAAGCACCCAGGACCAACA 240
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TOPOLOGY: Linear
MOLECULE TYPE: DNA (genomic)
US-08-669-524-2

Query Match 97.9%; Score 1676.6; DB 2; Length 1713;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGATTTTCACGTTAGTTGATGAGAAATTAATGAGAGTTAAATGATTTGAAAT 60
DB 1 ATGATTTTCACGTTAGTTGATGAGAAATTAATGAGAGTTAAATGATTTGAAAT 60
QY 61 AAGTTTAAATATGCTTAACTACCAATGAACGCTGTAGCTGAATATGCT 120
DB 61 AAGTTTAAATATGCTTAACTACCAATGAACGCTGTAGCTGAATATGCT 120
QY 121 AAGTGAAGGCGTTAAAGCTTAACTGTGTAGATGATTCCTACTACAGTTTGAGGGT 180
DB 121 AAGTGAAGGCGTTAAAGCTTAACTGTGTAGATGATTCCTACTACAGTTTGAGGGT 180
QY 181 ATACGCTACGCGCCACACCGCAGTGGGTGAGATTTAAAGCACCAGCGACCAACA 240
DB 181 ATACGCTACGCGCCACACCGCAGTGGGTGAGATTTAAAGCACCAGCGACCAACA 240
QY 241 CCCTGGGATGCTGCGGCATTTGCTCAATCAATAAGATTAAGTCAAGTGTATTT 300
DB 241 CCCTGGGATGCTGCGGCATTTGCTCAATCAATAAGATTAAGTCAAGTGTATTT 300
QY 301 ATACGCGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGATTAAT 360
DB 301 ATACGCGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGATTAAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTGTTTAAATACATACATAGTGTGTTTATATC 420
DB 361 CTAAATCCCGAACTAAACGTCCTGTTTAAATACATACATAGTGTGTTTATATC 420
QY 421 GGTGAAGATCATGCTGATGTATGATGCTGATTTTAAATGAGATGCTGCTG 480
DB 421 GGTGAAGATCATGCTGATGTATGATGCTGATTTTAAATGAGATGCTGCTG 480
QY 481 ATTAACATACATATGCTTGTGAGCTAGCTTCTAAGTTTAAATGAGATGCTGCT 540
DB 481 ATTAACATACATATGCTTGTGAGCTAGCTTCTAAGTTTAAATGAGATGCTGCT 540
QY 541 AATGTCCCGGTAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAATAAT 600
DB 541 AATGTCCCGGTAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAATAAT 600
QY 601 AATGTCCCGGTAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAATAAT 660
DB 601 AATGTCCCGGTAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAATAAT 660
QY 661 GCTGCTTACCACTACATGATGTTAACCGAACAACCTGCGGCTTTTCCATGCTG 720
DB 661 GCTGCTTACCACTACATGATGTTAACCGAACAACCTGCGGCTTTTCCATGCTG 720
QY 721 ATACTAATGCTGCGGTAATGCTTATTTGCTATGCTAATACCAATGTAACATGCTG 780
DB 721 ATACTAATGCTGCGGTAATGCTTATTTGCTATGCTAATACCAATGTAACATGCTG 780
QY 781 TTACCTTACCACTTGTGCTGAGATGCTGAGATTAAGATTAAGATGTTTGGAA 840
DB 781 TTACCTTACCACTTGTGCTGAGATGCTGAGATTAAGATTAAGATGTTTGGAA 840
QY 841 TTTCTTATGAAGCAAGCAGATTTTAAATGAGGAAATGTTTAACTCTA 900
DB 841 TTTCTTATGAAGCAAGCAGATTTTAAATGAGGAAATGTTTAACTCTA 900
QY 901 GAAGAGCGTACAATAAGTCAATGTTTCTTTGCTCCACTGTTGAGCAATACAGACC 960
DB 901 GAAGAGCGTACAATAAGTCAATGTTTCTTTGCTCCACTGTTGAGCAATACAGACC 960
QY 961 GCTGATTTGCTTACCCCAACATCTCGGGAATGTTTAAATGCTTGGGGTAAATTCG 1020

DB 961 GCTGATTTGCTTACCCCAACATCTCGGGAATGTTTAAATGCTTGGGGTAAATTCG 1020
QY 1021 ATACCACTATGATGCTTACCACTTATCATATGAGGCTTATTTTCTACTCAATCTTAAG 1080
DB 1021 ATACCACTATGATGCTTACCACTTATCATATGAGGCTTATTTTCTACTCAATCTTAAG 1080
QY 1081 CAATGCTATGCTTGTAAAGATTAAGTGAACCTGTGTCAATTTTGTCCAGTGAATG 1140
DB 1081 CAATGCTATGCTTGTAAAGATTAAGTGAACCTGTGTCAATTTTGTCCAGTGAATG 1140
QY 1141 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGAATGAGGCTTAAATGAAAGGCT 1200
DB 1141 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGAATGAGGCTTAAATGAAAGGCT 1200
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCAGATCTAT 1260
DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCAGATCTAT 1260
QY 1261 TTCTGTTCCCATGCTGCTTGTGCAATTAAGTGAACCTGCTGCTGCTGCTG 1320
DB 1261 TTCTGTTCCCATGCTGCTTGTGCAATTAAGTGAACCTGCTGCTGCTGCTG 1320
QY 1321 GCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1321 GCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1381 CTTAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1381 CTTAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 AATCAATTTGGCCAAACGATGCTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 AATCAATTTGGCCAAACGATGCTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 ACTGATATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1501 ACTGATATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 ATGGAAGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
DB 1561 ATGGAAGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 1621 ATTAGATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 ATTAGATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 TCGATGTTGAAAAACATGAGATTTATTTAG 1713
DB 1681 TCGATGTTGAAAAACATGAGATTTATTTAG 1713

RESULT 8
US-09-068-960-14
Sequence 14, Application us/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068, 960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 1710
TYPE: DNA
ORGANISM: Musca domestica
US-09-068-960-14

Query Match 55.8%; Score 955; DB 4; Length 1710;
 Best Local Similarity 73.3%; Pred. No. 3.4e-268;
 Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

QY 44 TTTAAATGCAATGAAAATGATTTTAAACATGCTTAACTACCAACATGAAACGGTGTAG 103
 DB 44 TTTAAATGCAATGAAAATGATTTTAAACATGCTTAACTACCAACATGAAACGGTGTAG 103
 QY 104 CTGAACGATGATGAAAGGCGTTAAACGTTTAACTGCTGACATGATTTCTT 163
 DB 104 TCGATACGAAATGACCAAAATTAAGGCTTTAAAGCAATGCAATGCAATGATTTCTT 163
 QY 164 ACTACAGTTTGGAGGCTTACCGTACCGCCCAACCGCGGAGTGTAGGATTAAG 223
 DB 164 ACTACAGTTTGGAGGCTTACCGTACCGCCCAACCGCGGAGTGTAGGATTAAG 223
 QY 224 CACCCACGAGCAACACCCCTGGATGGTGGCGGATTTGCAATGATTAAGT 283
 DB 224 CACCCACGAGCAACACCCCTGGATGGTGGCGGATTTGCAATGATTAAGT 283
 QY 284 CAGTCAAGTTGATTTTAAACGGCAAGTGTGCTCAGAGATTTGCTAATCTAA 343
 DB 284 CAGTCAAGTTGATTTTAAACGGCAAGTGTGCTCAGAGATTTGCTAATCTAA 343
 QY 344 GTGCTATACGAATTAATCCGAAACGTAACGCTGCTTTAGTATACATACAG 403
 DB 344 ATGCTATACGAATTAATCCGAAACGTAACGCTGCTTTAGTATACATACAG 403
 QY 404 GTGCTATTAATTAATCGGTAATATCGATATGATGATGCTTATTTTCAATTA 463
 DB 404 GTGCTATTAATTAATCGGTAATATCGATATGATGATGCTTATTTTCAATTA 463
 QY 464 AAAAGATGTGTGATTAACATACATATCGTTGGAGCTTACGTTTCTAAGTT 523
 DB 464 AAAAGATGTGTGATTAACATACATATCGTTGGAGCTTACGTTTCTAAGTT 523
 QY 524 TAAATTCGAAGACCTTAATGTCGCCGTAATGCCGCTTAAAGATCAAGTACGGCT 583
 DB 524 TAAATTCGAAGACCTTAATGTCGCCGTAATGCCGCTTAAAGATCAAGTACGGCT 583
 QY 584 TGCCTGGATTAATAAATTAATGCGCAACTTGTGGCAATCCGATATAATTACAGTCT 643
 DB 584 TGCCTGGATTAATAAATTAATGCGCAACTTGTGGCAATCCGATATAATTACAGTCT 643
 QY 644 TTGGTGAAGTCCGCTGCTTACCCACTACATGATTTAAACCAACAACTCCG 703
 DB 644 TTGGTGAAGTCCGCTGCTTACCCACTACATGATTTAAACCAACAACTCCG 703
 QY 704 GTCTTTCATCGTGTGATTAATGCGGTAATGCTATTTGTCATTTGGCTATACCC 763
 DB 704 GTCTTTCATCGTGTGATTAATGCGGTAATGCTATTTGTCATTTGGCTATACCC 763
 QY 764 AATGTCACATCGTGTCTTCACTTACCCAAATTTGGCCGCTATAAGGCTGAGTAATG 823
 DB 764 AATGTCACATCGTGTCTTCACTTACCCAAATTTGGCCGCTATAAGGCTGAGTAATG 823
 QY 824 ATAAGATGTTTGAATTTCTTATGAAGCCACAGAGATTTAATAAATTGAGG 883
 DB 824 ATAAGATGTTTGAATTTCTTATGAAGCCACAGAGATTTAATAAATTGAGG 883
 QY 884 AAAAAGATATCTGGAATTTCTTAATGAAGCAATCCCTATGATTTGATCAAAAGAGAGC 883
 DB 884 AAAAAGATATCTGGAATTTCTTAATGAAGCAATCCCTATGATTTGATCAAAAGAGAGC 883
 QY 884 CACAAGTTTTCACACCCCAAAAGATGCAAAATAGGTATGTTCTTTGGACCCACTG 943
 DB 884 CACAAGTTTTCACACCCCAAAAGATGCAAAATAGGTATGTTCTTTGGACCCACTG 943
 QY 944 TTGACCATATCAGACCCGCTGATTTGCTTACCCAAACATCTCTGGGAAATGTTAA 1003
 DB 944 TTGACCATATCAGACCCGCTGATTTGCTTACCCAAACATCTCTGGGAAATGTTAA 1003
 QY 1004 CTGCTGGGTAATTCGATACCCATATGATGGTAAACATTTCAATATAGAGGTCTAATTT 1063
 DB 1004 CTGCTGGGTAATTCGATACCCATATGATGGTAAACATTTCAATATAGAGGTCTAATTT 1063

QY 1064 TCACCTCAATTCCTTAAGCAAAATGCCATGCTTGTAAAGAAATGGAACCTTGCTCAAT 1123
 DB 1064 CCAATTAATTCCTTAAGCAAAATGCCATGCTTGTAAAGAAATGGAACCTTGCTCAAT 1123
 QY 1124 TTGTCGCAAGTGAATTTGCTGATGCTGAACGACCCGCCAGACACTTGGAAATGGGTT 1183
 DB 1124 ATGTCCTTGGAGTGTGCTGACAGTGAACGACGAGTCCCGGAAACCTGGAGAGGGCTG 1183
 QY 1184 CTAATAATTAAGGCTCATGTTACAGAGAAACCAACGCTATATTTTATGATC 1243
 DB 1184 CCATTTGTAAGGAGCCCATGATGATGGGAAACACCTACCTCTGATATTTTATGAGC 1243
 QY 1244 TTTGCTCACATCATTTTCTGCTGCTCCCATGACATGCTTTGTGAATTAAGTCAATC 1303
 DB 1244 TTTGCTCCTATTTCTATTTTCTTCCCTTCCCATGACATGCTTTCTAATTTGCTTCAAC 1303
 QY 1304 ACACCTCGGTACACCCGCTCACTTGTATCGCTTGCAGCTTGTGAAATGCTATATCA 1363
 DB 1304 ACACAGCTGGACCTCCATTTATTTGTAATGCTTGTGATTTGATTTCCGAAATTTATTA 1363
 QY 1364 ATCCCTATGCTATTTATGCTGATGAGTGTGTTAAGGCTTTAGTATGCTATGAT 1423
 DB 1364 ACCCTATGCTATTTATGCTGATGAGTGTGTTAAGGCTTTAGTATGCTATGAT 1423
 QY 1424 TAACCTATTTCTTGTGAATCATTTGGCCAAACGATGCTTAAGAAATGCGTGAATCA 1483
 DB 1424 TAACCTATTTCTTGTGAATCATTTGGCCAAACGATGCTTAAGAAATGCGTGAATCA 1483
 QY 1484 AAACATTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
 DB 1484 AAACATTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
 QY 1544 GCAATGAATTTGAAGTATGGAATTTCTTCTGCGATTCATTAAGAAATCCGATGAG 1603
 DB 1544 GCAATGAATTTGAAGTATGGAATTTCTTCTGCGATTCATTAAGAAATCCGATGAG 1603
 QY 1604 TATACAGTGTGTAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
 DB 1604 TATACAGTGTGTAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
 QY 1664 AGATTAAACATGAGTGCATGTTTGAAGAAACATAGAGATTTATTT 1710
 DB 1664 AATTAACATGAGTGCATGTTTGAAGAAACATAGAGATTTATTT 1710

RESULT 9
 US-08-747-221B-51
 : Sequence 51, Application US/08747221B
 : Patent No. 6063610
 : GENERAL INFORMATION:
 : APPLICANT: Silver, Gary W.
 : APPLICANT: Wisniewski, Nancy
 : TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
 : TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 : NUMBER OF SEQUENCES: 66
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Carol Talkington Verser, Ph.D.
 : ADDRESSEE: Heska Corporation
 : STREET: 1825 Sharp Point Drive
 : CITY: Fort Collins
 : STATE: Colorado
 : COUNTRY: USA
 : ZIP: 80525
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: Windows 95
 : SOFTWARE: Wordperfect for Windows, Version 7.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/747,221B
 : FILING DATE: No. 6063610ember 12, 1996
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:

TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-005-051-52

Query Match 10.4%; Score 178; DB 4; Length 1584;
Best Local Similarity 56.1%; Pred. No. 4.9e-42;
Matches 359; Conservative 0; Mismatches 275; Indels 6; Gaps 1;

QY 116 ATGCAAGTAAAGGCGTTAAAGTTTAACTGTGTCAGATGATCTCTACTACAGTTTG 175
DB 1556 AAGTACTTTAAAGGAAAGAGCAATTTAGTAAAAAGAAATGTTCTCATAGTTATT 1497
QY 176 AGGGTATACCGTACGCCCAACCGCCAGTGGTGAAGTAAAGCAACCCAGCGAC 235
DB 1496 CTGGAATTCATATGCCAAACCTCCTGTAGTGTAGTATTAAGCCACCTCAACTG 1437
QY 236 CAACACCCCTGGATGCTGTCGCCGATTTGTCATCATTAAGTAAAGTCAAGTCAAGTTG 295
DB 1436 CAGAACCTTGGTCAGGTTCTTGTATGCTAAGTAAAGAGGAAATAGTTGATCAGTAC 1377
QY 296 ATTTTAAACGGGCAAGTGTGCTGAGAGGATGTCATATCAAGTCTATACGA 355
DB 1376 ATTTTAAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1317
QY 356 ATATCTAAATCCCGAACTAAAGCTCCGTTTAAAGTAAAGTAAAGTAAAGTAAAGTAA 415
DB 1316 CAATAACATCAGAGAAATCACTCTTCAGTATGATGATGATGATGATGATGATGATGAT 1257
QY 416 TTATCGGTAAATCATCGATATGATGATGATGATGATGATGATGATGATGATGATGATG 475
DB 1256 TCTATGGATCTGGAATATGATATGATATGATCTGTAATTTGATGATGATGATGATGATG 1197
QY 476 TGTGATTAACATCAATATCGTTTGGAGCTCTAGTTTCTAAATTTAAATTTCAAG 535
DB 1196 TTTCTGTTACTTCAATATGATATGATGATGATGATGATGATGATGATGATGATGATG 1137
QY 536 ACCTTAATGCGCCGATATGCGCGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 595
DB 1136 AA-----GCGCTGGCAATGTTGTTTATGATGATGATGATGATGATGATGATGATG 1083
QY 596 AAATTAATGCGCACTTGTGTCAGATCCGATATATTAAGTCTTGTGGAAGTG 655
DB 1082 AAACAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1023
QY 656 CCGGTCCTGCTCTTACCACTACATGATGATGATGATGATGATGATGATGATGATGATG 715
DB 1022 CAGGTGCTGCAAGTGTTCATTTATGATGATGATGATGATGATGATGATGATGATGATG 963
QY 716 GTGCTTACTAATGCGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 755
DB 962 AAGCATCTCAAAAGTGAAGTCTTTAAATCCTTGGGC 923

RESULT 13
US-08-747-221B-36
Sequence 36, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS: Molecules, Proteins and Uses Thereof
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610e1 December 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 11..1594
US-08-747-221B-36

Query Match 10.4%; Score 178; DB 3; Length 2007;
Best Local Similarity 56.1%; Pred. No. 5.5e-42;
Matches 359; Conservative 0; Mismatches 275; Indels 6; Gaps 1;

QY 116 ATGCAAGTAAAGGCGTTAAAGTTTAACTGTGTCAGATGATCTCTACTACAGTTTG 175
DB 39 AAGTACTTTAAAGGAAAGAGCAATTTAGTAAAAAGAAATGTTCTCATAGTTATT 98
QY 176 AGGGTATACCGTACGCCCAACCGCCAGTGGTGAAGTAAAGCAACCCAGCGAC 235
DB 99 CTGGAATTCATATGCCAAACCTCCTGTAGTGTAGTATTAAGCCACCTCAACTG 158
QY 236 CAACACCCCTGGATGCTGTCGCCGATTTGCAATCATTAAGTAAAGTCAAGTTG 295
DB 159 CAGAACCTTGGTCAGGTGTTCTTGTATGCTAAGTAAAGAGGAAATGTTGATGATGATG 218
QY 296 ATTTTAAACGGGCAAGTGTGCTCAGAGATTTGCTATACCTAAGTGTCTATACGA 355
DB 219 ATTTTAAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 278
QY 356 ATATCTAAATCCCGAACTAAAGCTCCGTTTAAAGTAAAGTAAAGTAAAGTAAAGTAA 415
DB 279 CAATAACATCAGAGAAATCACTCTTCAGATATGATGATGATGATGATGATGATGATG 338
QY 416 TTATCGGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 475
DB 339 TCATGGATCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 398
QY 476 TGTGATTAACATCAATATCGTTTGGAGCTCTAGTTTCTAAGTTTAAATTTCAAG 535
DB 399 TTTCTGTTACTTCAATATATGATGATGATGATGATGATGATGATGATGATGATGATG 458
QY 536 ACCTTAATGCGCCGATATGCGCGCTTAAAGTAAAGTCAAGTCAAGTCAAGTCAAGTCA 595
DB 459 AA-----GCGCTGGCAATGTTGTTTATGATGATGATGATGATGATGATGATGATG 512
QY 596 AAATTAATGCGCAACTTGTGTCAGATCCGATATATTAAGTCTTGTGGAAGTG 655
DB 513 AAACAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 572

NAME/KEY: CDS
LOCATION: 11..1594
US-09-005-051-36

Query Match 10.4%; Score 178; DB 4; Length 2007;
Best Local Similarity 56.1%; Pred. No. 5,5e-42;
Matches 359; Conservative 0; Mismatches 275; Indels 6; Gaps 1;

```
QY 116 ATGGCAAGTGAAGGCTTAAACGTTTAACTGTACAGATGATCTTACTACAGTTTG 175
DB 39 AAGCTACTTAAAGAGAAAAGCAATTAAGTGAAGAAAGTGTCCATAGTTATT 98
QY 176 AGGGTATACCGTACGCCCAACGCCGAGGTGAGGTGATTTAAAGCACCACGAC 235
DB 99 CTGAATTCATATGCCCAACCTCGTAGGTGATTAAGATTAAAGCACCACGAC 158
QY 236 CAACACCCCTGGATGGTGGCCGATTTGCAATCATTAAGATAAGTCAGTCAAGTTG 295
DB 159 CAGAACCTTGTCAGGTGTCTTGTAGTAAAGCAAGCAATAGTTAGATCAGTAC 218
QY 296 ATTTTATACGGCAAGTGTGGCTCAGAGATGTCTATACCTAAGTCTATACGA 355
DB 219 ATTTTATTAATAAATTAAGTAGAGGCTGAGATGTTTATACCTCAATGCTATGTC 278
QY 356 ATATCTAAATCCGAAACTTAAACGTCCTTTTATATACATACATGTTGTTTGA 415
DB 279 CAAAACCTCAGAAATCACTTCTCCAGTAATGATGATACATGAGAGGCTTCT 338
QY 416 TTATCGTGAAATCATCGTATATGATATGTCCTGATTTATTCATTAAAGATGTG 475
DB 339 TCATGGGATCTGAAATAGTATGATGATGCTCTGATATTTGATGATGATGAAATTG 398
QY 476 TGTGATTACATACATATGCTTTGGAGCTTAGTTTCTAAGTTTAAATTCAGAA 535
DB 399 TTCTGTTACTTCAATATGATAGTGTGTTGGGATTTTGAACCTGGGAATGAA 458
QY 536 ACCTTAATGTGCGCGGTATGCGGCTTAAAGATCAAGTCATGCGCTTGGTGAATTA 595
DB 459 AA-----GCGCCTGCAATGTTGTTGATGACCAAGTGAAGCTTAATAGGTAA 512
QY 596 AAAATTAATGCGCAACTTTGGTGGCAATCCGATATATTAAGTCTTTGGTGAAGTG 655
DB 513 AAAACATATATGATGCTTTGGTGGTGAACCCCAATGATGATATTTTGGAGATCAG 572
QY 656 CCGGTCTGCTCTACCCCTACATGATGTTAACCAACCAACTGCGCTTTTCATC 715
DB 573 CAGGTGTCAGATGTTTCAATATTTGATGTTATCAGATCTTCCAAAGACCTTTTCATA 632
QY 716 GTGTATACTAATGCGGTAATGCTATTTGTCATTTGCG 755
DB 633 AAGCATCTCAAAAGTGAAGTCTTTAATCCTTGGGC 672
```

Search completed: April 11, 2003, 08:51:16
Job time : 46.5118 secs

Db 731 AATCCTAAAGTGAACCTCTCTTGGAGAAAGTCAGAGACGCTTC 777

RESULT 4

US-09-880-107-2271
Sequence 2271, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2271
LENGTH: 2381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474
US-09-880-107-2271

Query Match

3.6%: Score 62.2; DB 10; Length 2381;
Best Local Similarity 54.8%; Pred. No. 6e-06; Indels 9; Gaps 3;
Matches 190; Conservative 0; Mismatches 148;

QY 325 GAGATTGCTATACCTACGATGCTATACGAAATATCAATCCCGAAGCTAAACGTC 384
DB 427 GAAGACGCTTATATCTAAATGATGATCCAGACCTAAAC--AAAAATGCCCT 483
QY 385 GTTTAGTATACATACATGCTGCTGCTTTTATTCGCTGAAATCATCGATATGAT 444
DB 484 GTATTGATATGATTTATGCTGCTGCTTCAACCTGAAACATCATCTTTACATGTTAT 543
QY 445 GGTCTGATTTATTCATTAATAAGGA--TGTGCTGATTAATCAATCAATATCGTTG 501
DB 544 GATGCGAAGTTCTGCTCGGCTGGAAGATTTATGATGCTCAATGAACTATAGGCTG 603
QY 502 GGAGCTTAGGTTTCTAAGTTTAAATTCAGAGACCTTAATGCGCGTAAATGCCGC 561
DB 604 GGTGCGCTAGGATCTTCTAGCTT--GCCAGGAATCCTGAGGCTCCAGGACATGGGT 660
QY 562 CTAAAGATCAAGCATGCGCTGCTGATTAATAATTAATGCGCAACTTTGGTGGC 621
DB 661 TTATTGATCAACAGTTCCTTCACTGAGGCTTCAAAAAATATATAGACGCTTTGGTGA 720
QY 622 AATCCGATATATTAACAGTCTTTGGTGAAGTCCGCGTGCCTC 668
DB 721 AATCCTAAAGTGAACCTCTCTTGGAGAAAGTCAGAGACGCTTC 767

RESULT 5

US-09-748-739A-3
Sequence 3, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
METHOD OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748, 739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2416
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
NAME/KEY: CDS
LOCATION: (214)...(1935)
US-09-748-739A-3

Query Match
3.6%: Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6e-06; Indels 9; Gaps 3;
Matches 190; Conservative 0; Mismatches 148;

QY 325 GAGATTGCTATACCTACGATGCTATACGAAATATCAATCCCGAAGCTAAACGTC 384
DB 481 GAAGACGCTTATATCTAAATGATGATCCAGACCTAAAC--AAAAATGCCACT 537
QY 385 GTTTAGTATACATACATGCTGCTGCTTTTATTCGCTGAAATCATCGATATGAT 444
DB 538 GTATTGATATGATTTATGCTGCTGCTTCAACCTGGAACATCATCTTTACATGTTAT 597
QY 445 GGTCTGATTTATTCATTAATAAGGA--TGTGCTGATTAATCAATCAATATCGTTG 501
DB 598 GATGCGAAGTTCTGCTCGGCTGGAAGATTTATGATGCTCAATGAACTATAGGCTG 657
QY 502 GGAGCTTAGGTTTCTAAGTTTAAATTCAGAGACCTTAATGCGCGTAAATGCCGC 561
DB 658 GGTGCGCTAGGATCTTCTAGCTT--GCCAGGAATCCTGAGGCTCCAGGAAATGGGT 714
QY 562 CTAAAGATCAAGCATGCGCTGCTGCTGATTAATAATTAATGCGCAACTTTGGTGGC 621
DB 715 TTATTGATCAACAGTTCCTTCACTGAGGCTTCAAAAAATATATGACGCTTTGGTGA 774
QY 622 AATCCGATATATTAACAGTCTTTGGTGAAGTCCGCGTGCCTC 668
DB 775 AATCCTAAAGTGAACCTCTCTTGGAGAAAGTCAGAGACGCTTC 821

RESULT 6

US-09-748-739A-5
Sequence 5, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
METHOD OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748, 739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2416
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
NAME/KEY: CDS
LOCATION: (214)...(1935)
US-09-748-739A-5

Query Match
3.6%: Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6e-06; Indels 9; Gaps 3;
Matches 190; Conservative 0; Mismatches 148;

QY 325 GAGATTGCTATACCTACGATGCTATACGAAATATCAATCCCGAAGCTAAACGTC 384
DB 481 GAAGACGCTTATATCTAAATGATGATCCAGACCTAAAC--AAAAATGCCACT 537


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QY 385 GTTTAGTATACATACATGCTGCTTTTATATCGTGAAATCATCGTATATGAT 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 GTATTGATATGATTTATGAGTGAGTGTTTCAACCTGACATCATCTTTACATGTTAT 597
QY 445 GGTCCGTATATTTGATTAATAAAGA---TGTCGTGTTGATTAACATATATCGTTTG 501
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 GATGGCAAGTTCTGCGTCGGGTGAAGAGTTATTTAGTGTCAATGCACTATAGGGTG 657
QY 502 GGAGCTCTAGGTTTCTAAGTTAAATTCAGAGACCTTAATGCGCGTATATCGCGC 561
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 GGTGCCCTAGGATTTCTTACTTT---GCCAGGAATTCCTGAGCTCCAGGACATGSGGT 714
QY 562 CTAAAGATCAAGTCATGCGCTTGGCTTGATTAATAATATATGCGCCACTTTGGTGGC 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 715 TTATTTGATCAACAGTTGCTCTTCAGTGGTTCAAAAAATATAGCAGCCTTTGGTGA 774
QY 622 ATCCCGATATATTTACATCTTTGGTGAAGTGGCGGTGCTGCCG 668
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 775 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGACAGCTTC 821
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RESULT 7
US-09-748-739A-7
; Sequence 7, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1935)
; US-09-748-739A-7
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Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;
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QY 325 GAGCATTTGCTATACCTATAGTGTCTATACGAATATATCCGAAACTTAACGTCC 384
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Db 481 GAAGACTGTTATATCTTAATGATGATTCACAGCTTAAC---AAAAATGCCACT 537
QY 385 GTTTAGTATACATACATGCTGCTTTTATATCGTGAAATCATCGCATATGAT 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 GTATTGATATGATTTATGAGTGAGTGTTCAACTGGAACATCATCTTACATGTTAT 597
QY 445 GGTCCGTATATTTGATTAATAAAGA---TGTCGTGTTGATTAACATCAATATCGTTTG 501
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Db 598 GATGGCAAGTTCTGCGTCGGGTGAAGAGTTATTTAGTGTCAATGCACTATAGGGTG 657
QY 502 GGAGCTCTAGGTTTCTAAGTTAAATTCAGAGACCTTAATGCGCGTATATCGCGC 561
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 GGTGCCCTAGGATTTCTTACTTT---GCCAGGAATTCCTGAGCTCCAGGACATGSGGT 714
QY 562 CTAAAGATCAAGTCATGCGCTTGGCTTGATTAATAATATATGCGCCACTTTGGTGGC 621
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Db 715 TTATTTGATCAACAGTTGCTCTTCAGTGGTTCAAAAAATATAGCAGCCTTTGGTGA 774
QY 622 ATCCCGATATATTTACATCTTTGGTGAAGTGGCGGTGCTGCCG 668
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Db 775 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGACAGCTTC 821
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RESULT 8
US-09-748-739A-16
; Sequence 16, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-748-739A-16
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Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;
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QY 325 GAGCATTTGCTATACCTATAGTGTCTATACGAATATATCCGAAACTTAACGTCC 384
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Db 481 GAAGACTGTTATATCTTAATGATGATTCACAGCTTAAC---AAAAATGCCACT 537
QY 385 GTTTAGTATACATACATGCTGCTTTTATATCGTGAAATCATCGCATATGAT 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 GTATTGATATGATTTATGAGTGAGTGTTCAACTGGAACATCATCTTACATGTTAT 597
QY 445 GGTCCGTATATTTGATTAATAAAGA---TGTCGTGTTGATTAACATCAATATCGTTTG 501
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 GATGGCAAGTTCTGCGTCGGGTGAAGAGTTATTTAGTGTCAATGCACTATAGGGTG 657
QY 502 GGAGCTCTAGGTTTCTAAGTTAAATTCAGAGACCTTAATGCGCGTATATCGCGC 561
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 GGTGCCCTAGGATTTCTTACTTT---GCCAGGAATTCCTGAGCTCCAGGACATGSGGT 714
QY 562 CTAAAGATCAAGTCATGCGCTTGGCTTGATTAATAATATATGCGCCACTTTGGTGGC 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 715 TTATTTGATCAACAGTTGCTCTTCAGTGGTTCAAAAAATATAGCAGCCTTTGGTGA 774
QY 622 ATCCCGATATATTTACATCTTTGGTGAAGTGGCGGTGCTGCCG 668
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 775 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGACAGCTTC 821
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RESULT 9
US-09-893-519A-112
; Sequence 112, Application US/09893519A
; Publication No. US20030027243A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS PHARMACEUTICALS, INC.
; APPLICANT: THOMPSON, Craig
; APPLICANT: MOORE, Jeffrey
; APPLICANT: BURMAN, Ed T.
; APPLICANT: BRADLEY, John
; APPLICANT: DESILVA, Thamara
; APPLICANT: HARRIS, Sandra
; APPLICANT: KOMARNITSKY, Svetlana
; APPLICANT: MENDILLO, Marc
; APPLICANT: MOORE, Daniel
; APPLICANT: MCCOY, Melissa
; APPLICANT: SANDERSON, Karen
; APPLICANT: HAO, Taiq
; APPLICANT: ZHU, Shuhao
; APPLICANT: LONG, Fan
; APPLICANT: DAVIDOV, Eugene
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RESULT: 10
US-09-974-300-1107
; Sequence 1107, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitorin
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085,500-US
; CURRENT APPLICATION NUMBER: US/09/974, 3000
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO: 1107
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1107

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RESULT 12
US-09-934-323-1

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Sequence 1, Application US/09934323
Patent No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: Curtilis, Rofy A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
FILE REFERENCE: 10448-081001
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (420)...(2924)
US-09-934-323-1

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Query Match
Best Local Similarity 54.2%; Score 57.6; DB 10; Length 4667;
Matches 117; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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530 CAGAAACCTTAATGTCCTGCTTAAAGATCAAGTCATGCTTGGCT 589
1090 CCGGGACCCAGGCTGCAAAAGGACATATGCTGCTCCGACCATCAGGCTTGGTG 649
590 GGATTAATAATGTCCTGCTTAAAGATCAAGTCATGCTTGGCT 649
1150 GGCTGCTGTAATAATGTCCTGCTTAAAGATCAAGTCATGCTTGGCT 1209
650 AAGTCCCGCTGCTGCTTAAAGATCAAGTCATGCTTGGCT 709
1210 CCGGGACCCAGGCTGCTGCTTAAAGATCAAGTCATGCTTGGCT 1269
710 TCCATGCTGCTGCTTAAAGATCAAGTCATGCTTGGCT 745
1270 TCCAGAAAGGCTGCTGCTTAAAGATCAAGTCATGCTTGGCT 1305

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RESULT 13
US-09-954-531-1038
Sequence 1038, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
FILE REFERENCE: 689290-77
CURRENT FILING DATE: 2002-05-02
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1038
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-531-1038

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Query Match
3.3%; Score 56.8; DB 9; Length 2191;

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Best Local Similarity 53.2%; Pred. No. 0.00015;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;
322 TCAGAGATGCTCTATACCTAGCTCTATACGATATATCAATCCGAA---ACTAA 378
436 TCTGAGAGCTGCTCTATACCTAGCTCTATACGATATATCAATCCGAA---ACTAA 378
379 CTTCCGCTTTAGTATATACATAGCTGCTGCTTTATATGCTGTAATAATCTGAT 438
496 CTGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
439 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
554 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
499 TTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
613 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
559 GGCCTTAAGATCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 618
667 GCTTACCTGAGCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
619 GGCATCCGATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
727 GGCATCCGATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
679 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
767 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830

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RESULT 14
US-09-880-107-3854
Sequence 3854, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US 60/237,054
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3854
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y09616
US-09-880-107-3854

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Query Match
3.3%; Score 56.8; DB 10; Length 2191;
Best Local Similarity 53.2%; Pred. No. 0.00015;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;
322 TCAGAGATGCTCTATACCTAGCTCTATACGATATATCAATCCGAA---ACTAA 378
436 TCTGAGAGCTGCTCTATACCTAGCTCTATACGATATATCAATCCGAA---ACTAA 378
379 CTTCCGCTTTAGTATATACATAGCTGCTGCTTTATATGCTGTAATAATCTGAT 438
496 CTGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
439 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612

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GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 2944.03 Seconds

(Without alignments)
16933.650 Million cell updates/sec

Title: US-09-776-910-5

Perfect score: 1713

Sequence: 1 atgaattcaacgtagttt.....aacatagagattattttag 1713

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBml:*

1: gb_da:*

2: gb_da:*

3: gb_da:*

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41: gb_da:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	1706.6	99.6	1713	6	ARI53439
5	1698.6	99.2	1713	6	ARI53441
6	1698.6	99.2	1713	6	ARI53441
7	1698.6	99.2	1713	6	ARI53441
8	1673.4	97.7	1713	6	ARI53441
9	982.4	57.3	2160	3	ARI53341
10	961	56.1	2175	3	ARI53082
11	951.8	55.6	1710	6	ARI53445
12	677.2	39.5	2017	3	AY051473
13	375.4	21.9	2660	3	AY121675
14	373.8	21.8	2820	3	DMU51050
15	369	21.5	57335	2	AC015272
16	369	21.5	18459	3	AC008312
17	369	21.5	197597	3	AC011253
18	369	21.5	309023	3	AE003671
19	362.2	21.1	1962	3	AY051497
20	321.4	18.8	2122	3	AY058637
21	309.4	18.1	1906	3	AY058345
22	298.8	17.4	13044	2	AC014297
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26	286.6	16.7	2050	3	AF216210
27	276.8	16.2	1205	3	AF216215
28	271.6	15.9	1809	6	AX260182
29	239.8	14.0	1630	3	COESPA2EA
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32	236.6	13.8	188459	3	AC008312
33	236.6	13.8	197597	3	AC011253
34	236.6	13.8	309023	3	AE003671
35	229.2	13.4	2401	3	DMU51054
36	228	13.3	1724	3	AY069743
37	222.6	13.0	933	3	AF216216
38	222.6	13.0	1836	3	COSEKES1
39	220.8	12.9	3447	3	DMU51052
40	217.6	12.7	1630	3	COSEKES2
41	212.4	12.4	84252	2	AC009207
42	210.4	12.3	1401	3	CPU43544
43	205.8	12.0	6028	3	AF177382
44	203.2	11.9	1401	3	CPU43546
45	198.2	11.6	1401	3	CPU43545

ALIGNMENTS

RESULT 1

LOCUS ARI53440

DEFINITION Sequence 5 from patent US 6235515.

ACCESSION ARI53440

VERSION ARI53440.1 GI:15120972

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1713)

AUTHORS Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm., Robin,G.Charlesde,Quetteville., Claudianos,C., Smyth,K.A., Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.

TITLE Malathion carboxylesterase

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: US 6235515-A 5 22-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..1713
 BASE COUNT 516 a 305 c 369 g 523 t
 ORIGIN

Query Match 100.0%; Score 1713; DB 6; Length 1713;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTACACCTTGTGTTGATGAGAAATTTAAATGCAAGATTAAATGCAATTTGAAAT 60
 DB 1 ATGAATTTACACCTTGTGTTGATGAGAAATTTAAATGCAAGATTAAATGCAATTTGAAAT 60
 QY 61 AAGTTTAACTATGCTTAACTACCAATGAAGCGGTGTACTGAAACTGAAATGCG 120
 DB 61 AAGTTTAACTATGCTTAACTACCAATGAAGCGGTGTACTGAAACTGAAATGCG 120
 QY 121 AAAGTGAAGCGCTTAAAGCTTAACTGTGTACGATGATTCCTACTACAGTTTGAAGGT 180
 DB 121 AAAGTGAAGCGCTTAAAGCTTAACTGTGTACGATGATTCCTACTACAGTTTGAAGGT 180
 QY 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTTAAACACCCCAAGCAACA 240
 DB 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTTAAACACCCCAAGCAACA 240
 QY 241 CCCTGGGATGTTGTGGCTGATTTGCAATCATAAAGATTAAGTCAAGTGAATTTT 300
 DB 241 CCCTGGGATGTTGTGGCTGATTTGCAATCATAAAGATTAAGTCAAGTGAATTTT 300
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 QY 361 CTAAATCCCGAAACTAAGCTCCGTTTATGATACATCATGCTGGTGTATATATC 420
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 QY 421 GGTGAATAATCATGCTGATATGATGCTGCTGATTTATTTCAATTAAGATGTGTG 480
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 QY 721 ATACTAATGCGGTAATGCTATTTGCTATGCTGCTAATACCAATGCTAATCGTGGC 780
 DB 721 ATACTAATGCGGTAATGCTATTTGCTATGCTGCTAATACCAATGCTAATCGTGGC 780
 QY 781 TTACACCTTAGCCAAATTTGCGCGCTTAAAGGTGAGAAATATGATGATTTTGA 840
 DB 781 TTACACCTTAGCCAAATTTGCGCGCTTAAAGGTGAGAAATATGATGATTTTGA 840
 QY 841 TTTCTTATGAAGCCACAGCATTTAGTAAACCTTGAGGAAAAAGTTTAACTCTA 900
 DB 841 TTTCTTATGAAGCCACAGCATTTAGTAAACCTTGAGGAAAAAGTTTAACTCTA 900
 QY 901 GAAGAGCGTACAAATTAAGTCAATGTTTCTTTGCTTGGTCCACGCTTGAGCATATCGAGC 960
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DB 901 GAAGAGCGTACAAATTAAGTCAATGTTTCTTTGCTTGGTCCACGCTTGAGCATATCGAGC 960
 QY 961 GCTGATTTGTCTTACCACCAATCCCGGAAATGTTAAACCTGCTGGGTATTTG 1020
 DB 961 GCTGATTTGTCTTACCACCAATCCCGGAAATGTTAAACCTGCTGGGTATTTG 1020
 QY 1021 ATACCCATATGATGCTGTAACACTTATATGAGGCTCTATTTTCTCAATCTTAA 1080
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 QY 1081 CAATGCTATGCTTGTGAAGAAATGGAACCTTGTCTCAATTTTGTCCAGTAATG 1140
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 DB 1141 GCTGATGCTGAACGACCGCCCGAGAGACCTTGAATGAGTGTCTAAATTAAGAGCT 1200
 QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTCAATCTAT 1260
 DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTCAATCTAT 1260
 QY 1261 TTCTGTTCCCATGCTGATGCTTGTGCAATTAACGTTTCAATACACCTCCGTACACC 1320
 DB 1261 TTCTGTTCCCATGCTGATGCTTGTGCAATTAACGTTTCAATACACCTCCGTACACC 1320
 QY 1321 GTCATCTGATGCTGCTGCACTGATTCGAGAGATCTTATCAATCCCTATGATATG 1380
 DB 1321 GTCATCTGATGCTGCTGCACTGATTCGAGAGATCTTATCAATCCCTATGATATG 1380
 QY 1381 CGTAGTGACGCTGTTAAGGCTTGAATGCTGATGCTGATGAATTAACCTATTTCTG 1440
 DB 1381 CGTAGTGACGCTGTTAAGGCTTGAATGCTGATGCTGATGAATTAACCTATTTCTG 1440
 QY 1441 AATCAATGCGCAACGCTATGCTTAAAGAAATGCGGAATACAAACAAATGGAAGCTAG 1500
 DB 1441 AATCAATGCGCAACGCTATGCTTAAAGAAATGCGGAATACAAACAAATGGAAGCTAG 1500
 QY 1501 ACTGATATATGATATGATATTTGCGCACCTGATATCTTATGCAATGAATGAAGT 1560
 DB 1501 ACTGATATATGATATGATATTTGCGCACCTGATATCTTATGCAATGAATGAAGT 1560
 QY 1561 ATGGAATAATGTTTCTGCGGATCAATTAAGAAATCCGATGAAGTATACAAAGTGTGAAT 1620
 DB 1561 ATGGAATAATGTTTCTGCGGATCAATTAAGAAATCCGATGAAGTATACAAAGTGTGAAT 1620
 QY 1621 ATTAGATGATGAATTAAGAAATGATGCTGCGCAATGAGATTAAGCAATGGAG 1680
 DB 1621 ATTAGATGATGAATTAAGAAATGATGCTGCGCAATGAGATTAAGCAATGGAG 1680
 QY 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713
 DB 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713

RESULT 2
 AR153442 1713 bp DNA linear PAT 08-AUG-2001
 LOCUS AR153442
 DEFINITION Sequence 9 from patent US 6235515.
 ACCESSION AR153442
 VERSION AR153442.1 GI:15120974
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolm, Robin, G. Charlesde, Quetleville, Claudianos, C., Smyth, K. A., Boyce, T. Mark, Oakeshot, J. Graham, and Brownlie, J. Collin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 9 22-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..1713

BASE COUNT 515 a 305 c 370 g 523 t
ORIGIN
Query Match 99.7%, Score 1708.2, DB 6, Length 1713;
Best Local Similarity 99.8%, Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 ATGATTTTCAACGTTAGTTTGTATGAGAAATTTAAATGAAGATTAATGATTCATGTAAT 60
1 ATGATTTTCAACGTTAGTTTGTATGAGAAATTTAAATGAAGATTAATGATTCATGTAAT 60
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61 AAGTTTAACTATCGTTTAACTACCAATGAACGCTGTAGTGAACATGATATGAC 120
121 AAAGTGAAGGCGTTAAACGTTTAACTGTATGATGATTCCTACTACAGTTTGAAGGT 180
121 AAAGTGAAGGCGTTAAACGTTTAACTGTATGATGATTCCTACTACAGTTTGAAGGT 180
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361 CTAATCCCGCAACCTAACCGTCCCTTTTATATACATACATGCTGTGTATATAC 420
421 GGTGAAATTCATCGTATATGATGTGCTGATTTTATCATTAAGATGATGCTGTG 480
421 GGTGAAATTCATCGTATATGATGTGCTGATTTTATCATTAAGATGATGCTGTG 480
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541 AATGAGCCCGGATATGCGGCTTAAAGATCAAGTCATGCGCTGATTTGATTAAT 600
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901 GAAGGCGTACAAATTAAGTATGTTTCTTTGCTCCACGCTGTGACCATATAGACC 960
961 GCTGATTTGTCTTACCCAAACATCTCGGAAATGTTAAACGTGTGGGTATTCG 1020

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Oy 1021 ATACCCACTATGATGGGTATACACTTCAATATAGAGGCTATATTTTCACTCAATCTTAAG 1080
Db 1021 ATACCCACTATGATGGGTATACACTTCAATATAGAGGCTATATTTTCACTCAATCTTAAG 1080
Oy 1081 CAAATGCCATGCTTGTATAGCAATTTGCAATTTGCTGCAATTTGCTGCAATTTG 1140
Db 1081 CAAATGCCATGCTTGTATAGCAATTTGCAATTTGCTGCAATTTGCTGCAATTTG 1140
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Db 1141 GCTGATCTGAACGCGACCCCGCAGACCTTGAAGAAATGGGCTGCTAAATTTAAAGGCT 1200
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Oy 1261 TTCTGTTTCCCATGCTATGCTTTGTTGCAATTTACGTTTCAATACACCTCCGCTACACC 1320
Db 1261 TTCTGTTTCCCATGCTATGCTTTGTTGCAATTTACGTTTCAATACACCTCCGCTACACC 1320
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Db 1321 GTCFACCTGTATCGCTTGCATTCGATTCGAGAAATCTTATCAATCCCTATGCTATATG 1380
Oy 1381 CGTATGAGAGCTGTGTAAAGGCTTATGCTATGCTGATGAATTAACCTATTTCTTCTG 1440
Db 1381 CGTATGAGAGCTGTGTAAAGGCTTATGCTATGCTGATGAATTAACCTATTTCTTCTG 1440
Oy 1441 AATCAATTTGGCCAAACGATATGCTTAAAGATTCGCTGATTAACCAATTTAAGCTATG 1500
Db 1441 AATCAATTTGGCCAAACGATATGCTTAAAGATTCGCTGATTAACCAATTTAAGCTATG 1500
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Db 1501 ACTGATATGATGATCAATTTGCCACACTGCTATTCCTTATAGCAATGAATTTGAAGT 1560
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Db 1561 ATGAAATGTTTCTCGGATCCAAATTAAGAAATCCGATGAAGTATACAGTGTGTAAT 1620
Oy 1621 ATTAGTATGATTAAGATTAAGTATGCTGCTGAAGTGAAGTAAAGTAAAGTGAAG 1680
Db 1621 ATTAGTATGATTAAGATTAAGTATGCTGCTGAAGTGAAGTAAAGTAAAGTGAAG 1680
Oy 1681 TCGATGTTTGAAGAAACATAGATTTATTTAG 1713
Db 1681 TCGATGTTTGAAGAAACATAGATTTATTTAG 1713
RESULT 3
ARI53438 1713 bp DNA linear PAT 08-AUG-2001
LOCUS ARI53438
DEFINITION Sequence 1 from patent US 6235515.
ACCESSION ARI53438
VERSION ARI53438.1 GI:15120970
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Robinson,G.Charlesde,Quetleville., Claudianos,C., Smyth,K.A.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
TITLE Journal
FEATURES
JOURNAL Malatlon carboxylesterase
PATENT: US 6235515-A 1 22-MAY-2001;
LOCATION/Qualifiers
SOURCE 1. 1713
BASE COUNT 515 a 304 c 370 g 524 t
ORIGIN

Query Match 99.6%; Score 1706.6; DB 6; Length 1713;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 ATGAAATTCACGTTAGTTGATGAGAAATTAATGGAAGATTAATGATGAAAT 60
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 121 AAAGTGAAGGCGTTAAAGCTTAACTGATGATGATGATGATGATGAT 180
 121 AAAGTGAAGGCGTTAAAGCTTAACTGATGATGATGATGATGATGAT 180
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 901 GAAGAGCGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
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 1381 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
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RESULT 4
 AR153439 1713 bp DNA linear PAT 08-AUG-2001
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCES
 1 (bases 1 to 1713)
 Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolm, Robin, G. Charles, Ouellet, J. J. Graham, and Brownlie, J. Collin. Boyce, T. Mark, Oakeshott, J. Graham, and Brownlie, J. Collin. Malathion carboxylesterase
 Patent: US 6235515-A 3 22-MAY-2001;
 Location/Qualifiers
 FEATURES
 source
 1. 1713
 /organism="unknown"
 BASE COUNT 515 a 306 c 370 g 522 t
 ORIGIN
 Query Match 99.6%; Score 1706.6; DB 6; Length 1713;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 1 ATGAATTTTCACGCTAGTTGATGAGAAATTAATGAGATTAATGCTTGAAT 60
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DB 61 AAGTTTTTAACTATCGTTTAACTACCAATGAAACGGTGTGATGAACTGATATG 120
OY 121 AAAGTGAAGGCGTTAAAGCTTTAACTGTATGATGATCTTCTACTAGTTTGA 180
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DB 121 AAAGTGAAGGCGTTAAAGCTTTAACTGTATGATGATCTTCTACTAGTTTGA 180
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DB 181 ATACCGTACGCCCAACGCCCACTGGGTGAGCTGAGATTTTAAAGCCAGGACCA 240
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DB 241 CCTTGGATGTGTCGTGATGTTGCAATCATTAAGATTAAGTCAAGTGTATTT 300
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DB 481 ATTAACATATACATATGCTTTGGAGCTTAGTCTTTCTTAAGTTTAAATTCAG 540
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DB 901 GAAGAGCTACAAATTAAGTCAATGTTTCTTTGTCACAGTGTGAGCCATATAG 960
OY 961 GCTGATTTGCTTACCCAAACATCTCGGAAATGTTTAAACCTTTGGGGTAA 1020
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DB 961 GCTGATTTGCTTACCCAAACATCTCGGAAATGTTTAAACCTTTGGGGTAA 1020
OY 1021 ATACCCATATGATGGGTATACACTTATATGAGGGGTATTTTACCTTAATCT 1080
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DB 1021 ATACCCATATGATGGGTATACACTTATATGAGGGGTATTTTACCTTAATCT 1080
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DB 1081 CAATGCCCTATGCTTGTATAGAAATTTGCAATTTTGTGCAAGTGAATTC 1140
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DB 1141 GCTGATGCTGAAGCGACGCCGCCAGAGACCTTGGAAATGGGTCTAAATTTAA 1200
OY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTTGCTCACA 1260
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DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTTGCTCACA 1260
OY 1261 TTTCTGTTCCCATATCCTGTTGTTGCAATTTACCTTTCAATCACACCTCC 1320
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DB 1261 TTTCTGTTCCCATATCCTGTTGTTGCAATTTACCTTTCAATCACACCTCC 1320
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DB 1681 TCGATGTTTGAATAACATAGACATTTATTTT 1713

RESULT 5
AR062837 1713 bp DNA linear PAT 29-SEP-1999
LOCUS AR062837
DEFINITION Sequence 1 from patent US 5843758.
ACCESSION AR062837
VERSION AR062837.1 GI:5990528
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.,Joyce., Newcomb,R.David., Robin,G.,Charlesde,Queteville.,
Boyce,T.Mark., Campbell,P.,Malcolm., Parker,A.Gerard.,
Oakesholt,J.,Graham. and Smyth,K.-A.
Enzyme based bioremediation
PATENT: US 5843758-A 1 01-DEC-1998;
FEATURES
source 1..1713
BASE COUNT 516 a 305 c 370 g 522 t
ORIGIN
Query Match 99.2%; Score 1698.6; DB 6; Length 1713;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1 ATGAATTTTCACGCTAGTTTGAATGAGAAATTAATGAGATTAATGCTTGAAT 60
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Db	121	AAAGTGAAGGCCGTTTAAACGTTTAACTGTGTACAGATGATTCCTACTACTACAGTTTGAGGGT	180
Qy	181	ATACGGTACGCCCAACCGCAGTGGGTAGCTGAGATTTTAAAGCACCCACGACCAACA	240
Db	181	ATACGGTACGCCCAACCGCAGTGGGTAGCTGAGATTTTAAAGCACCCACGACCAACA	240
Qy	241	CCCTGGGATGTTGTGGCTGATTTGTTGCAATCATTAAGATAGTCAGTCAGTTCGATTTT	300
Db	241	CCCTGGGATGTTGTGGCTGATTTGTTGCAATCATTAAGATAGTCAGTTCGATTTT	300
Qy	301	ATPACGGGGAAGTGTGTGGGCTCAGAGATTTGCTATACCTAAGTGTATACGAATAT	360
Db	301	ATPACGGGGAAGTGTGTGGGCTCAGAGATTTGCTATACCTAAGTGTATACGAATAT	360
Qy	361	CTPAAATCCCGAAACTAAGATCCCGCTTTTATGATACATACATGCTGTGCTTTATATC	420
Db	361	CTPAAATCCCGAAACTAAGATCCCGCTTTTATGATACATACATGCTGTGCTTTATATC	420
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Db	421	GGTGAATAATCATCTGATATATGATATGTTTCTGATATTTTATTAAGAGATGGGTG	480
Qy	481	ATTACATTAATATGTTTGGAGCTCAGGTTTCTAAGTTTAAATTACAGAAGCTT	540
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Db	541	AATGTGCCGGGTATATGCGCGCTTTAAAGATCAAGTATGCGCTGATTTGGATTTAAAT	600
Qy	601	AATTGGCCCAACTTTGTGGCAATCCGATNAATTAACATCTTTGGTGAAGTGGCGGT	660
Db	601	AATTGGCCCAACTTTGTGGCAATCCGATNAATTAACATCTTTGGTGAAGTGGCGGT	660
Qy	661	GCTGCGCTACCCACTACATGATGTTTAAACGGAACAACTGGCGCTTTCCATCGGGT	720
Db	661	GCTGCGCTACCCACTACATGATGTTTAAACGGAACAACTGGCGCTTTCCATCGGGT	720
Qy	721	ATACTAATGTGGGTAAATGCTAATTTGTCCAAATTTGGCTAATCCCAATCTCAACATCGTGC	780
Db	721	ATACTAATGTGGGTAAATGCTAATTTGTCCAAATTTGGCTAATCCCAATCTCAACATCGTGC	780
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Db	781	TTTCACTTATGCAAAATTTGGCCGCTATTAAGGGTGAATAATGTATAGATGTTTGGAA	840
Qy	841	TTTTCTTATGAAGCAAGCCACAGATTTTATTAACCTGAGAGAAAGTTTAACTCTA	900
Db	841	TTTTCTTATGAAGCAAGCCACAGATTTTATTAACCTGAGAGAAAGTTTAACTCTA	900
Qy	901	GAAAGAGCTACAAATTAAGTATGTTTCTTTGGTCCCACTGTTGAGCCATACAGAC	960
Db	901	GAAAGAGCTACAAATTAAGTATGTTTCTTTGGTCCCACTGTTGAGCCATACAGAC	960
Qy	961	GCTGATTTGTCTTACCCAAACATCTCTGGGAAATGTTAAACGCTGGGGTAATTCG	1020
Db	961	GCTGATTTGTCTTACCCAAACATCTCTGGGAAATGTTAAACGCTGGGGTAATTCG	1020
Qy	1021	ATACCCAGTATGATGGGTAAACACTCAATGAGGGTCTATTTTTCATTTCAATTCCTTAAG	1080
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Db	1081	CAAAATGCGCTATGCTTTGAAGGAATGGAACTGTGTCAATTTTGTGCCAAGTGAATTCG	1140

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LOCUS	Sequence	7 from patent US 6235515.	
DEFINITION	AR153441		
ACCESSION	AR153441.1	GI:15120973	
VERSION			
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1713)		
AUTHORS	Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm., Roblin,G.Charlesde.,Quetleville.,Claudianos,C., Smyth,K.-A., Boyce,T.Mark., Oakeshot,J.Graham. and Brownlie,J.Colin. Malachion carboxylesterase Patent: US 6235515-A 7 22-MAY-2001; Location/Qualifiers 1..1713 "/organism="unknown"		
TITLE	JOURNAL		
FEATURES	source		
BASE COUNT	516 a 305 c 370 g 522 t		
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Best Local Similarity	99.5%; Pred. No. 0;		
Matches 1704; Conservative	0; Mismatches 9; Indels 0; Gaps 0		
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 Lucilia cuprina alpha esterase (lcaef) mRNA, implicated in
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 VERSION
 U56636.1 GI:1336079
 KEYWORDS
 ACCESSION
 U56636
 SOURCE
 ORGANISM
 Lucilia cuprina.
 Lucilia cuprina.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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 Oestroidea; Calliphoridae; Luciflia.
 REFERENCE
 1 (bases 1 to 2240)
 Newcomb, R.D., East, P.D., Russell, R.J. and Oakeshott, J.G.
 Isolation of alpha cluster esterase genes associated with
 organophosphate resistance in *Lucilia cuprina*
 Insect Mol. Biol. 5 (3), 211-216 (1996)
 TITLE
 JOURNAL
 Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
 MEDLINE
 97215578
 PUBMED
 9061925
 3 (bases 1 to 2240)
 Newcomb, R.D., Campbell, P.M., Ollis, D.L., Cheah, E., Russell, R.J. and
 Oakeshott, J.G.
 A single amino acid substitution converts a carboxylesterase to an
 organophosphorus hydrolase and confers insecticide resistance on a

JOURNAL blowfly
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
PUBMED 97352821
REFERENCE 9207114
AUTHORS 4 (bases 1 to 2240)
TITLE Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
Two different amino acid substitutions in the α -esterase, E3,
confer alternative types of organophosphorus insecticide resistance
in the sheep blowfly
JOURNAL Unpublished
REFERENCE 5 (bases 1 to 2240)
AUTHORS Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
TITLE Direct Submission
JOURNAL Submitted (24-APR-1996) Richard D. Newcomb, Molecular Genetics,
HortResearch, Private Bag 92 169, Auckland, New Zealand
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ORIGIN

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Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 481 ATTAACATACATATGCTTGGAGCTCTAGGTTTCTAAGTTTAATTCAGAACCTT 540
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LOCUS AR062838 Sequence 2 from patent US 5843758.
DEFINITION AR062838
ACCESSION AR062838
VERSION AR062838.1 GI:5990529
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Robin,G.Charlesde,Quetreville.,
Boyce,T.Mark., Campbell,P.Malcolm.,
Oakeshott,J.Graham. and Smyth,K.A.,
Enzyme based bioremediation
Patent: US 5843758-A 2 01-DEC-1998;
TITLE JOURNAL
FEATURES
source 1..1713
location/Qualifiers
BASE COUNT 506 a 299 c 363 g 515 t 30 others
ORIGIN

Query Match 97.7%; Score 1673.4; DB 6; Length 1713;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1677; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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QY	1261	TTCTGGTTCCTCCATGCATCGCTTTGTGGCAATTTACGTTCAATACACACTCCGGTACACC	1320
Db	1261	TTCTGGTTCCTCCATGCATCGCTTTGTGGCAATTTACGTTCAATACACACTCCGGTACACC	1320
QY	1321	GTCCTACTTGTATGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG	1380
Db	1321	GTCCTACTTGTATGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG	1380
QY	1381	CGTAGTGGACGTGGTGTAAAGGCGTTAGTCATGCTGATGAATTAACCTATTCTCTGG	1440
Db	1381	CGTAGTGGACGTGGTGTAAAGGCGTTAGTCATGCTGATGAATTAACCTATTCTCTGG	1440
QY	1441	AATCAATTTGGCCCAACGCTATGCTTAAGAAATCCGCTGAATACAAACAAATTTGAACGATG	1500
Db	1441	AATCAATTTGGCCCAACGCTATGCTTAAGAAATCCGCTGAATACAAACAAATTTGAACGATG	1500
QY	1501	ACTGCTATATGAGATACAAATTTGCCACCACTGCTATCTCTTATACCAATGAATGAAGGT	1560
Db	1501	ACTGCTATATGAGATACAAATTTGCCACCACTGCTATCTCTTATACCAATGAATGAAGGT	1560
QY	1561	ATGGAATAATGTTCTCGTGATCCAAATTAAGAAATCCGCTGAAGTATACAGTGTTTGAAT	1620
Db	1561	ATGGAATAATGTTCTCGTGATCCAAATTAAGAAATCCGCTGAAGTATACAGTGTTTGAAT	1620
QY	1621	ATTAGTGTATGATTAATTAATATGATGATGCTGCTGAATAGATTAATCAATATGGAG	1680
Db	1621	ATTAGTGTATGATTAATTAATATGATGATGCTGCTGAATAGATTAATCAATATGGAG	1680
QY	1681	TCGATGTTTGAAGAAACATAGAGATTTATTTTGA	1713
Db	1681	TCGATGTTTGAAGAAACATAGAGATTTATTTTGA	1713
RESULT 9	AF133341	2160 bp mRNA linear INV 17-AUG-2000	
LOCUS	AF133341	Musca domestica carboxylesterase MdaE7 (MdaE7) mRNA, complete cds.	
DEFINITION	AF133341		
ACCESSION	AF133341.1	GI:4768932	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
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Qy	661	GC	CCCTCTTACCACTACATGATGTAAACCGAAACAACTCGCGGCTTTTCCATCTG	720
Db	877	GG	GGCTTCAACCACTTACATGATGATTAACCGAAACGACCCGGTTTATTTCCATCTG	936
Qy	721	AT	ATCAATATGTGCGGTATGCTATTTGTCCATTGGGCTAAATACCATTGCAATCTG	780
Db	937	AT	CACTATGTATGTCGGTATTTCCATGTCTCTATGGGCTCTACAGAAATGCCAAATCTG	996
Qy	781	TT	TCACCTTTAGCCAAATTTGGCCGGCTATTAAGGTGAGAAATATGATMAGATGTTT	840
Db	997	CT	CAACCTATGGCCCAAAAGCTGTGGGCTATTAAGGAGAGACAAATGAATATCTG	1056
Qy	841	TT	TCCTTTTGAAGACCAAGCCACAGGATTATAGTAAAACTTGAGGAAATAGTTT	900
Db	1057	TT	CTCTTAATGAAGACCAATCCCTATGTATTTGATCAAAAAGACCCCAAGTTT	1116
Qy	901	GA	AGAGCGCTACAAATATAGTATGTTCCCTTTGGTCCACCTGTGAGCCATATCAG	960
Db	1117	GA	AGAAATGAACAATAATAGTATGTTCCCTTTGGACCCACTGTAGAACATACAG	1176
Qy	961	GC	CTATTTGTCTTTACCCAAACATCTCTGGGAAATGTTAAACTGTGGGTAATTC	1020
Db	1177	GC	CCACCTGTGTGGTACCCAAACATCAAGAAATGTGTAAAGGCGCTGGGAAATTC	1236
Qy	1021	AT	ATACCCACTATGATGGGTACACTTATATGTAGGGGTATTTTCTACTTAATCT	1080
Db	1237	AT	ATCCACATATGATAGGCAATACCTCTCTAGAAAGTTTGCTTTCAATCAATTC	1296
Qy	1081	CA	ATATGCTTATGCTTTTAAAGAAATTTGAAACTGTGTCAATTTTGTGCCAATG	1140
Db	1297	CA	ATATTCCTGAGGTGTGTAAAGATTTTGGATTCCTGTGTAAATATGTCTT	1356
Qy	1141	GC	TATGCTTAAAGCAACCGCCAGAGACTTGGAAATGGGTGTAAATTAAGAA	1200
Db	1357	GC	TATGCTTAAAGCAACCGCCAGAGACTTGGAAATGGGTGTAAATTAAGAA	1416
Qy	1201	CA	ATTTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTTTGTCTCA	1260
Db	1417	CA	ATTTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTTTGTCTCA	1476
Qy	1261	TT	TCGTTTCCCATGATCGTTTGTGTGAATACGTTTCAACACACCTCGGTAC	1320
Db	1477	TT	TCCTCTCCCATGATCGTTTGTGTGAATACGTTTCAACACACCTCGGTAC	1536
Qy	1321	GT	CTACTTGTATGCTTGCATTCGATTTGGAAAGATCTTATCAATCCCTATG	1380
Db	1537	AT	TATTTTGTATGCTTGCATTTGCATTTCCGAAAGAAATTAATTAACCCCT	1596
Qy	1381	CG	TATGCTGATGCTGTTTAAAGGTGTATGATCGTGTATTAACCTATTTCT	1440
Db	1597	CG	TATTTTGGCCGTGGCTTAAAGGTGTATTAACCTATGATGATGATGATG	1656
Qy	1441	AT	CAATTTTGGCCCAACCTATGCTTAAAGATGCGGTATCAAAACAAATGA	1500
Db	1657	AA	CAATTTTGGCCCAACCTATGCTTAAAGATGCGGTATCAAAACAAATGA	1716
Qy	1501	AC	TGTATATGATGATCAATTTGCCACACTGGTATCTTATAGCAATGAATG	1560
Db	1717	GT	TGTGTATGATGATCAATTTGCCACACTGGTATCTTATAGCAATGAATG	1776
Qy	1561	AT	GAATAATGTTTCTGTGATCCATTAAGAAATCGATGAGATATACAGGTT	1620
Db	1777	AT	GAATAATGTTTCTGTGATCCATTAAGAAATCGATGAGATATACAGGTT	1836
Qy	1621	AT	TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1680
Db	1837	AT	TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1896
Qy	1681	TC	GATGTTTGAAGAAACATATAGATTTATTTTA 1712	
Db	1897	AG	TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1928

RESULT 10	AF139082	2175 bp	mRNA	linear	INV 20-OCT-2000
LOCUS	AF139082				
DEFINITION	Haemaphysalis irritans irritans alpha E7 esterase (ae7) mRNA, complete cds.				
ACCESSION	AF139082				
VERSION	AF139082.1				
KEYWORDS	GI:5502938				
SOURCE	Haemaphysalis irritans irritans.				
ORGANISM	Haemaphysalis irritans irritans. Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidae; Muscidae; Haemaphysalis.				
REFERENCE	1 (bases 1 to 2175) Guerrero, F.D.				
AUTHORS	Cloning of a horn fly cDNA, H1alphaE7, encoding an esterase whose transcript concentration is elevated in diazinon-resistant flies				
TITLE	Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)				
JOURNAL	2 (bases 1 to 2175) Guerrero, F.D.				
MEDLINE	10989298				
PUBMED	20445807				
REFERENCE	2 (bases 1 to 2175) Guerrero, F.D.				
AUTHORS	Direct Submission				
TITLE	Submitted (30-MAR-1999) USDA-ARS, Knipling-Bushland U.S. Livestock				
JOURNAL	Insects Research Laboratory, 2700 Fredericksburg Rd., Kerrville, TX				
FEATURES	67028, US				
SOURCE	Location/Qualifiers				
gene	1..2175 /organism="Haemaphysalis irritans irritans" /strain="Camp Cooley 4/97" /sub-species="irritans" /db_xref="taxon:75445" /clone="HF41CC" /note="pyrethroid and diazinon-resistant" 1..2175 /gene="ae7" 282..1994 /gene="ae7" /note="similar to Lucilia cuprina and Drosophila melanogaster alpha E7 esterases" /codon_start=1 /product="alpha E7 esterase" /protein_id="AAFI14517.1" /db_xref="GI:5502938" /translation="MNFNVSFLERLKRIRKICVEKILNLTRETHIVDTEKGKINGVKRLIVYDSDSPREGIIPYAKPQVGLRFAKAPQRPVMDVKQCHASRSVQDFTSGNSGSEDCLILYNTNNLNTDTRKPIYLFVFFHGCGTICGANKRYTGADYFIKKDYVITAVYRLGVGEFSLNSENLNVENAGLKDQVMAIINIKNCASFQGDPCITLFGESAGASTHYMMITEQARGLFHRAYLMSGTACIMAHITQCOHRYTAKRIQKGENNDKYVDFELKANKYDILAREHEHYLTINEELRIVMEFQGTTPRYETPDCVLPRPNEMELKTAMNSIPILIGNTSYGLLEFISVGNKNPHILKELEFECEYVPEGLVEDRSPSELEIASILKRLIYRGERTLESPFELCSDPEYFVPMRPIQLRPNHIVGSPRIYLRPDPS EELINPRIMYRGVGVGASGHTDELTLYLFTMLSLKRPKRSREKRTIERMIGITQCA TTGAPYSPSELNGMENTTWDLSLKSDEYVCKANIGDELFTIDLPEMKLKYWQSVFNKKREL"				
BASE COUNT	690 a 365 c 435 g 685 t				
ORIGIN					
Query Match	56.1%; Score 961; DB 3; Length 2175;				
Best Local Similarity	72.6%; Pred. No. 1.2e-204;				
Matches 1243; Conservative	0; Mismatches 470; Indels 0; Gaps 0;				
1	ATGAAATTCACGCTAGTTGATGAGAAATTAATAAGATTAATGCAATGGAAT 60				
283	ATGAAATTCACGCTAGTTGATGAGAAATTAATAAGATTAATGCAATGGAAT 341				
61	AAATTTTAACTACCGCTATTTACCAATGAACGATATTTGATGATGCAATATGGA 401				
121	AAAGTAAAGCGCTTAAACGTTTAACCTGTACATGATGATTCCTACTACAGTTTGAGGCT 180				
402	AAATTTTAAAGCGCTTAAACGTTTAAACCTGTACATGATGATGATTCCTACTACAGTTTGAGGCT 461				

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OY 181 ATACGTAAGCCCAACCCAGTGGGTAGCTGAGATTAAAGCACCCAGGACCAACA 240
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Db 462 ATACCAATATGCGCAACCTCTGCGGCGCAATTAAGATTAAAGCTCCACCAAGCTCTGTC 521
OY 241 CCGTGGGATGAGTGGGTGATTTGTCATCAATTAAGATCAATGATGATGATTTT 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 522 CCGTGGGATGAGTGAAGATTTGTCATGCTGCTCCCGTCCGTTCCGTTCAACACATTTTC 581
OY 301 ATACGCGCAAGTGTGTGCTCAGAGATTGCTATACCTAAGTCTATACGATATAT 360
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Db 582 ATATCCGCAACTCAAGTGTGCGAGATTTGTTATATTGATCTATACGATATAT 641
OY 361 CTAAATCCCAACTAAGCTCCGTTTATATACATACATGATGATGATTTATATTC 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 642 TTAATACGTATCAAAAGCTCCGTTTCTTCTCATGATGATGATGATTTATTTGT 701
OY 421 GGTGAATATCATGCTATATGATGCTCTGATTTATTTCAATTAAGATGATGATG 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 702 GCGGAGCTATTAAGAACTATTAAGCGCTGATTTATTTCAATTAAGAGAGAGCTGCTTC 761
OY 481 ATTAACATACATATCTGTTGCGAGCTCTAGGTTTCTAGTTTAAATTCAGAGACCTT 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 762 ATATCTGCAATATCTGTTAGGGGTGTAGCTTTTCTAAGTTAAATTCGAAATCTC 821
OY 541 AATGCGCCGCTAATGCGCGCTTAAGATCAATGATGATGATGATGATTTAAAT 600
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Db 822 AATGCTACTGATATGCTGCGCTTAAGATCAATGATGATGATGATTTAAAT 881
OY 601 AATGCGCCCACTTTGCTGCGCAATCCGATTAATTAAGCTTTGGAAGAGCGCGT 660
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 882 AATGCTGCGAGCTTTGCTGCGCAATCCGATTTATTTCTATTTGCGAGAGTGTGGA 941
OY 661 GGTGCTACCCACTATCATATGATTTAAAGCAACAACTCGCGTCTTTTCAATCTGCT 720
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Db 942 GCTGCTCCAGCACTATATGATGATTAAGCAAGCTCGTGGCTATTCATCTGCTC 1001
OY 721 ATACTAATGCTGGTATATGCTATTTGCTCATTTGCTATACCAATGATCAATCTGCTC 780
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1002 GTTTTATGCTTGGAACCTCTATGCTATATGCGCCATACCAATGCTCAATCTGCTC 1061
OY 781 TTACCTTGAACCAATTTGCGCGCTATAAGGCTGATATGATAGATGATTTTGA 840
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Db 1062 TATACATTTGCCAAGATTTGTTACAAAGAAATTAATGACAAAGATCTCATAT 1121
OY 841 TTTCTTATGAAGCCAGCCAGAGATTAGTAAACTTGAGGAAAGTTTAACTCTA 900
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Db 1122 TTTCTATGAAGCAATCTCTATGATGCTGCGCGAGAGAGACAAAGTTTGAACAA 1181
OY 901 GAAGAGGCTCAATTAAGGATGATTTCTTTGCTCCAGCTGTGAGCCATATCAAGCC 960
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1182 GAGAGACTTGTATAGATTAATGATTTGCTTGGCTCCACACAGAACCTTATGAAACA 1241
OY 961 GCTGATTTGCTTACCAACATCTCTCGGAAATGTTAAAGCTTTGGGTTAATTCG 1020
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1242 CAGAGCTGTTTGGCCCAACCAATCGGAATGCTTTAAAGCTCTTGGGTTAATCTA 1301
OY 1021 ATACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
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Db 1302 ATACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1361
OY 1081 CAATGCTTATGCTTTGAAGAAATGGAATCTGTGCAATTTTGTGCAATGTAATG 1140
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Db 1362 CAATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1421
OY 1141 GCTGATGCTGAAGCAGCCGCGCCAGAGACCTTGAAGATGATGATGATGATGATG 1200
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Db 1422 TAGATTTGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1481
OY 1201 CATGTTACGAGAAACCAACAGCTGATTAATTTTATGATCTTCTGCTCATCTAT 1260
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Db 1482 TATGTAAGTGAAGACCAACATTTGGAAGTTTATGAGATTAATGCTGATTTCTAC 1541

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OY 1261 TTTGTTTCCCATGCTGTTTGTGCAATTAAGCTTTTCAATCAACAGCTCCGTAACCC 1320
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Db 1542 TTTTGGTATCCAAATGATCTTTTGTGCAATTAAGCTTTTCAATCAATCAATGCTCGGTCGCC 1601
OY 1321 GCTACTTTGATGCTTGCATCTGATTTGGAAGATCTTATCAATCCCTATGATTTAG 1380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1602 ATCTACTATATGTTTGTATTTGATTTCCGAGAGATTAATTAATCTATGATTTAG 1661
OY 1381 CGTATGAGAGCTGTTTAAAGGGGTGATGATGATGATGATGATGATGATGATG 1440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1662 CGTATGAGAGCTGTTTAAAGGGGTGATGATGATGATGATGATGATGATGATG 1721
OY 1441 AATCAATGGCCCAACGATGCTTAAGAAATCGGCTGATCAATCAAAACATTTAGCTATG 1500
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Db 1722 ACTATGCTCACCACAAAGATGCTCAAAAGATGAGCTGATTAATTAACATGAGAAATG 1781
OY 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
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Db 1782 ATAGGCAATTTGAGACCAATTTGCGCACTACGCGCAATCTATATGATGATGATGATG 1841
OY 1561 ATGGAATATGTTTCTGCGATCTCAATTAAGAAATCGATGATGATGATGATGATG 1620
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1842 ATGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1901
OY 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
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Db 1902 ATAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1961
OY 1681 TCGATGTTTGAAGAAACATAGAGATTAATTTAG 1713
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Db 1962 AGTGTTCATTAAGAGAGGGAATTTGTTAG 1994

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RESULT 11

AR153445

LOCUS AR153445 1710 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 14 from patent US 6235515.

ACCESSION AR153445

VERSION AR153445.1 GI:15120977

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1710)

AUTHORS Russell, J. Joyce., Newcomb, R. David., Campbell, P. Malcolm., Robin, G. Charles., Quetleville., Claudianos, C., Smyth, K. A., Boyce, I. Mark., Oakeshott, J. Graham, and Brownlie, J. Colin.

TITLE Malathion carboxylesterase

JOURNAL Patent: US 6235515-A 14 22-MAY-2001;

FEATURES

source location/Qualifiers

1..1710

BASE COUNT 498 a 369 c 394 g 449 t

ORIGIN

Query Match 55.6%; Score 951.8; DB 6; Length 1710;

Best Local Similarity 73.2%; Pred. No. 1.4e-202;

Matches 1220; Conservative 0; Mismatches 447; Indels 0; Gaps 0;

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OY 44 TTAATGATGAAATTAAGTTTAACTATGCTTTAACTACCAATGAACGCTGTG 103
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Db 104 TCGATATGCAATATGCAATTAATTAAGGCTTTAAAGCAATGACGCTGATGATGATGATG 163
OY 164 ACTAAGTTTGAAGGTTATACCGCAACGCGGAGTGGTGAAGTTTAAAG 223
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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OY 224 CACCCAGCAGCAACACCGCTGGATGCTGCTGATTTGCAATCAATGAATAGT 283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 224 CACCCAGCGGCTTACCATTGGAGGGTGTACGTATTTGCTGTGGGCGACCAACAGAT 283
 Oy 284 CAGTCCAGTTGATTTTAAAGGCAAAAGTGTGGCTCAGAGATTGTCTATACCTTA 343
 Db 284 CGGTACACAGATTTCATTAAGTGGCAAAACCCAGAGTTCGAGATTGTCTATACCTTA 343
 Oy 344 GTGTCTATACGAATATATTAATCCGGAACAACTAAAGTCCGTTTGTATATCAATACATG 403
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 Oy 404 GTGTGTATTTATTTATTCGTTGAAAAATCATGTATATGTATGTCTGCTATATTTTCATTA 463
 Db 404 GCGGAGATTTTATTTTTCGCGAAGCAAAATGTAATGTTGGTTCGCGACTTCTTATGA 463
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 Oy 524 TAAATTCAGAAAGACCTTAATGTGCGGTAATGCGGCTTAAAGATCAAGTCAAGGCT 583
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 Oy 644 TTGGTGAAGTGGCGGTCTGCTTACCCTACCTACATGATGTTAACCAACCAACTCGCG 703
 Db 644 TCGGGAAGATGCTGTGTGGGCTCAACCCATTTACATGATGATTAACCAACCAAGCCGCG 703
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 Db 704 GTTTATTCATCGTGTGTATCATGATGTCCGTAATTCATGTGCTCATATGGGCTCTACAG 763
 Oy 764 AATGTCAACATCGTGTCTTACCTTACCCAAATTTGGCGCTATTAAGGGTGAATTAATG 823
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 Oy 824 ATAAAGATTTTGAATTTCTTATGAAGCAAGCCACAGATTTAGTAAACCTTGAAG 883
 Db 824 AAAAAGATATCTGGAATTTCTTAATGAAGCAACCAATCCCTATGATTTGATCAAAAGAGAGC 883
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 Oy 1184 CTAAATTTAAAAAGGCTCATGTTACAGAGAAACCAACAGCTCATATTTTATGATGAT 1243
 Db 1184 CCATTTGAAAAAGGCCATGTGATGGGGAACACATACCTCTGATATATTTTATGAGAC 1243
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 Db 1244 TTGTCTCAATTTCTATTTCTCTTCCCATCATCGCTTCTCAATATTTGCGCTTCAAC 1303
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Oy 1364 ATCCCTATGCTATTTATGCTAGTACGACGTGCTGTTAAGGCTGTACTCATGCTGATGAT 1423
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 Db 1424 TAACCTATCTCTTGTGAACATTTTGTGGAACGCGCTGCAAAAGAAAGCCGCAATACA 1483
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 Db 1484 AAACATTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
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 Oy 1604 TATACAGTGTGTTGATATTTAGTATGATGATGATGATGATGATGATGATGATGATGAT 1663
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 Db 1664 AAATTAAACATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710

RESULT 12
 AY051473
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Direct Submission
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a polyA tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unsplined precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our web site
 (<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.

FEATURES
 source
 location/Qualifiers
 1..2017
 /organism="Drosophila melanogaster"
 /strain="y: cn bw sp"
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ACCESSION AV121675
VERSION AV121675.1 GI:21464397
KEYWORDS FLI cDNA.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Aspayani, A., Carlson, J.,
Champe, M., Chaver, C., Dorsett, V., Dresnek, D., Fartan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nuncio, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
and Celniker, S.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
COMMENT Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones, that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unsliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu

FEATURES
source location/Qualifiers
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IYRELYL"

BASE COUNT 724 a 632 c 650 g 654 t
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205 GGTGAGCTGAGATTAAGACACCCAGCAGCAACACCCCTGGAGATGCTGGGTATGTT 264
666 GCGAGACTCCGCTTCAAGCGCCCGCGGAGCCAGACACTGGTCAATGTCAGCGGTG 725
265 TSCAATCATTAAGATTAAGTCAAGTGAATTTATTAAGCGGCAAAAGTGTGTGCTCA 324
726 ACACATGTTGCGGCCAAGCCCTGCAGGTCAACATGCTTCTGAAGCAGGTGCAAGCAG 785
325 GAGGATGCTCTATACCTAAGTCTATACGATTAATCTTAATCCGAATCAAGCTGCC 384
786 GAGGACTGCTCTACCTCAATGTCTTAACACGAGGAGTTCATCCACAGACCTTTGCC 845
385 GTTTAGTATACATACATGCTGCTGTTTATATCGTGAAGAAATCATGCTGATATAT 444
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966 GCGCTGGGATCTCTTACCTTCTCAAGCAAGCTGAGTCTCGGAACCGCGGACATTA 1025
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1146 CTGACGAGATCAGCGCAAGGCGCTATTTCAAGACATATTAATTCGGGATCCGCATG 1205
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1386 ACCATGTTTCAAGTTTGACCCCACTGACCCCTATTTGACTTCCTCATTTGTGATTC 1445
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1446 AAGTGCCACATGAAATATGTCGGGACGTGTGGGGAACAGCATTCATGTCATCGGA 1505
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BASE COUNT      777 a 609 c 657 g 776 t 1 others

ORIGIN
Query Match      21.8%; Score 373.8; DB 3; Length 2820;
Best Local Similarity 54.6%; Pred. No. 36-73;
Matches 1054; Conservative 0; Mismatches 612; Indels 263; Gaps 5

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DB  890  AGACCATGAGCATTAAGTCCAGCAGTATCCGCACTCCACCAATGAACAGTTGTGCGC 949
QY  106  GAAACTGAATATGCGCAAGTGAAGGGCGTTAAACGTTTAACTGTGTGATGATTCCTAC 165
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DB  950  GACACGAGATAGCGCCCAAGTGAAGGGGTATCAACACCGCTACTCTCTACGATGCGCTAC 1009
QY  166  TACAGTTTGAAGGTATACCGTACGCGCCCAACCGGCACTGGGTGAGCTGATGATTAAGCA 225
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DB  1010  TTCAGCTTGAGAGGTATCCCGTACGCCACGCTCCGGTGGGAGATGGCGTTTAAAGGCC 1069
QY  226  CCCCAGCGACAACACCCGTGGAGTGGTGGCGTATGTTGGCAATCATMAAGATAAGTCA 285
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DB  1070  CCTCAGAGGCCCATTCCTCCGGGAGGAGATTCGCACTGCAGCCAGCCAGCAAGATTAAGGCC 1129
QY  286  GTGCAAGTTGATTTATTAACGGGCAAGTGTGTGGCTCAGAGAGATTGTTATTAACCTAACT 345
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QY  346  GCTATACGAATAAT----- 360
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QY  361  -----CTMAATCCCGAACAATAACG 380
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QY  381  TCCCGTTTATGATACATATACATGATGGTGGTATTATATCGGTGAATAATCATCGTGAATAT 440
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QY  501  GGGAGCTCT----- 509
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QY  510  -----AGGTTTCTAGTTTAAATTTAGAAGACCTTAATATGTGCGCGGTAAATGCCGCC 562
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RESULT 15
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DEFINITION	Drosophila melanogaster, *** SEQUENCING IN PROGRESS *** , in ordered			

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VERBON	AC015272 1

VERSION 01.045000
 KEYWORDS HTG; HTGS_PHASE2.
 SOURCE Drosophila melanogaster.

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Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
Direct Submission

Direct Submission JOURNAL
Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA

COMMENT This sequence was identified as CDM:10213452 by the submitter. For further information on this sequence e-mail to flye@elera.com.

- * NOTE: This is a 'working draft' sequence.
- * This sequence will be replaced
- * by the draft of the new sequence

FEATURES

- * by the finished sequence as soon as it is available and
- * the accession number will be preserved.

location/Qualifiers

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Matches 1051: Conservative	0;	Mismatches 615:	Indels 263: Gaps 5:
Query match	21.38;	Score 307;	DB 2; Length 37533;

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Db 36481 AGAACCATCGAGCATAAAGTCCAGCAGATTCGCCAGTCGACCAATGAAACAGTTGCGCC 36422

QY 106 GAAACTGAATATGGCAAAAGTGAAGGCCTTAAACGTTTAACTGTGTACGATGATTCCTAC 165

Db 36421 GACACGGAGTACGGCCCAAGTGAGGGGATCAAGCGTCTATCTCTACGATGCCCCAC 36362

QY 166 TACAGTTTGAGGGTATACCGTACGCCCAACCCAGCGGGGTGACGTGAGATTTAAACCA 225

Db 36361 TTTCAGCTTTCGAGGGATACCCCGTAGCCCAAGCCCTCCGGTGGGGGAATTTCGGCTTTAAAGGCC 36302

Db 36301 CCTCAGAGGCCATTTCCCTGGGAGGAGGTTTGGGACTGCAGGCAGCGGAGGATTAAGGCC 36242

QY 286 GTCCAGTGTGATTTTATTAACGGCCAAAGTGTGGCTCAGAGCATTGTCTATACCTAAGT 345

Db 36241 GTCCAGGTCGACGTTCTTCGATTAAGGTAGAAGGGCTCCGAGACCTGGCTCATCTCAAT 36182

QY 346 GTCTATACGAATAT----- 360
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Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG

XX WPI: 1995-263870/34.
 DR P-PSDB; AAR78142.
 XX pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 water, meat etc.
 XX
 PS Claim 5; page 12-17; 38pp; English.
 XX
 CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA
 CC library was amplified using cluster-specific esterase primers.
 CC Isolated clone Lc743, a probable full-length cDNA, was expressed
 CC using a baculovirus vector in insect cells and shown to encode
 CC an OP-susceptible E3 esterase, useful in bioremediation.
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 SQ Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;

Query Match 99.2%; Score 1698.6; DB 16; Length 1713;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 841 TTTCCTATGAAGCCAAAGCCAGAGATTTAGTAATAACTTGAGGAAAAAGTTTAACCTCA 900
DB 841 TTTCCTATGAAGCCAAAGCCAGAGATTTAGTAATAACTTGAGGAAAAAGTTTAACCTCA 900
QY 901 GAAGAGCTTACAAATTAAGTCATGTTCCCTTTGGTCCCACTGTGAGCCATATCAGACC 960
DB 901 GAAGAGCTTACAAATTAAGTCATGTTCCCTTTGGTCCCACTGTGAGCCATATCAGACC 960
QY 961 GCTATTTGCTCTTACCAAAACATCTCGGAAATGTTAAACCTGCTGGGTAATTCG 1020
DB 961 GCTATTTGCTCTTACCAAAACATCTCGGAAATGTTAAACCTGCTGGGTAATTCG 1020
QY 1021 ATACCACTATGATGGGTACACTTCATATGAGGCTATTTTCACTTCAATTTCTTAAG 1080
DB 1021 ATACCACTATGATGGGTACACTTCATATGAGGCTATTTTCACTTCAATTTCTTAAG 1080
QY 1081 CAATGCTATGCTTTAGGAATGGAATCTGTGCAATTTTGTGCCAAGTGAATG 1140
DB 1081 CAATGCTATGCTTTAGGAATGGAATCTGTGCAATTTTGTGCCAAGTGAATG 1140
QY 1141 GCTGATGCTGAACGACCGCCAGAGACCTTGAATGAGTGGTGAATTAATAAAGGCT 1200
DB 1141 GCTGATGCTGAACGACCGCCAGAGACCTTGAATGAGTGGTGAATTAATAAAGGCT 1200
QY 1201 CATGTTAAGGAGAAACCAACAGCTGATTAATTTATGATCTTCTGCTCATCATAT 1260
DB 1201 CATGTTAAGGAGAAACCAACAGCTGATTAATTTATGATCTTCTGCTCATCATAT 1260
QY 1261 TTCTGCTTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 TTCTGCTTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 GTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 GTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 CGTAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 CGTAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 AATCAATGTCGCAACGATATGCTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 AATCAATGTCGCAACGATATGCTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 ACTGCTATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 ACTGCTATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 ATGGAATATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 ATGGAATATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 ATTAGATATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 ATTAGATATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 TCGATGTTTGAATAACATAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAATAACATAGATTTATTTAG 1713

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RESULT 2
 AAT68596 standard; DNA: 1713 BP.
 AAT68596;
 08-Aug-1997 (first entry)

	Matches	1704:	Conservative	0:	Mismatches	9:	Indels	0:	Gaps	0:
QY	1	ATGAATTTCAACGTTAGTTTGATGAGAAATTTAAAAATGGAAGATTAATATCATTTGAAAAAT	60							
Db	1	ATGAATTTCAACGTTAGTTTGATGAGAAATTTAAAAATGGAAGATTAATATCATTTGAAAAAT	60							
QY	61	AAGTTTAAATCATACGTTTAACTACCAATGAAAGGTTGTAAGCTGAATCTAATATATGCC	120							
Db	61	AAGTTTAAATCATACGTTTAACTACCAATGAAAGGTTGTAAGCTGAATCTAATATATATGCC	120							
QY	121	AAAGTGAAGAGCGTTAAACGTTTAACTGTGTCGATGATGATCTACTACAGTTTGGAGGT	180							
Db	121	AAAGTGAAGAGCGTTTAAAGTTTAACTGTGTAAGATGATCTACTACAGTTTGGAGGT	180							
QY	181	ATACCGTACGCGCCCAACCGCAGTGGGTGAGCTAGCAATTTTAAAGCAACCCAGCAGACACA	240							
Db	181	ATACCGTACGCGCCCAACCGCAGTGGGTGAGCTAGCAATTTTAAAGCAACCCAGCAGACACA	240							
QY	241	CCCTGGGATGCTGTCCGTGATTTGTTGCAATCATAAAGATAAATGTCAGTCAATTTGATTTT	300							
Db	241	CCCTGGGATGCTGTCCGTGATTTGTTGCAATCATAAAGATAAATGTCAGTCAATTTGATTTT	300							
QY	301	ATTAAGGGGAAAGTGTGGGCTCAAGAGATGTCATACCTAAAGTGTATACGAAATAT	360							
Db	301	ATTAAGGGGAAAGTGTGGGCTCAAGAGATGTCATACCTAAAGTGTATACGAAATAT	360							
QY	361	CTAAATCCCGAAACATAACAGTCCCGTTTAACTATACATACATGATGTTGTTTATATATC	420							
Db	361	CTAAATCCCGAAACATAACAGTCCCGTTTAACTATACATACATGATGTTTATATATC	420							
QY	421	GGTGAATAATCATGCGATATATGATGTGCTGATTTATTTCAATTTAAAGATGTGTTG	480							
Db	421	GGTGAATAATCATGCGATATATGATGTGCTGATTTATTTCAATTTAAAGATGTGTTG	480							
QY	481	ATTAACTATCAATATGCTTTGGAGCTCTAGGCTTTTCTAAAGTTTAAATCAAGACCTT	540							
Db	481	ATTAACTATCAATATGCTTTGGAGCTCTAGGCTTTTCTAAAGTTTAAATCAAGACCTT	540							
QY	541	AATGTGCCCGGTAATGCGCGCTTAAAGATCAAGTCATAGCCCTTCATTTGATTTAAAT	600							
Db	541	AATGTGCCCGGTAATGCGCGCTTAAAGATCAAGTCATAGCCCTTCATTTGATTTAAAT	600							
QY	601	AATTTGCGCAACTTTGGTGGCAATCCCGATATATTACAGTCTTTGGTGAAGTGC	660							
Db	601	AATTTGCGCAACTTTGGTGGCAATCCCGATATATTACAGTCTTTGGTGAAGTGC	660							
QY	661	GCTGCTCTACCCACTACATGATGTTTAAACCGAACAACCTGGGCTTTTCCATGCTGT	720							
Db	661	GCTGCTCTACCCACTACATGATGTTTAAACCGAACAACCTGGGCTTTTCCATGCTGT	720							
QY	721	ATACTAATGTCGGGTAATGCTATTTTGTCCATTTGGCTAATACCAATATGTCACATGCTGC	780							
Db	721	ATACTAATGTCGGGTAATGCTATTTTGTCCATTTGGCTAATACCAATATGTCACATGCTGC	780							
QY	781	TTTACCTTAAGCCAAATTTGGCCGGCTATAAAGGTTGAGATATATGATATAGATGTTTGGAA	840							
Db	781	TTTACCTTAAGCCAAATTTGGCCGGCTATAAAGGTTGAGATATATGATATAGATGTTTGGAA	840							
QY	841	TTTCTTATGAAGAACCAAGCACAGATTTATAGTAAACCTTGAGAGAAATTTTAACCTCA	900							
Db	841	TTTCTTATGAAGAACCAAGCACAGATTTATAGTAAACCTTGAGAGAAATTTTAACCTCA	900							
QY	901	GAAAGAGCTACAAATAAAGTCAATGTTTCCATTTGGTCCACAGTTGAGCATATAGAC	960							
Db	901	GAAAGAGCTACAAATAAAGTCAATGTTTCCATTTGGTCCACAGTTGAGCATATAGAC	960							
QY	961	GCTGATGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAACATGCTGGGTAATTCG	1020							
Db	961	GCTGATGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAACATGCTGGGTAATTCG	1020							
QY	1021	ATACCACTATGATGGGTAAACACTTCAATATGAGGCTATATTTTACTTCAATTTCTTAAG	1080							
Db	1021	ATACCACTATGATGGGTAAACACTTCAATATGAGGCTATATTTTACTTCAATTTCTTAAG	1080							

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QY 1081 CAATGCTATGCTTGTAGGAATGAAACCTGTGTCATTTTGTGCCAAGTAATG 1140
DB 1081 CAATGCCCTATGCTTGTAGGAATGAAACCTGTGTCATTTTGTGCCAAGTAATG 1140
QY 1141 GCTGATGCTGAACGACGCGCCGACAGACCTTGGAAATGGGTCTTAAATTAAGGT 1200
DB 1141 GCTGATGCTGAACGACGCGCCGACAGACCTTGGAAATGGGTCTTAAATTAAGGT 1200
QY 1201 CAGTGTACAGGAAACACCAACAGCTGATTAATTTATGATCTTGTCTGATCATAT 1260
DB 1201 CAGTGTACAGGAAACACCAACAGCTGATTAATTTATGATCTTGTCTGATCATAT 1260
QY 1261 TTCTGCTCCCATGATGCTTGTGTGCAATTAACGTTCAATCACACCTCCGATACCC 1320
DB 1261 TTCTGCTCCCATGATGCTTGTGTGCAATTAACGTTCAATCACACCTCCGATACCC 1320
QY 1321 GTCTACTTGTATGCTTGTGCACTTGCATTCGGAAGATCTTATCAATCCCTATGATATG 1380
DB 1321 GTCTACTTGTATGCTTGTGCACTTGCATTCGGAAGATCTTATCAATCCCTATGATATG 1380
QY 1381 CGTAGTGTGAGTGTGTTAAGGGGTAGTGTGATGCTGATGATTAACCTATTTCTCTGG 1440
DB 1381 CGTAGTGTGAGTGTGTTAAGGGGTAGTGTGATGCTGATGATTAACCTATTTCTCTGG 1440
QY 1441 AATCAATTTGGCCAAACGATGCTTAAGAAATCGCGTGATACAAACAAATTAACGATATG 1500
DB 1441 AATCAATTTGGCCAAACGATGCTTAAGAAATCGCGTGATACAAACAAATTAACGATATG 1500
QY 1501 ACTGCTATATGATACAAATTTGCCACACGCTAATCCCTATAGCANTGAATTTGAAGT 1560
DB 1501 ACTGCTATATGATACAAATTTGCCACACGCTAATCCCTATAGCANTGAATTTGAAGT 1560
QY 1561 ATGGAATATGTTCTCGGATGATCAATTAAGAATCGCATGAATGAATGAATTTGAAT 1620
DB 1561 ATGGAATATGTTCTCGGATGATCAATTAAGAATCGCATGAATGAATGAATTTGAAT 1620
QY 1621 ATTATGATGATTAATTAATTAATGATGATGCTGAAATGATTAAGATTAACATGCGAG 1680
DB 1621 ATTATGATGATTAATTAATTAATGATGATGCTGAAATGATTAAGATTAACATGCGAG 1680
QY 1681 TCGATGTTGAATAACATAGATTAATTTTAG 1713
DB 1681 TCGATGTTGAATAACATAGATTAATTTTAG 1713

RESULT 3
AA091566
ID AA091566 standard; cDNA: 1713 BP.
XX
AC AA091566;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103con.
XX
KM Esterase; E3: bioremediation; organophosphate; carbamate;
KW Insecticide; pesticide; water decontamination; meat decontamination;
KW 89.
XX
OS Lucilia cuprina.
XX
FH Key 1.1713 Location/Qualifiers
FT CDS /tag= a
XX
XX WO9519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995. 95MO-AU00016.
XX
XX 13-JAN-1994. 94AU-0003347.
XX

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XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI: 1995-263870/34.
XX
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX eliminate residues of organo:phosphate and carbamate pesticides from
XX water, meat etc.
XX
XX Example 4: Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX Op-susceptible esterase E3 of L. cuprina) from a diazinon
XX resistant strain, Llandillo 103. 4 isolated clones were
XX sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
XX esterases; a consensus sequence is given in AA091566.
XX
XX
XX Sequence 1713 BP: 512 A; 307 C; 369 G; 525 T; 0 other;
XX

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Query Match 97.9% Score 1677.8; DB 16; Length 1713;
Best Local Similarity 98.7% Pred. No. 0; Mismatches 22; Indels 0; Gaps 0;
Matches 1691; Conservative

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QY 1 ATGAATTTCAAGCTTAGTTGATGAGAAATTAATGAAGATTAAATGCAATTAATGCAATTAAT 60
DB 1 ATGAATTTCAAGCTTAGTTGATGAGAAATTAATGAAGATTAAATGCAATTAATGCAATTAAT 60
QY 61 AAGTTTAACTATGCTTTAACTACCAATGAACGGTGTAGTGAACCTGAATATGGC 120
DB 61 AAGTTTAACTATGCTTTAACTACCAATGAACGGTGTAGTGAACCTGAATATGGC 120
QY 121 AAGTGAAGGGGCTTAAAGCTTAACTGTGTACATGATTCCTACTACAGTTTGAAGGT 180
DB 121 AAGTGAAGGGGCTTAAAGCTTAACTGTGTACATGATTCCTACTACAGTTTGAAGGT 180
QY 181 ATACGCTAGCCCAACCGCCAGTGGTGAGCTGATGAATTAAGCAACCCAGGACCAACA 240
DB 181 ATACGCTAGCCCAACCGCCAGTGGTGAGCTGATGAATTAAGCAACCCAGGACCAACA 240
QY 241 CCCTGGGATGAGTGTGCTGATGTTGCATCATTAAGATACATGATGATGATTTT 300
DB 241 CCCTGGGATGAGTGTGCTGATGTTGCATCATTAAGATACATGATGATGATTTT 300
QY 301 ATACGCGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGAATAT 360
DB 301 ATACGCGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCAACCTAAGCTCCGTTTATGATACATCATGATGATGATTTTATATC 420
DB 361 CTAAATCCCAACCTAAGCTCCGTTTATGATACATCATGATGATGATTTTATATC 420
QY 421 GGTAATATCATGCTGATGATGATGCTGATTAATTTATTAAGATGCTGCTTG 480
DB 421 GGTAATATCATGCTGATGATGATGCTGATTAATTTATTAAGATGCTGCTTG 480
QY 481 ATTAACATACATATGCTTTGGAGCTGTAGCTTTCTAGTTAAATCAGAACCTT 540
DB 481 ATTAACATACATATGCTTTGGAGCTGTAGCTTTCTAGTTAAATCAGAACCTT 540
QY 541 AATGTGCGCGGTATGCGCGCTTAAGATCAAGTCAAGTCCCTGATTTGATTAAT 600
DB 541 AATGTGCGCGGTATGCGCGCTTAAGATCAAGTCAAGTCCCTGATTTGATTAAT 600
QY 601 AATTGCGCAACTTTGGTGGCAATCCGATTAATTTACATGCTTTTGTGAAGTGGG 660
DB 601 AATTGCGCAACTTTGGTGGCAATCCGATTAATTTACATGCTTTTGTGAAGTGGG 660
QY 661 GCTGCTTACCCACTACATGATGTTAAGCAACCAACTGCGGCTTTTCCATCGTGT 720
DB 661 GCTGCTTACCCACTACATGATGTTAAGCAACCAACTGCGGCTTTTCCATCGTGT 720

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OY 721 ATACTAATGTGGGTAATGCTATTTGTCATTTGCTAATACCAATGCAACATGCTGCC 780
DB 721 ATACTAATGTGGGTAATGCTATTTGTCATTTGCTAATACCAATGCAACATGCTGCC 780
OY 781 TTCACCTTAGCCAAATTTGGCCGGCTATAAGGCTGAGAAATAGTAAGAGTCTTTGGAA 840
DB 781 TTCACCTTAGCCAAATTTGGCTATAGGCTGAGAGTAATAGTAAGAGTCTTTGGAG 840
OY 841 TTTCTTAGGAAGCCAGACAGATTTAGTAAACTTGAGGAAAGATTTTAACTCTA 900
DB 841 TTTCTTAGGAAGCCAGACAGATTTAGTAAACTTGAGGAAAGATTTTAACTCTA 900
OY 901 GAAGAGCGTACAAATTAAGTCAATTTCTTTGTCACAGTGGAGCATATACAGACC 960
DB 901 GAAGAGCGTACAAATTAAGTCAATTTCTTTGTCACAGTGGAGCATATACAGACC 960
OY 961 GCTGATTTGTCTTACCCAAACATCCTCGGGAATGTTAAACTGCTTGGGGTAATTCG 1020
DB 961 GCTGATTTGTCTTACCCAAACATCCTCGGGAATGTTAAACATGCTTGGGGTAATTCG 1020
OY 1021 ATACCCACATATGAGTGGTACACTTCATATGAGGCTATTTTTCACCTTCAATTCCTAAG 1080
DB 1021 ATACCCACATATGAGTGGTACACTTCATATGAGGCTATTTTTCACCTTCAATTCCTAAG 1080
OY 1081 CAAATGCGCTATGCTTTAAGGAATTTGAAACTTGTGCAATTTTGGCCAGTGAATTCG 1140
DB 1081 CAAATGCGCTATGCTTTAAGGAATTTGAAACTTGTGCAATTTTGGCCAGTGAATTCG 1140
OY 1141 GCTGATGCTGAACGCCACGCCGCCAGAGACCTTGAATGGTGTCTAAATTTAAAAAGGCT 1200
DB 1141 GCTGATGCTGAACGCCACGCCGCCAGAGACCTTGAATGGTGTCTAAATTTAAAAAGGCT 1200
OY 1201 CATGTTACGAGGAAACACCAACAGCTGATTAATTTATGAGTCTTCTCTACATCTAT 1260
DB 1201 CATGTTACGAGGAAACACCAACAGCTGATTAATTTATGAGTCTTCTCTACATCTAT 1260
OY 1261 TTTCTGTTCCCATGCTATGCTTTGCAATTTACGTTTCAATCACACCTCGGCTACAGCC 1320
DB 1261 TTTCTGTTCCCATGCTATGCTTTATGCAATTTACGTTTCAATCACACCTCGGCTACAGCC 1320
OY 1321 GTCTACTTGTATCGCTTTCGACTTCGATTCGAGAGATCTTATCAATCCCTATGCTATATG 1380
DB 1321 GTCTACTTGTATCGCTTTCGACTTCGATTCGAGAGATCTTATTAATCCCTATGCTATATG 1380
OY 1381 CGTAGTGGACGCTGCTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTTCTGG 1440
DB 1381 CGTAGTGGACGCTGCTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTTCTGG 1440
OY 1441 AATCAATTTGGCCAAACGCTATGCTTAAGAAATGCGTGAATACAAAACATTTGAACCTATG 1500
DB 1441 AATCAATTTGGCCAAACGCTATGCTTAAGAAATGCGTGAATACAAAACATTTGAACCTATG 1500
OY 1501 ACTGATATATGATACAAATTTGCGACCACTGTAATCCTTATAGCAATGAATTTGAAGT 1560
DB 1501 ACTGATATATGATACAAATTTGCGACCACTGTAATCCTTATAGCAATGAATTTGAAGT 1560
OY 1561 ATGGAATATGTTTCTGGGATCCAAATTAAGAAATCCGATGAAGTATACAAGTGTGTAAT 1620
DB 1561 ATGGAATATGTTTCTGGGATCCAAATTAAGAAATCCGATGAAGTATACAAGTGTGTAAT 1620
OY 1621 ATTAGATGAATTAAGAAATGATGATGCTGCTGAATGAGTAAAGTAAACAAATGGAG 1680
DB 1621 ATTAGATGAATTAAGAAATGATGATGCTGCTGAATGAGTAAAGTAAACAAATGGAG 1680
OY 1681 TCGATGTTGAAAAACATAGATTATTTAG 1713
DB 1681 TCGATGTTGAAAAACATAGATTATTTAG 1713

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RESULT 4
AA091564
ID AA091564 standard; cDNA: 1713 BP.

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XX AC AA091564;
XX DT 22-DEC-1995 (first entry)
XX DE OP-resistant esterase Lc7LI03C allele.
XX KW Esterase; E3; bioremediation; organophosphate; carbamate;
XX KM insecticide; pesticide; water decontamination; meat decontamination;
XX OS Lucilia cuprina.
XX FT Key Location/Qualifiers
XX FT CDS 1..1713
XX FT /*tag= a
XX PN W09519440-A1.
XX PD 20-JUL-1995.
XX PF 13-JAN-1995; 95WO-AU00016.
XX PR 13-JAN-1994; 94AU-0003347.
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX DR WPI; 1995-263870/34.
XX PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX PT eliminate residues of organo:phosphate and carbamate pesticides from
XX PS water, meat etc.
XX PS Example 4; Page 12-17; 38pp: English.
XX CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX CC resistant strain, Llandillo 103. 4 isolated clones were
XX CC sequenced (Lc7LI03 A-D, AA091562-65) that encoded diazinon-resistant
XX CC esterases. The esterases, or cells expressing them, are used
XX CC in bioremediation.
XX SQ Sequence 1713 BP; 512 A; 308 C; 368 G; 525 T; 0 other;
XX
XX Query Match 97.8%; Score 1674.6; DB 16; Length 1713;
XX Best Local Similarity 98.6%; Pred. No. 0;
XX Matches 1689; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
OY 1 ATGAATTTACGCTAGTTGATGAGAAATTAATGAAGATTAATGCAATGAAAT 60
DB 1 ATGAATTTACGCTAGTTGATGAGAAATTAATGAAGATTAATGCAATGAAAT 60
OY 61 AAGTTTAACTATCCTTAACTACTACCAATGAACGCTGTAAGCTGAATATGCG 120
DB 61 AAGTTTAACTATCCTTAACTACTACCAATGAACGCTGTAAGCTGAATATGCG 120
OY 121 AAAGTAAAGGCGTTAAAGTTTAACTGTGATGATGATTCCTACTACAGTTTGAAGGT 180
DB 121 AAAGTAAAGGCGTTAAAGTTTAACTGTGATGATGATTCCTACTACAGTTTGAAGGT 180
OY 181 ATACCGTACGCCCAACCGCAGTGGTGAAGTGAATTAAGCAACCCAGCAGCAACA 240
DB 181 ATACCGTACGCCCAACCGCAGTGGTGAAGTGAATTAAGCAACCCAGCAGCAACA 240
OY 241 CCTGGGATGCTGCTGCTATGTTGCATCATTAAGATTAAGTGAAGTGAATTTT 300
DB 241 CCTGGGATGCTGCTGCTATGTTGCATCATTAAGATTAAGTGAAGTGAATTTT 300
OY 301 ATAAAGGCAAGATGCTGCTAGAGATGCTATACCTAAGTCTATACGAATTAAT 360
DB 301 ATAAAGGCAAGATGCTGCTAGAGATGCTATACCTAAGTCTATACGAATTAAT 360

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Best Local Similarity 98.6%; Pred. No.: 0;
Matches 1689; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGATTTCAACGTAGTTGATGAGAAATTAATGAGCATTAATGCAATTGAAT 60
Db 1 ATGATTTCAACGTAGTTGATGAGAAATTAATGAGCATTAATGCAATTGAAT 60
QY 61 AAGTTTTAACTATCTTAACTACCAATGAACGGTGTAGTGAACATGATATGCG 120
Db 61 AAGTTTTAACTATCTTAACTACCAATGAACGGTGTAGTGAACATGATATGCG 120
QY 121 AAAGTGAAGCGTTAAAGCTTTAACTGTACGATGATCTTCACTACAGTTTGAAGGT 180
Db 121 AAAGTGAAGCGTTAAAGCTTTAACTGTACGATGATCTTCACTACAGTTTGAAGGT 180
QY 181 ATACCGTACGCCCAACCCGCGTGTAGTGAATTTAAAGCCCGCCAGCAGCA 240
Db 181 ATACCGTACGCCCAACCCGCGTGTAGTGAATTTAAAGCCCGCCAGCAGCA 240
QY 241 CCTGCGATGCGTGTGCGATTTGCAATCATAAAGATGAAGTCAAGTTGATTT 300
Db 241 CCTGCGATGCGTGTGCGATTTGCAATCATAAAGATGAAGTCAAGTTGATTT 300
QY 301 ATAAAGGCGCAAGTGTGTGCTCAGAGGATGTCTATACCTAAGTGTCTATACGAATAT 360
Db 301 ATAAAGGCGCAAGTGTGTGCTCAGAGGATGTCTATACCTAAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTTTTAACTATACATACATGCTGTGTTTATATTC 420
Db 361 CTAAATCCCGAACTAAACGTCCTTTTAACTATACATACATGCTGTGTTTATATTC 420
QY 421 GGTGAATATCATGCGATGATGATGCTGATTTTCAATTAAGAGTGTGTG 480
Db 421 GGTGAATATCATGCGATGATGATGCTGATTTTCAATTAAGAGTGTGTG 480
QY 481 ATTAACATACATATATGCTTTGGAGCTCTAGATTTTCTAAGTTTAAATTCAGAACCTT 540
Db 481 ATTAACATACATATATGCTTTGGAGCTCTAGATTTTCTAAGTTTAAATTCAGAACCTT 540
QY 541 AATGCGCCGGTAAATGCGGCTTAAAGATCAAGCATGCGCTTGCAATGATTAATAAT 600
Db 541 AATGCGCCGGTAAATGCGGCTTAAAGATCAAGCATGCGCTTGCAATGATTAATAAT 600
QY 601 AATTGCGCACTTTGCGGCAATCCGATATATTACAGTCTTGTGGAAGTCCCGT 660
Db 601 AATTGCGCACTTTGCGGCAATCCGATATATTACAGTCTTGTGGAAGTCCCGT 660
QY 661 GCTGCTCTACCCACATCATATGTTAAACGAACTCGCGGCTTTTCCATCGTGT 720
Db 661 GCTGCTCTACCCACATCATATGTTAAACGAACTCGCGGCTTTTCCATCGTGT 720
QY 721 ATACTAATGTGGGTAATGCTATTTGCTATGCTAATACCAATGTCACATGCTGCC 780
Db 721 ATACTAATGTGGGTAATGCTATTTGCTATGCTAATACCAATGTCACATGCTGCC 780
QY 781 TTACACTTAGCCAAATTTGGCGGCTATAAGGTTGAATGAATGAATGTTTGA 840
Db 781 TTACACTTAGCCAAATTTGGCGGCTATAAGGTTGAATGAATGAATGTTTGA 840
QY 841 TTTCTTATGAAGCCAGCCACAGATTTAGTAAACTTGAAGAAAAGTTTAACTTA 900
Db 841 TTTCTTATGAAGCCAGCCACAGATTTAGTAAACTTGAAGAAAAGTTTAACTTA 900
QY 901 GAAGAGCTACAAATTAAGTATGTTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
Db 901 GAAGAGCTACAAATTAAGTATGTTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
QY 961 GCTGATTTGTCTTACCCAAACATCTCTGGGAAATGTTAAACATGCTTGGGTAATTCG 1020
Db 961 GCTGATTTGTCTTACCCAAACATCTCTGGGAAATGTTAAACATGCTTGGGTAATTCG 1020
QY 1021 ATACCCACTATGATGGGTAAACACTTCATATGAGGCTATTTTTCACCTCGTTCTAAG 1080
Db 1021 ATACCCACTATGATGGGTAAACACTTCATATGAGGCTATTTTTCACCTCGTTCTAAG 1080

Db 1021 ATACCCACTATGATGGGTAAACACTTCATATGAGGCTATTTTTCACCTCGTTCTAAG 1080
QY 1081 CAAATGCCCTATGCTTGTAAAGAAATTTGAAACTTGTGTCAATTTTGTGCAAGTGAATG 1140
Db 1081 CAAATGCCCTATGCTTGTAAAGAAATTTGAAACTTGTGTCAATTTTGTGCAAGTGAATG 1140
QY 1141 GCTGATGCTGAAGCGACGCCGCCAGAGACCTTGAAGAAAGGGTGTAAATTTAAAGGCT 1200
Db 1141 GCTGATGCTGAAGCGACGCCGCCAGAGACCTTGAAGAAAGGGTGTAAATTTAAAGGCT 1200
QY 1201 CATGTTACAGAGGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCATCATAT 1260
Db 1201 CATGTTACAGAGGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCATCATAT 1260
QY 1261 TTTCTGTTTCCCATGATGCTTTGTTGCAATTTACGTTTCAATCACACCTCCGCTACACC 1320
Db 1261 TTTCTGTTTCCCATGATGCTTTGTTGCAATTTACGTTTCAATCACACCTCCGCTACACC 1320
QY 1321 GTCCTACTGATGCGCTTGACCTTGATTCGGAAGATCTATCATGCTATGCTATGAT 1380
Db 1321 GTCCTACTGATGCGCTTGACCTTGATTCGGAAGATCTTATTAATCCCTATGCTATGAT 1380
QY 1381 GCTAGTGACGCTGTGTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTTCTG 1440
Db 1381 GCTAGTGACGCTGTGTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTTCTG 1440
QY 1441 AATCAATTTGGCCAAACGATGCTTAAAGATGCGCTGAATACAAACAAATTAAGCTATG 1500
Db 1441 AATCAATTTGGCCAAACGATGCTTAAAGATGCGCTGAATACAAACAAATTAAGCTATG 1500
QY 1501 ACTGATATGATGATCAATTTTCCGACCACTGCTATGCTTATGAAATGAATTTGAAGT 1560
Db 1501 ACTGATATGATGATCAATTTTCCGACCACTGCTATGCTTATGAAATGAATTTGAAGT 1560
QY 1561 ATGAAAAATGTTTCTGCGGATCCAAATTAAGAAATCCGATGAAGTATACAGTGTGTAAT 1620
Db 1561 ATGAAAAATGTTTCTGCGGATCCAAATTAAGAAATCCGATGAAGTATACAGTGTGTAAT 1620
QY 1621 ATTACTGATGAATTTAAATATGATTTGCTGCTGAAGTGAATTAAGATTAACATGCGAG 1680
Db 1621 ATTACTGATGAATTTAAATATGATTTGCTGCTGAAGTGAATTAAGATTAACATGCGAG 1680
QY 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
Db 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713

RESULT 6
AA091563
ID AA091563 standard; cDNA; 1713 BP.
XX
AC AA091563;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103B allele.
XX
XX Esterase; E3: bioremediation; organophosphate; carbamate;
KW Insecticide; pesticide; water decontamination; meat decontamination;
KW ss.
XX
OS Lucilia cuprina.
XX
FH Key Location/Qualifiers
FT 1..1713
FT CDS /*tag= a
XX
PN W09519440-A1.
XX
XX 20-JUL-1995.
XX
PD 13-JAN-1995; 95WO-AU00016.
XX
PF
XX

PR 13-JAN-1994; 94AU-0003347.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI; 1995-263870/34.
DR
XX
PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
PT eliminate residues of organo:phosphorate and carbamate pesticides from
PT water, meat etc.
XX
PS
XX Example 4; Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC Op-susceptible esterase E3 of *L. cuprina*) from a diazinon
CC resistant strain, Llandillo 103. 4 Isolated clones were
CC sequenced (Lc7L103 A-D, AAC91562-65) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
XX in bioremediation.
XX
SQ Sequence 1713 BP; 513 A; 308 C; 368 G; 524 T; 0 other;

Query Match	Similarity	Score	DB	Length
Best Local	98.5%	Pred. No. 0.		
Matches 1688:	Conservative	0;	Mismatches 25;	Indels 0;
				Gaps 0
Qy	1	ATGAATTTTCACGTTAGTTTGATGAGAAATTTAAATGCMAGATTAAATGCAATTGGAAT	60	
Db	1	ATGATATTTTCACGTTAGTTTGATGAGAAATTTAAATGCAATTAAATGCAATTGGAAT	60	
Qy	61	AGTTTAAATCTATCGTTTAACTTACCAATGAAAGGGTGTGACTGAAACTGAATATGGC	120	
Db	61	AGTTTAAATCTATCGTTTAACTTACCAATGAAAGGGTGTGACTGAAACTGAATATGGC	120	
Qy	121	AAAGTGAAGGCGTTAAACGTTTAACTGTGTGCGATGATTCCTACTACAGTTTGAGGGT	180	
Db	121	AAAGTGAAGGCGTTAAACGTTTAACTGTGTGCGATGATTCCTACTACAGTTTGAGGGT	180	
Qy	181	ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTTAAAGCAACCCACGACCAACA	240	
Db	181	ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTTAAAGCAACCCACGACCAACA	240	
Qy	241	CCCTGGGATGGTGTCCGTGATTTGTTGCATTCATTAAGATTAAGTCACTGCAAGTGAATTT	300	
Db	241	CCCTGGGATGGTGTCCGTGATTTGTTGCATTCATTAAGATTAAGTCACTGCAAGTGAATTT	300	
Qy	301	ATTAAGGGCAAAAGTGTGGCTGCAGAGATGTCTATACCTAAAGTGTCTATACGAATAT	360	
Db	301	ATTAAGGGCAAAAGTGTGGCTGCAGAGATGTCTATACCTAAAGTGTCTATACGAATAT	360	
Qy	361	CTAATTCGCCGAACATAAACGTCGCCCTTTTAGTATACATACATAGTGGGTGTTATATTC	420	
Db	361	CTAATTCGCCGAACATAAACGTCGCCCTTTTAGTATACATACATAGTGGGTGTTATATTC	420	
Qy	421	GGTGAATATCATCGTATATGTATGTGCTGTATTTTCATTTAAAGAGATGTGCTGTG	480	
Db	421	GGTGAATATCATCGTATATGTATGTGCTGTATTTTCATTTAAAGAGATGTGCTGTG	480	
Qy	481	ATTTAAATATCAATATTCGTTTGGGAGCTCTAGTGTTCCTAAAGTTTAAATTCAGACCTT	540	
Db	481	ATTTAAATATCAATATTCGTTTGGGAGCTCTAGTGTTCCTAAAGTTTAAATTCAGACCTT	540	
Qy	541	AATGTGCGCGGTAAATGCGCGGCTTAAACATCAAGTCATGAGGCGTTCGATTTAAAT	600	
Db	541	AATGTGCGCGGTAAATGCGCGGCTTAAACATCAAGTCATGAGGCGTTCGATTTAAAT	600	
Qy	601	AATGTGCGGCAATTTGGTGTGCAATCCGATATATATTAACGCTTTTGGTGAAGAGTCCGGT	660	
Db	601	AATGTGCGGCAATTTGGTGTGCAATCCGATATATATTAACGCTTTTGGTGAAGAGTCCGGT	660	
Qy	661	GCTGCTCTTACCCATCATATGATGTTAAACGACAACTGCGGCTTTTTCATTCATGCTGT	720	

Dp	661	CGTGGCTACCCACTACATGATGTATTAACGAAACAAACTGGCGTCTTTCCATCGGGT	720
Qy	721	ATACTAATGTGGGGTAATGCTATTTGTCCATTGGCTATACCCATGTCAACATCGTGC	780
Dp	721	ATACGAATGTGGGGTAATGCTATTTGTCCATTGGCTATACCCATGTCAACATCGTGC	780
Qy	781	TTTCACCTTAGCCAAATTTGGCGGCTATTAAGGGTGAAGATATATGAATTAAGATGTTTGGAA	840
Dp	781	TTTCACCTTAGCCAAATTTGGCGGCTATTAAGGGTGAAGATATATGAATTAAGATGTTTGGAG	840
Qy	841	TTTTCTTATGAAGCCACGACAGAGATTACTAAACTGAGGAAAAAGTTTTAACTCTA	900
Dp	841	TTTTCTTATGAAGCCACGACAGAGATTATATAAACCTTAGGAAAAAGTTTTAACTCTA	900
Qy	901	GAAAGCGCTACAAATTAAGGTATGTTCCTTTGGTCCACTGTGAGCCATTCAGACC	960
Dp	901	GAAAGCGCTACAAATTAAGGTATGTTCCTTTGGTCCACTGTGAGCCATTCAGACC	960
Qy	961	GCTGATGTGTCTTACCCAACATCTGGGAAATGGTTAAACCTGGTGGGTAATTCG	1020
Dp	961	GCTGATGTGTCTTACCCAACATCTCGGGAAATGGTTAAACATGCTGGGTAATTCG	1020
Qy	1021	ATACCCACTATGATGGGTAACTCTCAATTAAGGGTCTATTTTCACCTCAATTCCTAAG	1080
Dp	1021	ATACCCACTATGATGGGTAACTCTCAATTAAGGGTCTATTTTCACCTCTGTTCTTAAG	1080
Qy	1081	CAAAATGCTATGCTTTTAAAGAAATTGGAAACTTGTCTCAATTTTGTGCCAAGTAATTG	1140
Dp	1081	CAAAATGCTATGCTTTTAAAGAAATTGGAAACTTGTCTCAATTTTGTGCCAAGTAATTG	1140
Qy	1141	GCTGATGTGAAAGCAGCCGCCAGACACCTTGGAAATGGGTGCTAAATTAAGAAAGCT	1200
Dp	1141	GCTGATGTGAAAGCAGCCGCCAGACACCTTGGAAATGGGTGCTAAATTAAGAAAGCT	1200
Qy	1201	CATGTTACAGAGAAAGACCAACAGCTGATTAATTTTATGATCTTTGCTCCACATCTAT	1260
Dp	1201	CATGTTACAGAGAAAGACCAACAGCTGATTAATTTTATGATCTTTGCTCCACATCTAT	1260
Qy	1261	TTTCGGTCCCCCATGCAATCGTTGTGCCAATTAAGTTCAATACACCTCCGCTACACC	1320
Dp	1261	TTTCGGTCCCCCATGCAATCGTTTATTTGCCAATTAAGTTTCAATACACCTCCGCTACACC	1320
Qy	1321	GTCCTACTGTATTCGCTTCGACTTCGATTCGAGGAATCTTATCAATCCCTATGATTAAG	1380
Dp	1321	GTCCTACTGTATTCGCTTCGACTTCGATTCGAGGAATCTTATTAATCCCTATGATTAAG	1380
Qy	1381	CGTAGTGCACGTGGTGTAAAGGCTTAAAGTCAATGCTGATGAATTAACCTATTTCTTGG	1440
Dp	1381	CGTAGTGCACGTGGTGTAAAGGCTTAAAGTCAATGCTGATGAATTAACCTATTTCTTGG	1440
Qy	1441	AATCAATTTGGCCAAACGTAATGCTTAAAGATTCGCGGAATACAAACAAATTAAGCTAAG	1500
Dp	1441	AATCAATTTGGCCAAACGTAATGCTTAAAGATTCGCGGAATACAAACAAATTAAGCTAAG	1500
Qy	1501	ACTGGTATATGAGATACAAATTTGGCCACACGTGTAATCTTATAGCAATGAATTAAGGT	1560
Dp	1501	ACTGGTATATGAGATACAAATTTGGCCACACGTGTAATCTTATAGCAATGAATTAAGGT	1560
Qy	1561	ATGAAATGTTTCCCTGGGATTCGAATTAAGAAATTCGATGAAGTATACAAAGTGTGAAT	1620
Dp	1561	ATGAAATGTTTCCCTGGGATTCGAATTAAGAAATTCGATGAAGTATACAAAGTGTGAAT	1620
Qy	1621	ATTAGTATGAATTTGAAATGATTTGATGTGCTCGAATGATGAATTAAGTATTAACAAATGGGAG	1680
Dp	1621	ATTAGTATGAATTTGAAATGATTTGATGTGAGCCTGAAATGATTAAGTATTAACAAATGGGAA	1680
Qy	1681	TCGATGTTTGAAGAAACATTAAGATTTATTTTAC 1713	
Dp	1681	TCGATGTTTGAAGAAACATTAAGATTTATTTTAC 1713	

[illegible]

Query Match	55.6%	Score 951.8	DB 18	Length 1710
Best Local Similarity	73.2%	Pred. No. 2.1e-250		
Matches 1220	Conservative	0	Mismatches 447	Indels 0
CC resistance. The resistant enzyme acts as a malathion				
CC carboxylesterase and can be formulated for use in degrading				
CC environmental carboxylester or dimethyl general organophosphates.				
XX				
XX Sequence 1710 BP; 498 A; 369 C; 394 G; 449 T; 0 other;				
QY 44	TTAAATGCATGAAATTAAGTTTAACTATTCGTTTAACTAACAAATGAAGGAGGTAG	103		
DB 44	TTAAATGCATGCAATTAATATACAAACTACCGCTGAGTCAATACAAACCAATTA	103		
QY 104	CTGAATAGTAATATGCAAGTGAAAGGGCTTAACGTTAACTGTAGCATATCTT	163		
DB 104	TCGATACGTAATATGCAATTAATGAGGTGTAAAGCATGACCGCTACATATCTT	163		
QY 164	ACTACAGTTTACAGGTATACCGTAGCCCAACCGCATAGGTGACGCGAGATTTAAG	223		
DB 164	ACTACAGTTTACAGGTATACCGTAGCCCAACCGCATAGGTGACGCGAGATTTAAG	223		
QY 224	CACCCACGACCAACACCCCGGATGTGGGTGATTTGTCATCATTAAGTAACT	283		
DB 224	CACCCACGACGCTTACCATGAGAGGTGTACGTGATTCGTGTGGCCAGCACACAT	283		
QY 284	CAGTACAGTTATTTAAACGGGCAAAAGTGTGCTCAGAGATTTCTATACCTAA	343		
DB 284	CGGTACAGACATTTTCAATAGTGCACCAACCGATGTGGAGGATGTCTATACCTGA	343		
QY 344	GTGTATACGANTATCTAAATCCCGAACTAAAGCCCGTTTAAGTATACATATG	403		
DB 344	ATGTATACCATGATCTTGAACCCAGCAAAAGCGCTCGTTATGTTTCATCATG	403		
QY 404	GTGTGTTTATTTATCGGTGAATAATCATCGTATATGATGTGCTCATATTATTA	463		
DB 404	GCGAGATTTTATTTTTCGGGCAAGCAATTCGTAATGTTTGGTCCCGACTCTTATGA	463		
QY 464	AAAAGATGTGTGTGATTAACATPACATTCGTTTGGAGGCTCTAGTTTTCTAAGTT	523		
DB 464	AGAAACCCGTTGTGTGTAACCGTGCATATCGTTTGGTGTGTGGTTTCTTAGCC	523		
QY 524	TAAATTCAGAAAGCTTAATGTGCCCGTATGCGGCTTAAAGATCAAGTACGGCCT	583		
DB 524	TGAATTCGAAATATCTCAATATGCCCCGCAACGCTGAGCTCAAGATCAATATGCGCT	583		
QY 584	TGCATTTGATTAATAATTAATTCGCCCAACTGTTGGGCAATCCGATATTAACACT	643		
DB 584	TCAGATTTGGGTAMAGATTAATTAATTCGATTTGCGTGGCATGTACAAATTTACGCTCT	643		
QY 644	TTGTGTAAGTGTGCGGTGCTGCTTACCCACTACATGATGATTTAACCAACAACTGGC	703		
DB 644	TCGGGGAAGTGTGTGTGGGCTCAACCCATTAATGATGATTAACCAACAACTGGC	703		
QY 704	GTCTTTTCCATGTGTATATCTATGTCCGGGTAAATGCTTTGTCCATTTGGCTAATACC	763		
DB 704	GTTTATTCATGTGTATATGATGTCCGGGTAAATGCTTTGTCCATTTGGCTAATACC	763		
QY 764	AATGTCAACATGTGCTTCACTTAGCAAAATTTGGCGGCTTAAGGTGAGATATG	823		
DB 764	AATGTCAACATGTGCTTCACTTAGCAAAATTTGGCGGCTTAAGGTGAGATATG	823		
QY 824	ATAGAGATGTTTGAATTTCTTATGAAGCCAAACGACAGGATTTAGTAATAAATCTAGG	883		
DB 824	AAAAAGATTCCTGTAATCTTAATGAAGCCAAATCCCTTGAATTTGATCAAAAGGAGAC	883		
QY 884	AAAAAGTTTAACTGTAGAAAGGCTACAAATAAGTATGATTTCTTTTGGTCCACAG	943		
DB 884	CACAAAGTTTGAACCCGAAACAAATGAATTAAGGTATGTTCTTTTGGACCCACAG	943		
QY 944	TTTGACCATATCAGACGCTGATGTGTCTTACCAAAATCTCCCGGAAATGTTAA	1003		
DB 944	TAGAACCATATCAGACGCTGATGTGTCTTACCAAAATCTCCCGGAAATGTTAA	1003		

OY	1004	CTCTTGGGGTAATTCGATACCCCATATGATGGGTAAACCTTCATATGAGGTCATATTT	1063
Db	1004	GGCGCTGGGAAATTCGATACCCACATATGATGGCAATTCCTCCACAAAGGTTTGCTTT	1063
OY	1064	TCACCTCAATTCCTAAMCAAAATGCTATGCTGTGTAAAGAAATTTGGAACCTTGTCATTT	1123
Db	1064	CCAAATTCATATGCCAAMCAATATCCGAGGTTGTAAAGAGTTGGAAATCTGTGAAAT	1123
OY	1124	TTTGTCCAAGTGAATTTGGCTGATGCTGAAAGCAGCGCCAGAGACCTTGGAAATGGGTG	1183
Db	1124	ATGAGCCTTGGGAAATTTGGCTGAAAGAAAGCAGTGGCCCGGAAACCTTGGAGAGCGCTG	1183
OY	1184	CTAAATTTAAAAAGGCTCATGTTACAGAGAAACACCAACACTGTATATTTATATGATGC	1243
Db	1184	CCATTTGGAAAAAGGCCCATGTGGATGGGAAACACTTACTCTGATATATTTATGAGAGC	1243
OY	1244	TTTGCTCTCACATCTATTTCTGTGGTCCCATGCAATGCTTTGTGGAAATTAACGTTCAATC	1303
Db	1244	TTTCTCTCATTTTCTATTTCTCTCTCTCCATGCATGCTCTCTCAAAATGAGCCTTCAAC	1303
OY	1304	ACACCTCGGAGACACCGCTACTGTATGATGCGTGTGACATTCGATTCGGAAAGATCTTATCA	1363
Db	1304	ACACAGCTGCACATCCCATTTATTTGATGTCGATTTGCAATTTGCAATTCGAGAAATTAATTA	1363
OY	1364	ATCCCATTCGTATTTACCGTAGTGAAGCGTGGTTAAAGGTTTATGCTATGCTATGAT	1423
Db	1364	ACCCTATCGATATATCTGTTTGGCCGTTGGCGTTAAAGSTGTAAGCCATGCCATGAGC	1423
OY	1424	TAACTATTTCTTGGAATCAATTTGGCCAAACGTTATGCTTAAGAAATTCGCTGAATCA	1483
Db	1424	TAACTATCTCTTTGGAAACATTTTGTTCGAAAGCGCTGCGAAAGAAACCGCGATATTA	1483
OY	1484	AAACAATTTGAACGTATACACTGTATATGATATACAAATTTGCCACCACTGTATATCTTATA	1543
Db	1484	AAACCATTTGAACGCGATGTTGGCATTTGGACGGAATTTGCCACCAACCGGCAAAACCATCA	1543
OY	1544	GCATTTGAATTTGAAGGTATGGAAATTTTCTCGGGATCCCAATTAAGAAATCCCATGAAG	1603
Db	1544	GCAATGATATAGCCGCGATGGAACCACTCACCTCGGGATCCCAATAAAAAATCCGATGATG	1603
OY	1604	TATACAGTGTTTTGAATTTATAGTATGCAATTTGAAATGATATGTCCTCGAAATGGATA	1664
Db	1604	TCTATATATGTTTAAATATATGGGAGTAATGAAATTTATGATTTGCCAGAAATGATA	1664
OY	1664	AGATTTAAACAATGGGAGTCGATGTTTGGAAACATAGAGATTTATTT	1710
Db	1664	AAATTTAAACAATGGGACAGTATATTCGATTTAAAAAGAAAGAAATTTGTTT	1710

RESULT 9	
ABL02067	
ID	ABL02067 standard; cDNA; 2001 BP.
XX	
AC	ABL02067;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster expressed polynucleotide seq ID NO 683.
XX	
KM	Drosophila; developmental biology; cell signalling; insecticide
KW	pharmaceutical; gene; ss.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO20017042-A2.
XX	
PD	
XX	
XX	27-SEP-2001.
PF	
XX	
XX	23-MAR-2001; 2001WO-US09231.
PR	
XX	
XX	23-MAR-2000; 2000US-191637P.
PR	
XX	
XX	11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li FWD, Myers EW;
PI
XX
XX MPI: 2001-656860/75.
DR P-PSDB; ABB57964.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
PS Claim 1; SEQ ID NO 683; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB161675) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcc_sequences.
XX
XX Sequence 2001 BP: 502 A; 488 C; 521 G; 490 T; 0 other;

Query Match	39.5%	Score 677.2;	DB 23;	Length 2001;
Best Local Similarity	62.6%	Pred. No. 3.8e-175;		
Matches 1073; Conservative	0;	Mismatches 638;	Indels 3;	Gaps 1;

OY	1	ATGAATTTCACCGTTAGTTCGATGGACAATTAATAATGAAAGATTAAATGCATTGAAAAT	60
Db	95	ATGATAAAGAACCCTCGGCTTTGTGGAGCGCTTGCGGGCGCCCTCAAAACCATCGAGCAT	154
OY	61	AAGTTTTAAACTATCGTTTAACTACCAATGAATAAACGGTGGAGCTGAACTGAAATATGGC	120
Db	155	AAAGTCCAGCAGTATCCGCAATGCACCAATGAAACAGTTGTCCGCCACACGGAGTACGGC	214
OY	121	AAAGTAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACACAGTTTGAAGGT	180
Db	215	CAAGGAGAGGGTATCAAGACCGCTATCTCTCTACAGATGTGCCCTACTTCACGCTTCGAGGT	274
OY	181	ATACCGTCGCGCCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCACCCCAGCACCAACA	240
Db	275	ATCCCGTACGCCCAAGCCCTCCGCGTGGGGAAGTGGCGTTTAAAGGCCCTCCAGAGGCCATT	334
OY	241	CCCTGGATGGTGTGCGCGATGTGTGGCAATCATAAAGATTAAGTCAGTCGACAGTTGATTTT	300
Db	335	CCCTGGAGCGCAGTTTCGGGACATGCAAGCCAGCCGAAGATTAAGGCCGCTCCAGGTGCAGTTT	394
OY	301	ATMACGGGCAAAAGTGTGTGCTCAGAGGATTTCTATACCTAAGTGTCTATACGAATAAT	360
Db	395	GTCCTTCGATTAAGTAGAGAGGCTCCGAGAGACGCTCTATCTATCATATGTACACCAACAAT	454
OY	361	CTAAATCCCCGAACATAAACGTCGCCGTTTAACTATACATACATAGTGGTATTATATC	420
Db	455	GTTGAAGCCCGCAAGAGCGCTGCCCGGTATGTGTTGGATTACACGAGGAGGCTTCATTATC	514
OY	421	GGTGAATAATCATCGGATATGTATAGTCTGATATTTCAATTAAAAAGAGATGGCTTG	480
Db	515	GCGGAGGCCATCCGGAATGATATGGCCCGSATTACTTTATGAAGAAGATGTTGTTCTC	574
OY	481	ATTAACTACAATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAGAAGCTT	540
Db	575	GTCACGATACAGTACCGCACTTGGGGCTTTGGGATTTATGATCTTAAAGTCCCCGAGCTA	634
OY	541	AATGCGCCCGTAATCCCGGCGCTTAAAGATCAACTCATGGCCCTTGATTTGATTTAAAT	600
Db	635	AATGTACCAAGAAATGCTGGCGCTCAAGCATAGGTGCTGCGCCCTCAAGTGGAATCAAGAAC	694
OY	601	AATTGCGCAACTTGTGGCAATCCGATTAATTAACAGTCTTGGTGAAGATGCCGGT	660

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Db 695 AATTGGCGTAGTTTCGGCGAGATCCCACTGCATCTGTTTGGAGAGAGTGTGCA 754
Qy 661 GCTGCTCTACCCACTACATGATGTTAACCAGAACTGGCGTCTTTCCATCGTGT 720
Db 755 GGGCGCTCCACTACATGATGATGATGATGATGATGATGATGATGATGATGAT 814
Qy 721 ATACTAATGCGGGTATGCTATTTGCTATGCTGCTGCTGCTGCTGCTGCTGCTG 777
Db 815 ATCTTGCACTGCGGCGATGCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 874
Qy 778 GCTTCACCTTACCAATTTGGCGGCTATTAAGGATGAGATTAAGATGATGATG 837
Db 875 CCTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 934
Qy 838 GAATTTCTTATGAAGCAAGCCAGAGATTTAGTAAACTTGAAGAAAGTTTAAC 897
Db 935 GAGTTCTTGCAAGCAAGCCAGAGATTTATGCGCTGAGAGAAAGTTGCTGACA 994
Qy 898 CTAGAAGAGCGTACAAATTAAGTATGATGATGATGATGATGATGATGATGATG 957
Db 995 CTGAGAGAGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1054
Qy 958 ACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1017
Db 1055 ACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1114
Qy 1018 TCGATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1077
Db 1115 TCGATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1174
Qy 1078 AAGCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137
Db 1175 AAGCTTATGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 1234
Qy 1138 TTGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
Db 1235 TTGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1294
Qy 1198 GCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
Db 1295 GCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1354
Qy 1258 TATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1317
Db 1355 TATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1414
Qy 1318 CCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
Db 1415 CCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1474
Qy 1378 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
Db 1475 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1534
Qy 1438 TGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1497
Db 1535 AGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1594
Qy 1498 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1557
Db 1595 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1614
Qy 1558 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1617
Db 1655 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1714
Qy 1618 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
Db 1715 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1774
Qy 1678 GAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1711

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Db 1775 GAGAGCCTCTATGACGACAAAGATTTATGCT 1808
RESULT 10
ABL02081
ID ABL02081 standard; cDNA; 1704 BP.
XX
AC ABL02081;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 725.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PE 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EM;
XX
DR WPI; 2001-656860/75.
XX
DR P-PDOB; ABB57978.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 725; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 1704 BP; 417 A; 445 C; 460 G; 382 T; 0 other;
XX
Query Match 22.1%; Score 378.6; DB 23; Length 1704;
Best Local Similarity 53.9%; Pred. No. 2, 4e-93;
Matches 877; Conservative 0; Mismatches 729; Indels 21; Gaps 4;
Qy 85 ACCAATGAACGGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 144
Db 64 AGCAATGACAAAGGTCATGCGGACACGCTGACGAAAGGTGAAGGGGGTGAAGTGCAC 123
Qy 145 ACTGTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 204
Db 124 TCCATCTACGCAACAACTACATGATGATGATGATGATGATGATGATGATGATGATG 183
Qy 205 GGTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 264
Db 184 GCGAGCTCGCTTCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 243
Qy 265 TGCATATGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 324
Db 244 ACACATGTTGCGCGCAAGCCCTGCCAGGTCAACATCTGTTGAAGGACGATGCAAGGCGC 303

```

OY	325	GAGGTTGTGATATACCCAAAGTGTCTATACGAATAATCTAAATCCGGAACCTAAAGCTCC	384
Db	304	GAGAGCTGTCTTGACTCTCAATGTCTACACCGAGGATTCATCTACACAGACTTTGGCG	363
OY	385	GTTTATAGTATACATACATGCTGGTGGTTTATATATGCGTGAATAATCATGTGATATGAT	444
Db	384	GTTCGTGGTTTGGATCTATGCGGGTGGATTCCAATGGGAAAGCATCGCGGATCTGTAC	423
OY	445	GGTCTGATTAATTTTCATTTAAAGATGTGGTGTGGATTACATCAATATCGTTTGGGA	504
Db	424	AGCCCCGACTACATTATGATGAAACATGTCTGCTACTGTGTAATATCCATCGGTTAGA	483
OY	505	GCTCTAGTTTTCTCAACTTTTAATTCAGAAAGACTTAATGTGCCCGGTAAATCCGGCTT	564
Db	484	GCCCTGGGATTCCTTACTCTTGGCAGACGAAGAACTGGATGTCTCGGAAGCCCGGACTA	543
OY	565	AAATATCAAGTCATGCGCTTCGATTTGGATTAAATAATATGGCCCACTTTGGTGGCAT	624
Db	544	AAGATATCAAGTATAGGCTTGGCGGTGGTGCACAAAGGAATTTGCCAGTTCTTTGGTGGCAT	603
OY	625	CCCGATATATTTACAGTCTTTTGGTGAAGTCCCGGTGCTGCCCTACCCACTACATATAGT	684
Db	604	CCCGATATATAAACCGTTTTTGGTGAAGTGTGGAGTGTGAGTCCACAAATATATATAGT	663
OY	685	TTAACCCAAACAACCTGCCGCTTTTTCATCGTGATATCTATGTGCGGTATATGCTATT	744
Db	664	CTGACGATCAAGGCCAAGGGCTATTTTTCACAAACATATTTATATGTGGGATCCGCACTG	723
OY	745	TGTCCATTTGGCTAATATACCCTCAATGTCA---ACATCGTGCTTACCTTATGGCCAAATGGCC	801
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Db	784	GGCTACACAGAGATGCTATACGATCGGACATTTTTGCCCATCTCACAAATATGTAAGGCC	843
OY	862	CAGATTTAGTAAAACTTGAGGAAAAAGTTTACTCTTGAAGAGCGTACAAATATAGT-	920
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OY	979	AAACATCTCTGGGGAATGTGTTAAAACTGCTGGGGTAATTTGATCAACCATATGATGGGT	1038
Db	964	AAATGCCCACTGGAAATGATGCGGAGCTGTGGGGCAACAGATTTCCATGTCTATCGGA	1023
OY	1039	AACACTTCAATGAGGGTCTAATTTTTCACCTCAATTTCTTAAGCAAAATGCTATGCTGTT	1098
Db	1024	GGAACCTCTTCGAAAGGTCTCTCATGTTTCCGAAAGTGAACAAGTGGCCGGAACCTGTT	1083
OY	1099	AAGGAATTTGAAACTTGTGTCAATTTTGTGCCAAGTGAATTTGGTGTATGTGAAGCACCC	1158
Db	1084	TGCCAGTGGGTGACTCCGGAACCTGGGCCCTTCAGAGATGCCACAGTATGATGACAGCA	1143
OY	1159	GCCCCAGAGACCTTGAAATAGGGTGTCTAAATTTAAAAAAGTCAATGTTACAGAGAAACA	1218
Db	1144	AGAAAAGCGTTTGGAAAGAAAGTACAGAGACTATATTTTGGCGATAGGACTCTTGGCAGG	1203
OY	1219	CCAACAGCTGATTAATTTATGATCTTTTGTCTCAACATATTTTGTGGTCCCATGAT	1278
Db	1204	AAGACCATATTTGAGGTACACGATCTCTCTGTGTACAAATATTTTGTGGCATGCAATTCAT	1263
OY	1279	CGTTTGTGCAATTTAGCTTTCAATCAACCTCGGTACACCCGCTACTGTATCGCTTC	1338
Db	1264	AGGACTTTGTCTCGCTGCTGTCAACAGCCCATTTGGCCCCCAACATTTCTGTACGATTC	1323
OY	1339	GACTTGTGATGGAAGATCTTATCAATCCCTATATGATTAATGATGATGAGAGCTGTGTT	1398
Db	1324	GATTTGACTGTG---AAGCACTTCAATATATATGCAATATATACCTGTGGCCGCAAGGTG	1380

[illegible]

RESULT 11
 ABL02066
 ID ABL02066 standard, cDNA; 6175 BP.
 XX
 AC ABL02066;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 680.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.
 XX Drosophila melanogaster.
 OS
 PN WO200171042-A2.
 PM
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR P-PSDB: ABB57963.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT
 PS Claim 1; SEQ ID NO 680; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB161176-AB130511), expressed DNA
 CC sequences (AB101840-AB161715) and the encoded proteins
 CC (AB55737-AB872072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 779.
 XX
 KM Drosophila: developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 XX
 XX WO200171042-A2.
 PD 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 XX WPI: 2001-656860/75.
 DR P-PSDB; ABB57996.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX Claim 1: SEQ ID NO 779; 21bp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB57737-AB872072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
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 XX Sequence 1665 BP; 397 A; 446 C; 468 G; 354 T; 0 other:
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 Best Local Similarity 52.3%; Pred. No. 4.6e-90;
 Matches 860; Conservative 0; Mismatches 774; Indels 9; Gaps 2;
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 DB 5 TCGACTTTAAGTCCACACAGCAGCATACAGACCAAGAAAGACTGTCGACAGCA 64
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 DB 65 CCTAGGACCCCAATCAAGGCTTAAGAGGAAGTCCATCTACGCGACGTCTACTTCA 124
 OY 173 TTGAGGATATACCGTACGCGCAACCGCGGTGAGTGAAGTTTAAAGCAACCCAGC 232
 DB 125 TCGACGGGATCCCTTCGCAACACCAACGCGTGGGAGCTACGATCAAGGCTCCCAAC 184
 OY 233 GACCAACACCCGTGAGTGTGCTGATTTGCAATCATAAAGATAGTCAAGT 292
 DB 165 CCCCCGAGGTCTGACAGGAGGTGAGAGTGCACCTCCAGAGGTCCCAAGCCACTGCA 244
 OY 293 TTGATTTTATAAGGGCAAGTGTGTGCTCAGAGATTTGTATACCTTAAGTGTCTATA 352
 DB 245 AGCATCTGTGTTGAGATGACCGAGTGTCCGAGAGTGTCTTACCTCAATGTCTACA 304
 OY 353 CGAATATATCAATCCGCAACTAAACGTCCTTTTATATACATACATGCTGTGTT 412
 DB 305 CAAGAATTTTGTATCCCAACCAACCAATGCCGTGATGTCTGATCATGTGCGGTGCT 364

OY 413 TTATTATCGGTGAANAATCATCTGATATGTATGATGCTGCTGATTATTTCAATAAAGATG 472
 DB 365 TCCAGTTTGGCAGAGGCTTCACGGGAATGTTACAGTCCGATTATTTGCGCGAGAGATG 424
 OY 473 TGTGTTGATTAACTATATATCGTTTGGAGCTCTAGCTTTTCTTAAGTTTAAATTCAG 532
 DB 425 TGTGTGTCATTTCTATCACTACAGGTTGGGACCACTGGATTTTCTGCTCGAGCATC 484
 OY 533 AAGACCTTATATGTCGCCGTAATGCCGCTTAAAGATCAAGTCAAGTCCCTGATGGA 592
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 OY 593 TTAATAATATATGCGCAACTTTGGTGAATCCGATATATTAACAGTTTGGGAA 652
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 OY 653 GTGCGGTGCTGCTCTTACCCACTACATGATGTTAAACCAAACTCGCGTCTTTCC 712
 DB 605 GTGCGGAGTGTGCTGCTGCTTCACTACATGATGATCAGACAGACGATGACCTTTCC 664
 OY 713 ATCGTGTATTAATATGTCGGGTAATGCTATTTGTCATTTGCTTAATACCAATGTCAC 772
 DB 665 ACAAGGCCATCTGCAATGCTGGTAAATACGTTTCCCTGCGGAGTGAATCCTCAGAGAA 724
 OY 773 ATCGTGTCTTACCTTACGCAAAATGGCCGCTATTAAGGCTGAGATTAATGAATG 832
 DB 725 ACTGCGCATATGCTGTGCTGTCAGGCGGCTTACGAGTGAACCAACCCCGGATG 784
 OY 833 TTTTGAATTTCTTATGAAGCCAAAGCCACAGATTTTACTAAACTTGAAGAAAGTTT 892
 DB 785 TCTGGAGTTCTGAAGAAGCCCAAGGAGTCCGAATATCAAAAGCATGAGAACTCT 844
 OY 893 TTAATCTAAGAAAGCTAATTAAGTATGTTTCTTTGCTTCCACTGTTGAGCCAT 952
 DB 845 GCATTGACAGGAGAGAAAGAGCGGATTTGATTTCTTTTGGCCGTAATCGAATCGT 904
 OY 953 ATCAGCGCTGATGTTGCTTATCCCAACATCTCTGGGAAATGTTAAACGTGCTGG 1012
 DB 905 ATGTAAACCAAGCCACTGTGTGCTGCGAGCAAAACCAATGATGAACCGCTGGA 964
 OY 1013 GTAATTCGATTAACCACTATGATGAGTAACTATGATGAGGCTATATTTTCACTTCA 1072
 DB 965 GCAATATATATCCACTATATCATGCGGAGGCTTCCAAAGAGGCGCTTCTGTTACTCAG 1024
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 DB 1025 AGACCAAGCAAGTCCGAAGTGTCTAAACGATTTGACACTGCCGTTTGTGTGCTTA 1084
 OY 1133 GTGAATGCTGATGCTGAAGCCACCGC-----CCAGAGACCTTGAAGATGGTGTGA 1186
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 OY 1187 AATTTAAAGGCTCATGTTACAGAGAAACCAACAGCTGATTAATTTATGATCTTT 1246
 DB 1145 AGTGTACTACGCGATTAAGACGCGCCAGTCTGAGACACCTGATGAATACCTTCAATG 1204
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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1663.49 seconds
(without alignments)
16677.553 Million cell updates/sec

Title: US-09-776-910-5

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 33308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
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2: em_esthum:
3: em_estin:
4: em_estinv:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hlc:
9: gb_est1:
10: gb_est2:
11: gb_hlc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_gss:
18: em_gss_hum:
19: em_gss_inv:
20: em_gss_pln:
21: em_gss_vrt:
22: em_gss_fun:
23: em_gss_mam:
24: em_gss_mus:
25: em_gss_other:
26: em_gss_pro:
27: em_gss_rod:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315.2	18.4	778	9	AT062034 GH01076.5
2	280.8	16.4	649	9	AT1388926 GH19977.5
3	266.8	15.6	688	9	AT1403569 GH23036.5
4	256.6	15.0	671	9	AT1517692 GH28740.5
5	254.4	14.9	569	13	BI609541 RH14337.5
6	250	14.6	674	13	BI628316 RH56682.5

7	249.4	14.6	676	13	BI635372
8	248.4	14.5	673	13	BI614181
9	247	14.4	660	13	BI639486
10	246.8	14.4	672	13	BI614443
11	246.4	14.4	670	13	BI233202
12	245	14.3	648	9	AT113763
13	245	14.3	648	9	AT1403098
14	243.4	14.2	646	9	AT109901
15	243.4	14.2	646	9	AT293416
16	242.6	14.2	526	9	AT108080
17	241.4	14.1	516	9	AT108156
18	239.2	14.0	658	13	BI564586
19	238.4	13.9	656	13	BI619037
20	236.8	13.8	656	13	BI614821
21	236.6	13.8	669	13	BI588370
22	236.2	13.8	656	13	BI621302
23	233.2	13.6	628	9	AT109573
24	231.4	13.5	619	9	AT1516869
25	231	13.5	638	13	BI564361
26	230.8	13.5	628	9	AT1513346
27	230.6	13.5	630	9	AT403830
28	230	13.4	614	12	BG641228
29	230	13.4	647	13	BI575862
30	229.6	13.4	614	9	AT107729
31	229.6	13.4	614	9	AT1134360
32	229.2	13.4	622	9	AT134524
33	228	13.3	633	13	BI370683
34	222.6	13.0	670	9	AT389766
35	219.8	12.8	615	13	BI617897
36	219.2	12.8	615	13	BI588504
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38	218.6	12.8	588	13	BI638519
39	218.6	12.8	607	13	BI624437
40	218.6	12.8	607	13	BI673399
41	218.6	12.8	609	13	BI607309
42	218.6	12.8	609	13	BI622392
43	218.6	12.8	609	13	BI630054
44	218.6	12.8	611	13	BI572606
45	217.8	12.7	612	13	BI631806

ALIGNMENTS

RESULT 1
LOCUS AT062034 778 bp mRNA linear EST 19-APR-2001
DEFINITION GH01076.5prine GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH01076.5prine similar to U51050:
Drosophila melanogaster alpha esterase (aET) gene, partial cds,
mRNA sequence.

ACCESSION AT062034
VERSION AT062034.1 GI:3337873
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 778)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.

TITLE BDGP/HMT Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, estfruitfly@berkeley.edu
Plate: 10 row: G column: 4
High quality sequence stop: 363.
Location/Qualifiers

QY	908	GAACAATATGATGCTATGTTCTCTTCTTGGGCGCACGTTGAGGCATATACAGCCGGTATT	967
Db	484	GCATGACACAGTAATGTTTGCCCTTTGGCCCATCCCTGGACCATCTTCACGCCGGAAT	543
QY	968	GTGCTTACCCAAACATCCTCGGAAATGGTTAAACTGCTTGGGGTAATTGATACCA	1027
Db	544	GTGTGATATCCAAAGCCTCCAAAGAGATGATTAAGACCGCCCTGGAGTAATCTCATCCCA	603
QY	1028	CTATGATGGGTACACATCTCATATGAGAGGCTCATATTTT	1063
Db	604	TGTTATATAGGAACACCTTCGTACGAGGCGCTCTGT	639
RESULT 3			
A1403569			
LOCUS	GH23036	5prime GH Drosophila melanogaster head por2	Drosophila melanogaster alpha esterase (aer) gene, partial cds, mRNA sequence.
DEFINITION	GH23036	5prime GH Drosophila melanogaster head por2	Drosophila melanogaster alpha esterase (aer) gene, partial cds, mRNA sequence.
ACCESSION	A1403569	GI:4246656	EST.
VERSION	A1403569.1	GI:4246656	EST.
KEYWORDS	fruit fly		
SOURCE	Drosophila melanogaster		
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	Harvey,D., Brockslein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.		
AUTHORS	BDGP/HMT Drosophila EST Project		
TITLE	Unpublished (2001)		
JOURNAL	Contact: Stapleton, M.		
COMMENT	BDGP		
	Lawrence Berkeley National Lab		
	One Cyclotron Rd, Berkeley, CA 94720, USA		
	Fax: 510 486 6798		
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu		
	Plate: 230 row: C column: 12		
	High quality sequence stop: 648.		
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	/clone="GH23036"		
	/clone_lib="GH Drosophila melanogaster head por2"		
	/sex="male and female"		
	/dev_stage="adult"		
	/lab_host="DHS - alpha"		
	/note="Organ: head; Vector: POR2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into POR2. Plasmid cDNA library."		
BASE COUNT	161 a 174 c 197 g 156 t		
ORIGIN			
Query Match	15.6%;	Score 266.8;	DB 9; Length 688;
Best Local Similarity	65.4%;	Pred. No. 1.9e-63;	
Matches	391; Conservative	0; Mismatches 207;	Indels 0; Gaps 0;
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Db	91	ATGAATATAGAAACCTCGGCTTGTGCGAGCCCTTGGCGGTGCGGCTCAAAACATCGAGCAT	150
QY	61	AAGTTTAAATATGCTTAACTACTCCATGGAAGCGGTGATGCGAATCGAATATATGC	120
Db	151	AAAGTCACGACATATGCGCAGTCGACCAATGAAACAGTTGTGCGGACGAGATACGCGC	210
QY	121	AAAGTGAAGGCGTTAAAGCTTAACTGTATGATGATGATCTTACTACAGATTGAGGCT	180
Db	211	CAAGTGAAGGCGTATCAAGGCTCTATCTCTCTAGATGATGCTCCTACTTCAAGCTTCAGGCT	270
QY	181	ATACCGTACGCCCAACCGCCACTGGGTGAGTCTGAGATTTTAAAGCAACCCAGGACCAACA	240

[illegible]

Matches	376:	Conservative	0:	Mismatches	199:	Indels	0:	Gaps	0:
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Db	95	ATGATTAAGAAACCTCGGCTTTGTGAGCGCTTGGCGGCTCAAAACCAATGAGCACT	154						
Qy	61	AAGTTTTTAAATCTATCGTTTAACTACCAATGAACCGTGGTGGCTGAATCAATATATGC	120						
Db	155	AAAGTCAGCAGTATCCGCCAGTCCGACCAATGAACAGTTGTGCCCAACAGGATAGGCG	214						
Qy	121	AAAGCAAAAGCGTTAAACGTTTAACTGTGTAGCATATCTACTACAGATTTTAGGCT	180						
Db	215	CAAGTAGAGGGGTATCAACGCTCTATCTCTACAGATGTGCCCTACTTACAGCTTCAGGCT	274						
Qy	181	ATACCGTACGCCCAACCGCCAGTGGGTGACGTAGATTTAAAGCAACCCAGCAGCAACA	240						
Db	275	ATCCCGTACGCCCAACCGCTCCGGTGGGGAAGTTTGGGTTTAAAGGCCCTCAGAGCCATT	334						
Qy	241	CCCTGGGATGCTGTCGCGATTTGTTGCAATATTAAGATTAAGTCAGTCAAGTTGATTTT	300						
Db	335	CCCTGGGACCGAGTTTCGGCATCTCAGCAACGCAAGCAAGATTAAGGCCGCTCAGGTTC	394						
Qy	301	ATTAACGGCCAAAGTGTGGCTCAGAGATTTGTCTATACCTAACTGCTATACCAATAT	360						
Db	395	GCTTCGATTAAGTATAGAGGCTCCAGAGACCTCCCTATATCAATGTGTATACCAACAT	454						
Qy	361	CTAAATCCCGAAACCTAAAGCTCCGTTTAACTATACATATATGTTGTTTATATATC	420						
Db	455	GTTAAGCCCGACAAAGCTGCGCCGGTTATAGTTTGATTCAGTACGAGGAGGCTTATATC	514						
Qy	421	GGTGAATAATCATGCTGATATATATGTGCTCTGATTTATTCATTTAAAGATGGTGTG	480						
Db	515	GCGCAGGCGCAATGGGAATATGATGCGCGGATTTACTTATGAAGAAAGATGTTGCTC	574						
Qy	481	ATTAACTAATAATATGTTTGGAGCTCATAGTTTCTAAGTTTAATTCAGAACACTT	540						
Db	575	GTCACGATACGATACCCACTTGGGCGCTTTGGGATTTATGACGTTAAAGTCCCGCAGCTA	634						
Qy	541	AATGTGCCCGGTAATGCCGCTTAAAGATCAAGT	575						
Db	635	AATGTACGAGAAATGCTGGCTCAAGATCAAGT	669						
RESULT 5	Bt09541	569 bp	mRNA	linear	EST 07-SEP-2001				
LOCUS	RH4337	569 bp	mRNA	linear	EST 07-SEP-2001				
DEFINITION	Drosophila melanogaster, normalized Head pRc-1, 5' similar to alpha-EST7.								
ACCESSION	Bt09541	569 bp	mRNA	linear	EST 07-SEP-2001				
VERSION	Bt09541.1	569 bp	mRNA	linear	EST 07-SEP-2001				
KEYWORDS	fruit fly.								
SOURCE	Drosophila melanogaster								
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.								
REFERENCE	1 (bases 1 to 569)								
AUTHORS	Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champagne, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mitra, S., Mungall, C. J., Nuno, J., Pacle, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S., and Rubin, G. M.								
TITLE	BDGP/HMIT RH Drosophila EST project								
JOURNAL	Unpublished (2001)								
COMMENT	Contact: Stapleton, M.								
	BDGP								
	Lawrence Berkeley National Lab								
	One Cyclotron Rd, Berkeley, CA 94720, USA								
	Fax: 510 486 6798								
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu								

FEATURES	source	Location/Qualifiers
1. 569	/organism="Drosophila melanogaster"	
	/db_xref="taxon:7227"	
	/clone="RH14337"	
	/clone.lib="RH Drosophila melanogaster normalized Head	
	plc1-1"	
	/sex="male and female"	
	/dev_stage="Adult"	
	/lab_host="DH5-alpha,Tona"	
	/note="Origin: head, Vector: pRc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."	
BASE COUNT	126 a 147 c 167 g 129 t	
ORIGIN		
Query Match	14.98;	Score 254.4; DB 13; Length 569;
Best Local Similarity	65.58;	Pred. NO. 5.1e-60;
Matches 372; Conservative	0;	Mismatches 196; Indels 0; Gaps 0;
QY	17 GTTGTATGAGAAATTAATAATGAAAGATTAAATGCAATTTGAATTAAGTTTAACTATC	76
Db	1 GCTTTGTGAGGCGCTTGGGTGGCGCTCAAAACATCGACATTAAGTCCAGCAGTATC	60
QY	77 GTTTAACTACCAATGAACGGGTGAGTGTGAATGATATGCAAGGATTAAGGCGTTA	136
Db	61 GCCAGTCGACCAATGAACAGATGTGCGCCGACACGAGTACGGCAAGTGAAGGGTATCA	120
QY	137 AACGTTAACTGTGACGATGATTCCTACTACGATTTTGAAGGATATACCGTACGCCAAC	196
Db	121 AGCGTCTATCTCTPACGATGTGCCCTCTTACGCTTCGAGGATATCCGTACGCCACG	180
QY	197 CGCCATGGGTAGCTGAGATTTAAAGCACCCGACGACCAACCCCTGGATGTGTGC	256
Db	181 CTCGGGTGGGGAGTGGCGGTTAAAGGCCCTTTAAAGGCCCATTTCCGTGGAGCGAGTTTC	240
QY	257 GTGATTTGTCATTCATTAAGATTAAGTCAGTCAAGTTGATTTATTAAGCGGCAAAAGTGT	316
Db	241 CGCAGTCGACCCAGCGAAGAGATTAAGCGCGTCAGGTGACGTCTTCATTAAGGTAG	300
QY	317 GTGCGCTCAGAGAGATGTCTATTAACCTAAGGTCTATATACAAATATCTAAATCCGAAACTA	376
Db	301 AGGGCTCCGAGGACTGCTTATCTATCTAATGTGTACACCAACAATGTGAAGCCGACAAGG	360
QY	437 ATATGATGTCTCGATTTATTTCAATTAAGAGATGTGTTGATTTAATCATACATATTC	496
Db	421 AATGATTAAGCCCGGATTAATCTTAATGAAGAATGTGTCTCGACAGATAGTACC	480
QY	497 GTTGTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAACCTTATATGCGCCGGTATG	556
Db	481 GACTTGGGGCTTGGGATTTATGATCTTAAGTCCCCGAGTAATATGACAGGAATG	540
QY	557 CCGGCTTAAAGATCAAGTCAATGGCCTT	584
Db	541 CTGGCCTCAAGATCAGGTGCTGGCCCT	568
RESULT 6		
LOCUS	B1628316	674 bp mRNA
DEFINITION	RH56682.5prime RH Drosophila melanogaster normalized Head plc1-1	linear EST 10-SEP-2001
	Drosophila melanogaster cDNA clone RH56682.5 similar to alpha-B57.7	
	FBa0100112 GO: [catboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5; 08/22/2001, mRNA sequence.	
ACCESSION	B1628316	
VERSION	B1628316.1	GI:15530524

[illegible]

DB	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	531 GGGGAGCCAAATCGGGAATGTATGATGCCCGGAGTAATCTTATGAAAGAGATGTTTCTC	590						
QY	481 ATTAACATACATATATCGTTTGGAGCTCTAGATTCTTAAGTTAAATTCAGAACACCTT	540						
Db	591 GTCAGAGTACACTACCGACTTGGGCTMTGGATTTATGAGTCTTAAGTCCCGGAGCTA	650						
QY	541 AATGTGCCCCGTAATGCGGCT	563						
Db	651 AATGTACCAAGAAATGCTGGCT	673						
RESULT 7								
LOCUS	Bi635372							
DEFINITION	SD16705.5,prine SD Drosophila melanogaster cDNA clone SD16705 5 similar to alpha-Est: Fban000112.G0: [carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5: 05/18/2001							
ACCESSION	Bi635372							
VERSION	Bi635372.1							
KEYWORDS	EST.							
SOURCE	fruit fly.							
ORGANISM	Drosophila melanogaster							
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peleiyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.							
AUTHORS	1 (bases 1 to 676) Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.							
TITLE	BDGP/HMT Drosophila EST Project							
JOURNAL	Unpublished (2001)							
COMMENT	Contact: Stapleton, M. BDGP Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu Plate: SD.167 row: A column: 5 High quality sequence stop: 641. Location/Qualifiers 1. 676 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="SD16705" /clone_lib="SD Drosophila melanogaster Schneider L2 cell culture pot2" /lab_host="DH5-alpha" /note="Vector: pot2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into pot2. Plasmid cDNA library." BASE COUNT 155 a 173 c 194 g 154 t ORIGIN							
Query Match	14.6%;	Score 249.4;	DB 13;	Length 676;				
Best Local Similarity	65.2%;	Pred. No. 1.4e-58;						
Matches 367;	Conservative 0;	Mismatches 196;	Indels 0;	Gaps 0;				
QY	1 ATGAATTCACAGTTAGTTGATGGAGAAATTAATAATGGAAGATTAAATGCAATTGAAT	60						
Db	114 ATGAATTAAGAACCTCGCTTTTGAGAGCGCTGCGGTGCGGCTCAAAAACATCGAGCAT	173						
QY	61 AAGTTTAAATCTTCGTTAACTACCATGAAAGCGGTGTGATGAAACGTGAATATGATG	120						
Db	174 AAAGTCACAGCACTATCGCCAGTCGACCAATGAAGAAAGTTGTGCGGACAGGATGACG	233						
QY	121 AAAGTAAAGGCGGTTAAAGCTTAACTGATGATGATGATTCCTACTAGAGTTTGAGGT	180						
Db	234 CAAGTGAGGGGATCAAGAGGTCTATCTCTCTACGATGTGCGCTACTCTAGCTTGAGGGT	293						
QY	181 ATACGTCAGCCCAACCGGCACTGGGTGAGCTGAGATTAAAGCAACCCGACGACCAACA	240						

Db 294 ATCCGTCAGCCACCCCTCCGGTGGGAGATTCCGTTAAGGCCCTCAGAGGCCCAT 353
Qy 241 CCTGGGATGTCGTCGATGTTGTCATCATTAAGATAGTCAGTCAGTCAGTCATTT 300
Db 354 CCTGGGACGAGTTCGTCGATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 413
Qy 301 ATACGCGCAAGTGTGTGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 360
Db 414 GTCCTGCAATAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 473
Qy 361 CTAAATCCGAACTAAAGTCCTGTTTATGATATACATATGTCAGTCAGTCAGTCAGTC 420
Db 474 GTGAGGCCGACAGAGCTGCGCCGTTATGTTGATTCAGGAGAGGCTTCATTTATC 533
Qy 421 GGTCAAAATCATGTCATGATGTCGTCATGATATATGTCATATTAAGATGTCAGTCAGTC 480
Db 534 GCGGAGCCCAATGCGGATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 593
Qy 481 ATTAACATACATATGTCGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 540
Db 594 GTCAGATACAGTACGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 653
Qy 541 AATGTCGCCGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 563
Db 654 AATGACAGGAAATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 676

RESULT 8
B1614181 673 bp mRNA linear EST 07-SEP-2001

LOCUS
DEFINITION RH43493.5prime RH Drosophila melanogaster normalized head p1c-1:
Drosophila melanogaster cDNA clone RH43493.5 similar to alpha-Est7:
Fbano001112 GO:[carboxylesterase (GO:0004091); carboxylesterase
(GO:0004091)] located on: 3R 84D5-84D5.1: 08/18/2001, mRNA sequence.

ACCESSION
B1614181 GI:15509706

VERSION
B1614181.1 GI:15509706

KEYWORDS
EST.

SOURCE
fruit fly.

ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1 (bases 1 to 673)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frisoe, E., George
R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
Mungall, C.J., Nunoo, J., Pacheco, J., Paragas, V., Park, S.,
Phonenuayong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S. and Rubin
G.M.

TITLE
JOURNAL
COMMENT BDGP/HMT RH Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.

BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: RH.434 row: H column: 9
High quality sequence stop: 553.

FEATURES
Location/Qualifiers
1..673

Source
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH43493"
/clone_1bp="RH Drosophila melanogaster normalized head
p1c-1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DHS-alpha Tona"
/note="Organ: head; Vector: p1c1; Site: 1; XhoI: Site 2;
BamHI: Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

BASE COUNT 153 a 169 c 195 g 155 t 1 others
ORIGIN

Query Match 14.5%; Score 248.4; DB 13; Length 673;
Best Local Similarity 65.0%; Pred. No. 2.6e-58;
Matches 366; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

Qy 1 ATCAATTTACAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 60
Db 111 ATCAATTAAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 170

Qy 61 AAGTTTAACTATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 120
Db 171 AAGTTCAGAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 230

Qy 121 AAGTGAAGGCGCTTAAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 180
Db 231 CAGTGAAGGCGCTTAAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 290

Qy 181 ATACCGTACGCCCAAGCCGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 240
Db 291 ATCCCGTACGCCCAAGCCGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 350

Qy 241 CCTGGGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 300
Db 351 CCTGGGAGCGATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 410

Qy 301 ATACGCGCAAGTGTGTGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 360
Db 411 GTCCTGCAATAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 470

Qy 361 CTAAATCCGAACTAAAGTCCTGTTTATGATATACATATGTCAGTCAGTCAGTCAGTCAGTC 420
Db 471 GTGAGGCCGACAGAGCTGCGCCGTTATGTTGATTCAGTCAGTCAGTCAGTCAGTCAGTC 530

Qy 421 GGTCAAAATCATGTCATGATGTCGTCATGATGTCGTCATGATGTCGTCATGATGTCGTCGTC 480
Db 531 GCGGAGCCCAATGCGGATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 590

Qy 481 ATTAACATACATATGTCGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 540
Db 591 GTCAGATACAGTACGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 650

Qy 541 AATGTCGCCGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 563
Db 651 AATGACAGGAAATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 673

RESULT 9
B1639486 660 bp mRNA linear EST 10-SEP-2001

LOCUS
DEFINITION SD22067.5prime SD Drosophila melanogaster Schneider I2 cell culture
POT2 Drosophila melanogaster cDNA clone SD22067.5 similar to
alpha-Est7: Fbano001112 GO:[carboxylesterase (GO:0004091)] located on: 3R 84D5-84D5.1: 05/19/2001
carboxylesterase (GO:0004091)

ACCESSION
B1639486 GI:15541696

VERSION
B1639486.1 GI:15541696

KEYWORDS
EST.

SOURCE
fruit fly.

ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1 (bases 1 to 660)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.

TITLE
JOURNAL
COMMENT BDGP/HMT Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.

BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA

QY 361

TAAATCCCGAAACTAAAT

D	471	GTGAAGCCGACAGGGCTGGCCGGTATGGTTTGATTCACGGAGGAGGGCTTATATTC	530
Q	421	GGTGAATATCATCTGATATATATGTCCTGATTAATTCATTAAAGAGATGTGGTGG	480
D	531	GGCGAGCGGCATCGGATGATGCGCCGATTAATTAATGAAGATCTTGTCTC	590
Q	481	ATTAAATACAAATATATGTTGGAGCTTACGTTTCAAGTTTAATTCACAAACCTT	540
D	591	GTCAAGATACAGTACACGACTTGGGCTTTGGGATTATGAGCTTAAGTCCCGCAGCTA	650
Q	541	AATGTGCCCCGGTAAATGCCGCC	562
D	651	AATGACCAAGAAATGCTGCC	672
RESULT 11			
LOCUS	B1233202		
DEFINITION	B1233202	670 bp	linear
ACCESSION	RE29491	prime RE Drosophila melanogaster	normalized Embryo pf1c-1
VERSION	Phan0001112	located on: 3R 84D5-84D5; 04/12/2001,	mRNA sequence.
KEYWORDS	B1233202		
ORGANISM	B1233202.1	GI:14700784	
REFERENCE	EST.		
AUTHORS	Fruit fly.		
JOURNAL	Drosophila melanogaster		
COMMENT	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
	1 (bases 1 to 670)		
	Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Lao, G., Mista, S., Mungall, C. J., Nuno, J., Paclob, J., Pargasa, V., Park, S., Pounanenavong, S., Wan, K., Yu, C., Lewis, S. E., Celinker, S. and Rubin, G. M.		
	BCSP/HHMI RE Drosophila EST Project		
	Unpublished (2001)		
	Contact: Stapleton, M.		
	BDSP		
	Lawrence Berkeley National Lab		
	One Cyclotron Rd, Berkeley, CA 94720, USA		
	Fax: 510 486 6798		
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu		
	Plate: RE:294	row: H	column: 7
	High quality sequence stop: 534.		
FEATURES	Location/Qualifiers		
source	1..670		
	/organism="Drosophila melanogaster"		
	/db_xref="taxon:7227"		
	/clone="RE29491"		
	/clone_lib="RE Drosophila melanogaster normalized Embryo pf1c-1"		
	/sex="male and female"		
	/dev_stage="0-24 hours mixed stage embryonic"		
	/lab_host="DH5-alpha Tona"		
	/note="Organ: embryo; Vector: pf1c1; Site:1; XhoI; Site:2 BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."		
BASE COUNT	152 a	168 c	194 g
ORIGIN			155 t
			1 others
Query Match	14.4%	Score 246.4	DB 13; Length 670;
Best Local Similarity	64.9%	Pred. No. 9.4e-58;	
Matches 364;	Conservative 0;	Mismatches 197;	Indels 0;
		Gaps 0;	
Q	1	ATGAATTCACGCTAGTTTGATGAGAGAATTAATGAGAGATTAATGATGAAAT	60
D	110	ATGATATGAACCTCGCTTTGTGAGAGCGCTTGGCGGCTCAAAACATCGACAT	169
Q	61	AAGTTTAAACTATCGTTTAACTACATGCAATGACGCTGATGCTGAATGATATGCT	120

Db 170 AAGGCCAGCAGTATGCCGACATCGACCAATGAACACATGTCGCCGACACGAGATACGCC 229

Qy 121 AAGTGAAGAGCGTTAAACGTTTAACCTGTATACATGATATTCCTACTACAGTTTAAAGGT 180

Db 230 CAAGTGAAGGGGTATACACCGCTCTATCTCTACAGATGTGCCCTACTTACGCTTCAGAGGT 289

Qy 181 ATACCGTACGGCCCAACGCCACAGTGGGTGAGCTGAGATTTTAAAGCACCCACGACGACACACA 240

Db 290 ATCCCGTACGCCCAACGCCCTCCGGTGGGGAGTTTCCGGTTTAAAGCCCCCTACAGAGCCCAT 349

Qy 241 CCCGTGGATGGTGTGCGCTGATTTGTCATATATAAAGATTAAGTCAGTCCAAAGTTGATTTT 300

Db 350 CCCGTGGAGCGCAGATTCGCGACATGCGACGCCAGCGAAGGATTAAGGCCGTCCAGTGCAGTTC 409

Qy 301 ATAAACGGCCAAAGTGTGTGGCTCAGAGGATTTGCTATACCTAAAGTCTATATGCAATAT 360

Db 410 GTCTTCGTAAGATGATGAGAGGCTCGAGGACGCTGCTCTATCTCATATGTGTACACCAACAT 469

Qy 361 CTAAATCCCGAAGCAATAAACGTCGCCGTTTATATACATACATAGTGCTGTGTTTATATC 420

Db 470 GTGAAGCCCGCAAGAGCGCTCGCCCGGTTATGTTTGGATTTCACGAGGAGGCTTCATATC 529

Qy 421 GGTGAATATCTGCTGATATGATGCTGCTGATTTTTCATTAATAAGATGSGTGTG 480

Db 530 GGGCAGGCCCAATCGGGAATGATATGCCCGGATTACTTTATGANAAGAAATGTTGTCTC 589

Qy 481 ATTAACATCAATATATCGTTTGGAGCTCAGTGTCTTAAGTTTAATTCAGAACACCTT 540

Db 590 GTCAAGATACAGTACCGACACTTGGGCTTTGGGATTTATGAGCTTAAGTCCCGACGTA 649

Qy 541 AATGTGCCCCGCTAATGCCGC 561

Db 650 AATGTACCGAAGATGTGCG 670

RESULT 12

LOCUS A1113763

DEFINITION GH10213.5,prime GH Drosophila melanogaster head por2 Drosophila melanogaster cDNA clone GH10213 5prime similar to U51050;

ACCESSION A1113763

VERSION A1113763.1

KEYWORDS EST.

SOURCE

ORGANISM Drosophila melanogaster

REFERENCE

AUTHORS Harvey,D., Brokslein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.

TITLE BDP/HHMT Drosophila EST Project

JOURNAL Unpublished (2001)

COMMENT Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Plate: 102 row: B column: 1

High quality sequence stop: 435.

Location/Qualifiers

1..648

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="GH10213"

/clone_lib="GH Drosophila melanogaster head por2"

/sex="male and female"

/dev_stage="adult"

/lab_host="DHS - alpha"

/note="Organ: head; Vector: por2; Site_1: EcoRI; Site_2:

VERSION A1109901.1 GI:3478225
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 646)
 Harvey, D., Broksstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G. M.
 BDGP/HHMI Drosophila EST project
 Unpublished (2001)
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: 92 row: H column: 8
 High quality sequence stop: 513.
 Location/Qualifiers
 1..646
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 /db_xref="taxon:7227"
 /clone="GH09292"
 /clone_lib="GH Drosophila melanogaster head pot2"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="DHS - alpha"
 /note="Organ: head; Vector: pot2; Site: 1; Ecor1; Site_2:
 Xho1; Sized fractionated cDNAs were directly ligated into
 pot2. Plasmid cDNA library."
 152 a 163 c 182 g 149 t

BASE COUNT 152 a 163 c 182 g 149 t

ORIGIN

Query Match 14.2% Score 243.4; DB 9; Length 646;
 Best Local Similarity 64.8%; Pred. No. 6.4e-57;
 Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

1 ATGAATTTCAAGCTTAACTGATGAGAAATTAATGAACATTAATGATGAAAT 60
 89 ATGAATTAAGAACCTCGGCTTTGTGAGCCGCTTCGGTGGCCCTCAACCATCGAGAT 148
 61 AAGTTTAACTATCTGTTAACTACCAATGAACGTTGAGTGAACATGAATATGCG 120
 149 AAAGTCCAGAGTATCGCGACGACCAATGAACAGTTGTCCCGACAGAGTACGCG 208
 121 AAAGTGAAGCGTTAAAGCTTTAACTGTAGCATGATCTTCACTACAGTTTGAAGGT 180
 209 CAAGTAGAGGGTATCAACGCTCTATCTCTACGATGTGCCCTACCTTCGAGGGT 268
 181 ATACGCTACGCCCAACCCCGACGTGGAGTGAATTTAAAGCACCACCGACCAACA 240
 269 ATCCCTACGCCACCTCCGCTGGGAGAGTTGGGTTTAAAGCCCTCAGAGGCCCAT 328
 241 CCTGGATGTGTGCTGATGTTGCAATCAATAAGTAAGTACAGGCAAGTATTT 300
 329 CCTGGAGAGAGTTGGCAGTACGACGACGAGGAGTAAGGCGGCTCAGAGTTC 388
 301 ATACGGGCAAGTGTGTGCTCAGAGGATGTCTATACCTAAGTGTCTATACGAATAT 360
 389 GCTTCGATAGGTAGAGGCTCCGAGGACCTCTATCTATCTCAATGTACACCAACAT 448
 361 CTAAATCCGAACATTAAGCTCCGCTTTAGTATACATACATGATGATGTTTATATC 420
 449 GTGAAGCCCAACAGGTGCGCGGTATGTTGATGATCAAGGAGGAGGCTTCAATTTC 508
 421 GGTAAATATCATGTATATGATGCTGATTTATTTATTAAGAGATGTGTTG 480
 509 GCGCAGGCGCAATCGGAGTATGAGCGCGGATTAATCTTATGAAGAAATGTGTCTC 568
 481 ATTAACATACAAATGCTTGGAGCTCTAGGTTTCTTAAGTTAAATTCAGAACCTT 540

Db 569 GTACAGATACAGTACCGACCTTGGGCTTTGGATTTATAGTCTTAACTCCCGAGCTA 628
 541 AATGTCCCGGTAAATGC 557
 629 AATGTACCAAGAAATGC 645

RESULT 15
 A1293416 646 bp mRNA linear EST 19-APR-2001
 LOCUS LP06524.5prine LP Drosophila melanogaster larval-early pupal pot2
 DEFINITION Drosophila melanogaster cDNA clone LP06524.5prine similar to
 051050: Drosophila melanogaster alpha esterase (aef) gene, partial
 cds, mRNA sequence.
 A1293416
 A1293416.1 GI:3942823

ACCESSION A1293416
 VERSION A1293416.1 GI:3942823
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 646)
 Harvey, D., Broksstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G. M.
 BDGP/HHMI Drosophila EST project
 Unpublished (2001)
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: 65 row: B column: 12
 High quality sequence stop: 493.
 Location/Qualifiers
 1..646
 /organism="Drosophila melanogaster"
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 /clone="LP06524"
 /clone_lib="LP Drosophila melanogaster larval-early pupal
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 /sex="male and female"
 /dev_stage="larvae-pupae"
 /lab_host="DHS-alpha"
 /note="Organ: whole body; Vector: pot2; Site: 1; Ecor1;
 Site_2: Xho1; Sized fractionated cDNAs were directly
 ligated into pot2. Plasmid cDNA library."
 151 a 163 c 184 g 148 t

BASE COUNT 151 a 163 c 184 g 148 t

ORIGIN

Query Match 14.2% Score 243.4; DB 9; Length 646;
 Best Local Similarity 64.8%; Pred. No. 6.4e-57;
 Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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 149 AAAGTCCAGAGTATCGCGACGACCAATGAACAGTTGTCCCGACAGAGTACGCG 208
 121 AAAGTGAAGCGTTAAAGCTTTAACTGTAGCATGATCTTCACTACAGTTTGAAGGT 180
 209 CAAGTAGAGGGTATCAACGCTCTATCTCTACGATGTGCCCTACCTTCGAGGGT 268
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 269 ATCCCTACGCCACCTCCGCTGGGAGAGTTGGGTTTAAAGCCCTCAGAGGCCCAT 328
 241 CCTGGATGTGTGCTGATGTTGCAATCAATAAGTAAGTACAGTCAAGTATTT 300

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2	1708.2	99.7	1713	4	US-09-068-960-9		Sequence 9, Appl1
3	1706.6	99.6	1713	4	US-09-068-960-1		Sequence 1, Appl1
4	1706.6	99.6	1713	4	US-09-068-960-3		Sequence 3, Appl1
5	1698.6	99.2	1713	2	US-08-669-524-1		Sequence 1, Appl1
6	1698.6	99.2	1713	2	US-09-068-960-7		Sequence 7, Appl1
7	1673.4	97.7	1713	2	US-08-669-524-2		Sequence 2, Appl1
8	951.8	55.6	1710	4	US-09-068-960-14		Sequence 14, Appl1
9	181.2	10.6	1584	3	US-08-747-221B-51		Sequence 51, Appl1
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37	139.6	8.1	1.515	4	US-09-005-051-16	Sequence 16, Appl
38	139.6	8.1	1.515	4	US-09-005-051-17	Sequence 17, Appl
39	139.6	8.1	1.982	3	US-08-747-221B-13	Sequence 13, Appl
40	139.6	8.1	1.982	3	US-08-747-221B-15	Sequence 15, Appl
41	139.6	8.1	1.982	4	US-09-005-051-13	Sequence 13, Appl
42	139.6	8.1	1.982	4	US-09-005-051-15	Sequence 15, Appl
43	87.2	5.1	1.694	3	US-07-926-852-11	Sequence 11, Appl
44	87.2	5.1	2.889	1	US-07-926-852-11	Sequence 11, Appl
45	87.2	5.1	2.989	1	US-08-453-323-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
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: Sequence 5, Application US/09068960A
: Patent No. 6235515
: GENERAL INFORMATION:
: APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
: TITLE OF INVENTION: MALATHION CARBOXYLSTERASE
: FILE REFERENCE: Attorney Docket No. 6235515 50179-051
: CURRENT APPLICATION NUMBER: US/09/068,960A
: CURRENT FILING DATE: 1998-05-20
: EARLIER APPLICATION NUMBER: PCT/AU96/00746
: EARLIER FILING DATE: 1996-11-22
: EARLIER APPLICATION NUMBER: AU 6751
: EARLIER FILING DATE: 1995-11-23
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 1713
: TYPE: DNA
: ORGANISM: Lucilia cuprina
US-09-068-960-5

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Matches 1713;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-9

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Best Local Similarity 99.8% Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 ; Sequence 3, Application US/09068960A
 ; Patent No. 623515
 ; GENERAL INFORMATION:
 ; APPLICANT: Commonwealth Scientific and Industrial Rarch. Org.
 ; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
 ; FILE REFERENCE: Attorney Docket No. 623515 50179-051
 ; CURRENT APPLICATION NUMBER: US/09/068,960A
 ; EARLIER FILING DATE: 1998-05-20
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746
 ; EARLIER FILING DATE: 1996-11-22
 ; EARLIER APPLICATION NUMBER: AU 6751
 ; EARLIER FILING DATE: 1995-11-23
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 3
 ; LENGTH: 1713
 ; TYPE: DNA
 ; ORGANISM: Lucilia cuprina
 US-09-068-960-3
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 Best Local Similarity 99.84; Pred. No. 0;
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Qy 1441 AATCAATTTGCCCAACGATATGCTTAAAGATCGCTGAATACAAACAAATGAAGCTATG 1500
Db 1441 AATCAATTTGCCCAACGATATGCTTAAAGATCGCTGAATACAAACAAATGAAGCTATG 1500
Qy 1501 ACTGATATGATGATCAATTTGGCCACACTGTAATCCTTATAGCAATGAATTTGAAGT 1560
Db 1501 ACTGATATGATGATCAATTTGGCCACACTGTAATCCTTATAGCAATGAATTTGAAGT 1560
Qy 1561 ATGGAATATGTTTCCCTGGGATCAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
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Db 1561 ATGGAATATGTTTCCCTGGGATCAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
Qy 1621 ATTAGTATGAATTTGAATAATGATGATGTCCTGTAATGATTAAGATTAACATGGAG 1680
Db 1621 ATTAGTATGAATTTGAATAATGATGATGTCCTGTAATGATTAAGATTAACATGGAG 1680
Qy 1681 TCGATGTTTGAATAACATAGATTTATTATG 1713
Db 1681 TCGATGTTTGAATAACATAGATTTATTATG 1713

RESULT 5
US-08-669-524-1
? Sequence 1, Application US/08669524
? Patent No. 5843758
? GENERAL INFORMATION:
? APPLICANT: RUSSELL, Robyn J.
? APPLICANT: NEWCOMB, Richard D.
? APPLICANT: ROBIN, Geoffrey C.
? APPLICANT: BOYCE, Thomas M.
? APPLICANT: CAMPBELL, Peter M.
? APPLICANT: PARKER, Anthony G.
? APPLICANT: OAKESHOT, John G.
? APPLICANT: SMYTH, Kerrie A.
? TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
? NUMBER OF SEQUENCES: 22
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lowe Price Leblanc & Becker
? STREET: 99 Canal Center Plaza, Suite 300
? CITY: Alexandria
? STATE: Virginia
? COUNTRY: USA
? ZIP: 22314
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/669,524
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Price, Robert L.
? REGISTRATION NUMBER: 22,685
? REFERENCE/DOCKET NUMBER: 1451-021
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 703-684-1111
? TELEFAX: 703-684-1124
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1713 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
US-08-669-524-1

Query Match 99.2%; Score 1698.6; DB 2; Length 1713;
Best Local Similarity 99.5%; Pred. NO. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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181 ATACCGTACGCCAACCGCAGTGGTGAGCTGAGATTTAAAGCACCCGAGCACCACA 240
181 ATACCGTACGCCAACCGCAGTGGTGAGCTGAGATTTAAAGCACCCGAGCACCACA 240
241 CCTGGGATGCTGCTGCTGATTTGCAATCATTAAGATTAAGTCAAGTGAATTTT 300
241 CCTGGGATGCTGCTGCTGATTTGCAATCATTAAGATTAAGTCAAGTGAATTTT 300
301 ATACCGGCAAAAGTGTGTGCTGAGAGATGCTATACCTAAGTCTATACGATTAAT 360
301 ATACCGGCAAAAGTGTGTGCTGAGAGATGCTATACCTAAGTCTATACGATTAAT 360
361 CTAAATCCCGAAATCAAGTCCCGCTTTAGTATACATACATAGTGTGTTTATATC 420
361 CTAAATCCCGAAATCAAGTCCCGCTTTAGTATACATACATAGTGTGTTTATATC 420
421 GGTGAATATCATGCTGATATGATGCTGCTGATTTATTCATTAAGATGAGTGTG 480
421 GGTGAATATCATGCTGATATGATGCTGCTGATTTATTCATTAAGATGAGTGTG 480
481 ATTAACATATCATGCTGATTTGAGAGCTGATGCTTTCTAAGTTTAAATCAGAACCT 540
481 ATTAACATATCATGCTGATTTGAGAGCTGATGCTTTCTAAGTTTAAATCAGAACCT 540
541 AATGCGCCGTAATGCTGCTGCTTAAAGATCAAGTCAAGTCCCTGCTGATTAATAAT 600
541 AATGCGCCGTAATGCTGCTGCTTAAAGATCAAGTCAAGTCCCTGCTGATTAATAAT 600
601 AATGCGCCCAATTTGCTGCTGCTAATATTAAGTCTGCTGCTGCTGCTGCTGCTG 660
601 AATGCGCCCAATTTGCTGCTGCTAATATTAAGTCTGCTGCTGCTGCTGCTGCTG 660
661 GCTGCTCTTACCCATCATGATGTTTAAACGCAAACTGCGCTGCTTCCATCGGTG 720
661 GCTGCTCTTACCCATCATGATGTTTAAACGCAAACTGCGCTGCTTCCATCGGTG 720
721 ATACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
721 ATACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
781 TTTACCTTACCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
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841 TTTCTTATGAAGCAAGCAGAGATTTAGTAAACTTGAAGAAAAGTTTAACTCTA 900
841 TTTCTTATGAAGCAAGCAGAGATTTAGTAAACTTGAAGAAAAGTTTAACTCTA 900
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901 GAAGAGGCTACAAATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
961 GCTGATGCTGCTTACCCAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
961 GCTGATGCTGCTTACCCAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
1021 ATACCCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1021 ATACCCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1081 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
1081 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
1141 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1141 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1201 CATGTTACAGAGAACCAACCAAGCTGATTAATTTTATGATCTTCTGCTGCTGCTGCTG 1260
1201 CATGTTACAGAGAACCAACCAAGCTGATTAATTTTATGATCTTCTGCTGCTGCTGCTG 1260

1261 TTTGCTTCCCATGATGCTGTTGTTGCAATTAAGTCTTTCATACACCTCGGTACACCC 1320
1261 TTTGCTTCCCATGATGCTGTTGTTGCAATTAAGTCTTTCATACACCTCGGTACACCC 1320
1321 GCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1321 GCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1381 CGTAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1381 CGTAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1441 AATCAATGCGCAACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1441 AATCAATGCGCAACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1501 ACTGATATGATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1501 ACTGATATGATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
1621 ATTAGTATGATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
1621 ATTAGTATGATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
1681 TCGATGTTGGAATACATAGATTAATTTTATG 1713
1681 TCGATGTTGGAATACATAGATTAATTTTATG 1713

RESULT 6
US-09-068-960-7
Sequence 7, Application US/09068960A
Patent No. 623515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 623515 50179-051
CURRENT APPLICATION NUMBER: US/09/068, 960A
EARLIER FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ. ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ. ID NO 7
LENGTH: 1713
TYPE: DNA
ORGANISM: *Lucilia cuprina*
US-09-068-960-7

Query Match 99.2%; Score 1698.6; DB 4; Length 1713;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGAAGAATTAATGATTAATAAT 60
1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGAAGAATTAATGATTAATAAT 60
61 AAGTTTTTAACATATGCTTTAACTACCAATGAACGCTGCTAGCTGAACCTGAATATG 120
61 AAGTTTTTAACATATGCTTTAACTACCAATGAACGCTGCTAGCTGAACCTGAATATG 120
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121 AAGTGAAGGCTTTAAAGCTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
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181 ATACCGTACGCCAACCGCAGTGGTGAGCTGAGATTTAAACACCCGAGCACCACA 240

Db 181 ATACCGTACGCCCAACCCGCAAGTGGTGAGCTGAGATTAAAGACACCCAGGACCAACA 240
Oy 241 CCCGCGAGTGTGCGCGATGTTGGCAATCATTAAGTAAGTGTGTCAGTGTATTTT 300
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Oy 301 ATAAAGGCGCAAGTGTGCGCGATGTTGGCAATCATTAAGTGTGTCAGTGTATTTT 360
Db 301 ATAAAGGCGCAAGTGTGCGCGATGTTGGCAATCATTAAGTGTGTCAGTGTATTTT 360
Oy 361 CTAAATCCCGCAAGTGTGCGCGATGTTGGCAATCATTAAGTGTGTCAGTGTATTTT 420
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Oy 421 GGTGAATTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
Db 421 GGTGAATTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
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Oy 541 AATGCGCCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
Db 541 AATGCGCCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
Oy 601 AATGCGCCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
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Oy 661 GGTGCGCTACCCACTACATGATGATGATGATGATGATGATGATGATGATGATG 720
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Oy 721 ATACTAATGTCGGGTAATGCTATTTGTCATGCTGCTAATACCAATGTCACATGTC 780
Db 721 ATACTAATGTCGGGTAATGCTATTTGTCATGCTGCTAATACCAATGTCACATGTC 780
Oy 781 TTCACCTTAGCCAAATTTGGCGGCTAATAGGTAAGGTAAGGTAAGGTAAGGTAAG 840
Db 781 TTCACCTTAGCCAAATTTGGCGGCTAATAGGTAAGGTAAGGTAAGGTAAGGTAAG 840
Oy 841 TTTCTTAAGAAAGCCAGCAGATTTAGTAAACTTGAGAAAGTAACTTAACTGTA 900
Db 841 TTTCTTAAGAAAGCCAGCAGATTTAGTAAACTTGAGAAAGTAACTTAACTGTA 900
Oy 901 GAAGAGCGTACAAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 GAAGAGCGTACAAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Oy 961 GGTGATGTCCTTACCCAAATCTGCGGAAATGTTAAAGCTGTTGGGTAATGCG 1020
Db 961 GGTGATGTCCTTACCCAAATCTGCGGAAATGTTAAAGCTGTTGGGTAATGCG 1020
Oy 1021 ATACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 ATACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Oy 1081 CAAATGCTATGCTGTTAAGAAATGGAATGGAATGGAATGGAATGGAATGGA 1140
Db 1081 CAAATGCTATGCTGTTAAGAAATGGAATGGAATGGAATGGAATGGAATGGA 1140
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Oy 1261 TTTCTGTTCCCATGCTGTTGTTGCAATTAAGTAACTGTAACACACACACACAC 1320
Db 1261 TTTCTGTTCCCATGCTGTTGTTGCAATTAAGTAACTGTAACACACACACACAC 1320

Oy 1321 GTCATCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 1321 GTCATCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
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Oy 1441 AATCAATGCGCAAGCGATGCTGATGATGATGATGATGATGATGATGATGATG 1500
Db 1441 AATCAATGCGCAAGCGATGCTGATGATGATGATGATGATGATGATGATGATG 1500
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Db 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Oy 1561 ATGAAATGTTTCTGCGATGCTGATGATGATGATGATGATGATGATGATGATG 1620
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Db 1621 ATTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Oy 1681 TCGATGTTGAAACATAGATGATGATGATGATGATGATGATGATGATGATG 1740
Db 1681 TCGATGTTGAAACATAGATGATGATGATGATGATGATGATGATGATGATG 1740

RESULT 7
US-08-669-524-2
; Sequence 2, Application US/08669524
; Patent No. 5843758
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, Robyn J.
; APPLICANT: NEWCOMB, Richard D.
; APPLICANT: ROBIN, Geoffrey C.
; APPLICANT: BOYCE, Thomas M.
; APPLICANT: CAMPBELL, Peter M.
; APPLICANT: PARKER, Anthony G.
; APPLICANT: OAKESHOTT, John G.
; APPLICANT: SMYTH, Kerrie A.
; TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe Price Leblanc & Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 1451-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-669-524-2

Query Match 97.7%; Score 1673.4; DB 2; Length 1713;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1677; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGGAATTAATGACATTTGAAT 60
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61 AAGTTTTAACTACTGTTAACTACCAATGAACGTTGTTGTTGTTGTTGTTGTTGTT 120
121 AAGTGAAGGCGTTAAAGCTTTAACTGTTGATGATGATGATGATGATGATGATGAT 180
121 AAGTGAAGGCGTTAAAGCTTTAACTGTTGATGATGATGATGATGATGATGATGAT 180
181 ATACCGTACGCGCCAGCGGAGTGGTGAAGTATTTAAAGCCCGCCAGCCAGCAACA 240
181 ATACCGTACGCGCCAGCGGAGTGGTGAAGTATTTAAAGCCCGCCAGCCAGCAACA 240
241 CCCGTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 300
241 CCCGTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 300
301 ATACGGGCAAAAGTGTGGCTGAGAGATTTGCTATACCTAGTCTATACCAATAT 360
301 ATACGGGCAAAAGTGTGGCTGAGAGATTTGCTATACCTAGTCTATACCAATAT 360
361 CTAAATCCCGAACTAAACGTCCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 420
361 CTAAATCCCGAACTAAACGTCCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 420
421 GGTGAATAATCATCGTATGATGATGATGATGATGATGATGATGATGATGATGATG 480
421 GGTGAATAATCATCGTATGATGATGATGATGATGATGATGATGATGATGATGATG 480
481 ATTAACATACAAATATCGTTGGAGCTCTAGTTTCTAAGTTTAAATTCAGAGACCT 540
481 ATTAACATACAAATATCGTTGGAGCTCTAGTTTCTAAGTTTAAATTCAGAGACCT 540
541 AATGCGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
541 AATGCGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
601 AATGCGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
601 AATGCGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
661 GCTGCTTACCCACTACATGATGATGATGATGATGATGATGATGATGATGATGATG 720
661 GCTGCTTACCCACTACATGATGATGATGATGATGATGATGATGATGATGATGATG 720
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721 ATACTAATGCTGGGTAATGCTATTTGCTCATGCTTAATACCAATGTCACATGTCG 780
781 TTCACCTTACCAATTTGGCGGCTATTAAGGTTGAGATTAAGATTAAGATTTTGA 840
781 TTCACCTTACCAATTTGGCGGCTATTAAGGTTGAGATTAAGATTAAGATTTTGA 840
841 TTTCTTATGAAGCCAGCAGAGATTTAGTAAACTTGAAGAAAGTTTAACTGA 900
841 TTTCTTATGAAGCCAGCAGAGATTTAGTAAACTTGAAGAAAGTTTAACTGA 900
901 GAAGAGCGTAAATTAAGTATGTTTCTTTGCTCCACTGTTGAGCCATATAGACC 960
901 GAAGAGCGTAAATTAAGTATGTTTCTTTGCTCCACTGTTGAGCCATATAGACC 960
961 GGTGATTTGTTCTTACCCAAACATCTCGGAAATGTTTAAACATGCTTGGGTAATTCG 1020

1020 GGTGATTTGTTCTTACCCAAACATCTCGGAAATGTTTAAACATGCTTGGGTAATTCG 1020
1021 ATACCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
1021 ATACCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
1081 CAAATGCGCTATGCTTTGTTAGGAATTTGGAATTTGTTGTTGTTGTTGTTGTTGTT 1140
1081 CAAATGCGCTATGCTTTGTTAGGAATTTGGAATTTGTTGTTGTTGTTGTTGTTGTT 1140
1141 GCTGATGCTGAAGCAGCCCGCCAGAGACCTTGAATGCTGCTAAATTTAAAGGCT 1200
1141 GCTGATNTGAGCAGCAGCCCGCCAGAGACCTTGAATGCTGCTAAATTTAAAGGCT 1200
1201 CATGTTACAGGAAACACCAACAGTATTTTATGATGATGATGATGATGATGATGATG 1260
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1261 TTTCTGTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
1261 TTTCTGTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
1321 GTCATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1321 GTCATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1381 CGTAGTGAAGGCTGTTTGAAGGTTTGAAGGTTTGAAGGTTTGAAGGTTTGAAGGTT 1440
1381 CGTAGTGAAGGCTGTTTGAAGGTTTGAAGGTTTGAAGGTTTGAAGGTTTGAAGGTT 1440
1441 ATCAATTTGGCCAAACGATGCTTAAAGATGCTGATGATGATGATGATGATGATGATG 1500
1441 ATCAATTTGGCCAAACGATGCTTAAAGATGCTGATGATGATGATGATGATGATGATG 1500
1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
1561 ATGGAATAATGTTTCTGCGGATGATGATGATGATGATGATGATGATGATGATGATG 1620
1561 ATGGAATAATGTTTCTGCGGATGATGATGATGATGATGATGATGATGATGATGATG 1620
1621 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
1621 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
1681 TCGATGTTGAAAAACATAGATTTATTTAG 1713
1681 TCGATGTTGAAAAACATAGATTTATTTAG 1713

RESULT 8
US-09-068-960-14
Sequence 14, Application us/09068960A
Patent No. 623515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYLISERASE
FILE REFERENCE: Attorney Docket No. 623515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 14
LENGTH: 1710
TYPE: DNA
ORGANISM: Musca domestica
US-09-068-960-14

Query Match 55.6%; Score 951.8; DB 4; Length 1710;
 Best Local Similarity 73.2%; Pred. No. 1.3e+264;
 Matches 1220; Conservative 0; Mismatches 447; Indels 0; Gaps 0;

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OY 44 TTTAAATGCAATGAAAATAGTTTAACTATCGTTAACTACCAATGAAGAGGTGGTAG 103
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DB 44 TTTAAATGCAATGAAAATAGTTTAACTATCGTTAACTACCAATGAAGAGGTGGTAG 103
OY 104 CTGAATCGAATATGCGCAAGTGAAGAGGTAAAGCTTTAACTGTGACATGATTCCT 163
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DB 104 TCGATACGTAATATGCAAAATTAAGGCTTTAAAGCGAATGACCGCTCAACGATATTCCT 163
OY 164 ACTACAGTTTGGAGGTATACCGTACGCCAACCGCCAGTGGGTAGATGAGATTAAAG 223
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DB 164 ACTACAGTTTGGAGGTATACCGTATACCGTATGCTAAGCTTCACATGGGTAGATTCAAG 223
OY 224 CACCCAGGACCAACACCCCTGGATGCTGCTGATTTGCAATCAATAAGATTAAGT 283
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 224 CACCCAGGACGCGCTGTACCATGGAGGGGTGATGATGCTGCTGAGCCACCAAGAT 283
OY 284 CAGTCAAGTTGATTTTAAAGGGCAAGTGTGGCTCAGAGATTTCTATACCTTA 343
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 284 CAGTCAAGTCAATATCAATCCGAAACTAAGCGTCCGTTAGTATACATACATAG 403
OY 344 GTGTATATCAAGATATCAATCCGAAACTAAGCGTCCGTTAGTATACATACATAG 403
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 344 ATGTATATCAAGATATCAATCCGAAACTAAGCGTCCGTTAGTATACATACATAG 403
OY 404 GTGTGTTTTTAAATTCGCGTAAATCAATCGTATATGATGCTGCTGATTTTCAATTA 463
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 404 GCGGAGATTTTAAATTCGCGTAAATCAATCGTATATGATGCTGCTGATTTTCAATTA 463
OY 464 AAAAGAGTGTGTGATTAACATACATATCGTTGGAGACTAGTTTCTAAAGTT 523
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DB 464 AAAAGAGTGTGTGATTAACATACATATCGTTGGAGACTAGTTTCTAAAGTT 523
OY 524 TAAATTCAGAAACCTTAATGTGCGGTAATGCGCGCTTAAGATCAAGTACATGGCCT 583
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DB 524 TGAATTCGAAATATCAATGTCGCCGCAACGCTGCGCTCAAGATCAAGTATGCGCT 583
OY 584 TGCATTTGATTAATAATTAATGCGCAACTTTGTTGGCAATCCGATATATTAAGTCT 643
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DB 584 TGAATTCGAAATATCAATGTCGCCGCAACGCTGCGCTCAAGATCAAGTATGCGCT 643
OY 644 TTGGTGAAGTCCGCTGCTGCTACCCACTACATGATGTTAAACCGAACAACTCCG 703
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DB 644 TCGGGGAAAGTCTGTGGGGCTCAACCCATTAATGATTAACCGAACAACTCCG 703
OY 704 GTCTTTTCATGCTGATTAATGATGCGGTAATGCTATTTGCTCATTTGGCTAATGCC 763
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DB 704 GTCTTTTCATGCTGATTAATGATGCGGTAATGCTATTTGCTCATTTGGCTAATGCC 763
OY 764 AATGTCAACATGCTGCTTACCTTACCAATTTGGCGGCTAATGAAGGTGAGATTAATG 823
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DB 764 AATGTCAACATGCTGCTTACCTTACCAATTTGGCGGCTAATGAAGGTGAGATTAATG 823
OY 824 ATAAGATGTTTGAATTTCTTATGAAGAACCAAGCAGAGATTAGTAAACTTGAGC 883
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 824 AAAAAGATATCTCGAATTCCTTAATGAAGAACCAATCCATGATTTGATCAAGAGAGC 883
OY 884 AAAAGTTTTTAACTCTAGAGAGGTACAAATTAAGTCAATTTCTTTGCTCCACATG 943
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 884 CACAAGTTTTGACACCCGAAAGAAATGCAAAATTAAGTCAATTTCTTTGACACATG 943
OY 944 TTGACCATATCAGACCGCTGATTTGCTTACCCAAACATCTCGGGAAATGTTAAAA 1003
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 944 TAGAACCATATCAGACCGCTGATTTGCTTACCCAAACATCTAGAGAAATGGAAGA 1003
OY 1004 CTGCTTGGGTATTCGATACCATATGATGCTGAACATCTCAATGAGGCTCATTTT 1063
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1004 GCGCTTGGGAAATTCGATACCATATGATGAGCAATACCTCTCAAGAGTTTGCCTT 1063

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OY 1064 TCACCTTCATTTCTTAAGCAAAATCCCTATGCTTTGAAGAAATGGAACCTGTCATTT 1123
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DB 1064 CCAATTCATTTCTCCCAACAAATATCCGGAGGTTGTAAAGAGTTGGATCTCTGTGCAATTT 1123
OY 1124 TTGTGCCAAGTGAATTTGGCTGATGCTGAACGACCGCCCGCAAGACCTTTGAAATGGCTG 1183
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1124 ATGTGCTCTGGAGGTTGGCTGACATGAACGACGATGCCCGGAAACCTCGAGAGGCTG 1183
OY 1184 CTAAATTTAAAGGCTCATGTTTACAGGAGAAACCAACACACTGATTAATTTTATGATTC 1243
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1184 CCATTTGTGAAGAAAGGCCCATGATGAGGGAACACCTTCTGTGATTAATTTTATGAGAC 1243
OY 1244 TTGCTCTCACAATCTATTTCTGTTCCCATCATCGTTGTTGTCATTAACGTTTCAATC 1303
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DB 1244 TTGCTCTCATTCTATTTCTTCCCTTCCCTCCATCATGCTCTCTACATATGGCTTCAAC 1303
OY 1304 ACACCTCGGTACACCCGCTCTACTTGTATACGCTTGACCTTGATTCGAAGATCTTATCA 1363
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DB 1304 ACACAGCTGGACCTCCCATTTATTTGTATCGTTGATTTGATTCGAAGAAATATATTA 1363
OY 1364 ATCCCTATGCTATTTATGCTAGTGAACGCTGCTGTTAAGGCTGTTAGTCTGATGAT 1423
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DB 1364 ACCCTATGCTATTTATGCTGTTGGCCGCTTAAAGGTGAAGCCATGCGGATGAGC 1423
OY 1424 TAACCTATTTCTTCTGGAATCAATTTGGCCCAACGATAGGCTTAAGAAATGCGGATTA 1483
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1424 TAACCTATTTCTTCTGGAATCAATTTGGCCCAACGATAGGCTTAAGAAATGCGGATTA 1483
OY 1484 AAACATTTGAACGATATGACTGTATATGATTAACATTTTGCACACACTGGTAAATCTTATA 1543
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DB 1484 AAACATTTGAACGATATGACTGTATATGATTAACATTTTGCACACACTGGTAAATCTTATA 1543
OY 1544 GCAATGAATTTGAAGTATGAGAAATGTTTCCCTGGGATCCATTAAGAAATCCGATGAG 1603
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DB 1544 GCAATGAATTTGAAGTATGAGAAATGTTTCCCTGGGATCCATTAAGAAATCCGATGAG 1603
OY 1604 TTATCAAGTGTGATTAATTAATGATGAATTAAGAAATGATGCTCGTGAATGATGA 1663
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1604 TCTATTAAGTTTAAATATATGCGGATGAATTAAGAAATGATGATTTTCCGAAATGATGA 1663
OY 1664 AGATTAAACATGAGGATGATGTTGAAAAACATAGACATTTATTT 1710
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DB 1664 AAATTAAACATGAGGATGATGTTGAAAAACATAGACATTTATTT 1710

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RESULT 9
 US-08-747-221B-51
 : Sequence 51, Application US/08747221B
 : Patent No. 6063610
 : GENERAL INFORMATION:
 : APPLICANT: Silver, Gary W.
 : APPLICANT: Wisniewski, Nancy
 : TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
 : TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 : NUMBER OF SEQUENCES: 66
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Carol Takington Verser, Ph.D.
 : ADDRESSEE: Heska Corporation
 : STREET: 1825 Sharp Point Drive
 : CITY: Fort Collins
 : STATE: Colorado
 : COUNTRY: USA
 : ZIP: 80525
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: Windows 95
 : SOFTWARE: WordPerfect for Windows, Version 7.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/747,221B
 : FILING DATE: No. 6063610ember 12, 1996
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:


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NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1584
US-08-747-221B-51

Query Match      10.6%; Score 181.2; DB 3; Length 1584;
Best Local Similarity 56.4%; Pred. No. 1.7e-42;
Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

QY 116 ATGGCAAGTGAAGGCGTTAAAGCTTAAGTGTACATGATGATCTCTACTACAGTTTG 175
DB 29 AAGTACTTTAAAGGAAAGCAAAATAGTGAAGAAAGAAATGCTTCATAGTATT 88
QY 176 AGGTATACCGTACGCCCAAGCCAGTGGGTAGCTGAGATTAAAGCAAGCCAGCGAC 235
DB 89 CTGGAATTCATATGCCAAACCTCCTGTAGCTGATTAAGATTAAAGCCAGCTCAACCTG 148
QY 236 CAACACCCCTGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 295
DB 149 CAACACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 208
QY 296 ATTTTAAGGGGCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 355
DB 209 ATTTTAAGGGGCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 268
QY 356 ATATCTAATATCCCAAGTAAAGCTCCGTTTATGATACATACATGATGATGATGAT 415
DB 269 CAAGAACCTGCAAGAAATCACTCTTCAGTAAATGATGATGATGATGATGATGATGAT 328
QY 416 TTATCGTGAATATCATCGATATGATGATGATGATGATGATGATGATGATGATGATGAT 475
DB 329 TCATGGATCTGCAATATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 388
QY 476 TGTGATTAACATACATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAG 535
DB 389 TTCTGTTACTTTCATATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 448
QY 536 ACCTTAATGCGCCGATATGCGGCTTAAAGATCAAGTCATGAGCTGATGATGATGATGAT 595
DB 449 AA-----GCGCTGGCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 502
QY 596 AAATTAATTTGGCCAACTTTGGTGGCAATGCCATATATATACAGTCTTTGGTGAAGTG 655
DB 503 AAACATATTTGATCTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 562
QY 656 CCGGTCTGCTCTACCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715
DB 563 CAGGTGTGCAAGTGTCTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 622
QY 716 GTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
DB 623 AAGCATCTCACAAAGTGAAGTGTGTTAATCTTGGGCG 662

RESULT 10
US-08-747-221B-52/c
; Sequence 52, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
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APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Carol Talkington Verser, Ph.D.
ADDRESS: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610e1, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-747-221B-52

Query Match      10.6%; Score 181.2; DB 3; Length 1584;
Best Local Similarity 56.4%; Pred. No. 1.7e-42;
Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

QY 116 ATGGCAAGTGAAGGCGTTAAAGCTTAAGTGTACATGATGATCTCTACTACAGTTTG 175
DB 1556 AAGTACTTTAAAGGAAAGCAAAATAGTGAAGAAAGAAATGCTTCATAGTATT 1497
QY 176 AGGTATACCGTACGCCCAAGCCAGTGGGTAGCTGAGATTAAAGCAAGCCAGCGAC 235
DB 1496 CTGGAATTCATATGCCAAACCTCCTGTAGCTGATTAAGATTAAAGCCAGCTCAACCTG 1437
QY 236 CAACACCCCTGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 295
DB 1436 CAAGAACCTGCAAGAAATCACTCTTCAGTAAATGATGATGATGATGATGATGATGAT 1377
QY 296 ATTTTAAGGGGCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 355
DB 1376 ATTTTAAGGGGCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1317
QY 356 ATATCTAATATCCCAAGTAAAGCTCCGTTTATGATACATACATGATGATGATGATGATGAT 415
DB 1316 CAAGAACCTGCAAGAAATCACTCTTCAGTAAATGATGATGATGATGATGATGATGATGAT 1257
QY 416 TTATCGTGAATATCATCGATATGATGATGATGATGATGATGATGATGATGATGATGAT 475
DB 1256 TCATGGATCTGCAATATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1197
QY 476 TGTGATTAACATACATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAG 535
DB 1196 TTCTGTTACTTTCATATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1137
QY 536 ACCTTAATGCGCCGATATGCGGCTTAAAGATCAAGTCATGAGCTGATGATGATGATGATGAT 595
DB 1136 AA-----GCGCTGGCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1083
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Page 12

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1 TELEPHONE: 970/493-7272
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3 TELEFAX: 970/484-9505
4
5 INFORMATION FOR SEQ ID NO: 52
6
7 SEQUENCE CHARACTERISTICS:
8
9 LENGTH: 1584 nucleotides
10
11 type: nucleic acid
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13 STRANDEDNESS: single
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15 TOPOLOGY: linear
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17 MOLECULE TYPE: cdna
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Query Match	10.6%;	Score 181.2;	DB 4;	Length 1584;
Best Local Similarity	56.4%;	Pred. No. 1.7e-42;		
Matches 361; Conservative	0;	Mismatches 273;	Indels 6;	Gaps 1.

OY	116	ATGCAACAGTAAAGGCGTTAAACGTTACCTGATAGTACGATGATCCCTACTACAGTTTG	145
Db	1556	AAGGTACTTTTAAAGGAAAAAGACAAATTAAGTGAAGAAATGCTGTCATAGTAAT	1497
OY	176	AGGGATACCGGTACGCCCAACCCACGAGTGGTACGTAGATTTAAAGCAACCCAGGAC	235
Db	1496	CTGGATATCCATATAGCCCAACCTCCGTAGAGTACTAGATTTTAAAGCAACCTGAC	1437
OY	236	CAACACCCCTGGAGTGTGCTGCTGATGTTGTTCATCATTAACATAGTCACTGCAAGTTG	295
Db	1436	CAGAACTTGGTCAAGTGTCTTGAATGCTAGTAAAGAGGAAATGTTAGATCAGTAC	1377
OY	296	ATTTTATACGGCAAGTGTGGGTCAGAGATGTGTATACCTAAGTGTATACGA	355
Db	1376	ATTTTATTTAAAAAATTAAAGTACGGGCTGAGATGTTTAACTCATGTATGTAC	1317
OY	356	ATTAATCTAATCCGAAACTAAACGTCCGTTTAACTATACATACATGGTGGTTTAA	415
Db	1316	CAAAAAACATCAGAGAAATCACTTCCAGTAATGTATAGATACATGGAGAGAGGCTTCT	1257
OY	416	TTATGGGTAAATATCATGCTATATGTATGTCCTGATTTATTTCAUAAAAAGATGTGG	475
Db	1256	TCATGGGATCTGGAAATAGTATATGATATGTCCTGAAATTTGATGAGTATTTGAAATTG	1197
OY	476	TGTTGATTACATACATATGCTTTGGAGACTCAGGTTTTCCTAACTTAAATTAATTCAGAG	535
Db	1196	TTCTGGTATCTTTCAATTAATGATATAGTGTGTTTGGGATTTTGAACCTGGGAATAGAA	1137
OY	536	ACCTTAATGTGCCGATATGCCGCGCTTAAAGATCAAGTCATGCGCTTCATTTGGATTA	595
Db	1136	AA-----GGCGCTGGCAATGTGGTTTGAATGAGACAGGTTGAAGCTTAAATGGGTAA	1081
OY	596	AAATATATTCGCGCAACTTGGTGGCCAAATCCGGAATATTTAAAGTCTTTGGTGAAGTG	655
Db	1082	AAAAATATTTGATCTCTTTGGTGGTGAACCCACAAATATGATATTTTGGAGAAATCAG	1021
OY	656	CCGCTGCTGCCCTTACCCACTACATGATGTTTAAACGAACAACTCGCGGCTCTTTCATC	715
Db	1022	CAGGTGTGCAAGTGTTCATTTATTTGAATGTTATAGATCTTTCCAAAGCACTTTTTCATA	963
OY	716	GTGTTATCTAATGTGGGTAATGCTAATTTGGATTTGCAATTCG	755
Db	962	AAGCATCTCAAAATGGAAGTGGTAACTTAACTCTTGGGC	923

RESULT 13
US-08-747-221B-36
; Sequence 36, Application US/08747221B
; Patent No. 6063610

GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Minszewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Takington Verser, Ph.D.
ADDRESSEE: Heska Corporation

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

APPLICATION NUMBER: US/08/747, 221B
FILING DATE: No. 6063610eember 12, 1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Vester, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:

Query Match	10.6%;	Score 181.2;	DB 3;	Length 2007;
Best Local Similarity	56.4%;	Pred. No. 1.9e+42;		
Matches 361;	Conservative	0;	Mismatches 273;	Indels 6;
				Gaps 1;

QY	116	ATGCGAAGTGAAGAGCGCTTAAACGTTTAACTGCTGTACGATGATTCCTCACTCAAGCTTTG	175
Db	39	AAGGTACTTTAAAGGAAAGAGCAATTAAGTAAAGAAAGAAATGCTTCATAGTATT	98
QY	176	AGGGTATACCGTAGCCCAACCGCCACTGGGTAGCTGAGATTTAAAGCACCCCAAGCAC	235
Db	99	CTGGATTTCCATATATGCCAAACCTCCTAGGTATCTAAAGATTTAAGCCACTCAACTG	158
QY	236	CACACCCCTGGAGNGTGTGGCTATGTTGCATCTCAAGATTAAGTCAAGTCAAGTTC	295
Db	159	CAGAACCTTTGGCAGGTCTTTTATCTAGTAAAGAAAGGAAATAGTGTAGATCAAGTAC	218
QY	296	ATTATTATACGGGCAAGCTGTGTGCTTCAGAGATTTGTTATATACCTAAGTCTAATACGA	355
Db	219	ATTTTATTAAAAAAATTAAGATAGAGGGCTGAAAGATTTTATTAACCTCAATGCTTATGTAC	278
QY	356	ATATATCTAATCCGAAACTAAAGCTCCGTTTATGATATACATCAATCAATGCTGTGTTTAA	415
Db	279	CAAAAACATCAGAGAAATCACTCTTCCAGTAATGATGATCAATGAGAGAGCGTTC	338
QY	416	TTATCGGTAAAAATCATCGTATATATATGTCTCTGATTAATTCATTAAGAAAGATGTG	475
Db	339	TCATGGGATCTGGAATATATGATATATGTATGTGCTCGAATATTTATGATTAATGAAATTC	398
QY	476	TGTTGATTAACATACAAATATGCTTTGGAGAGCTCTAGTTTTCTAAGTTTAAATTCAGAC	535
Db	399	TTCTGTGTACTTCAATTTCCATTAGTGTTTGCGATTTTTCACCTGGGAATTAACG	458
QY	536	ACCTTAATGTGCCGGTAAATGCCGCGCTTAAGATCAAGTCATGCGCTTGATGGATTA	595
Db	459	AA-----GCGCGCTGCGCATGTGTGTTCATGTAGCAGAGGTGAAGCTCTAAATGGGTAA	512
QY	596	AAATATATTCGCCCACTTGTGGCAATCCCGATCAATATTACAGTCTTTTGGTAAAGTG	655
Db	513	AAAACAATATTGATCTTTTGGTGGTACAGCCCAACAAATGTGACTTTTGGAGAATCAG	572

NAME/KEY: CDS
LOCATION: 11..1594
US-09-005-051-36

Query Match 10.6%; Score 181.2; DB 4; Length 2007;
Best Local Similarity 56.4%; Pred. No. 1.9e-42;
Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

```
OY 116 ATGGCAAGTGAAGCGTTAAAGCTTAACTGTACGATGATCCCTACTACAGTTTG 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 39 AAGTACTTTAAAGAGAAAGACCAATAGTAAAGAAAGAAATGTGTCAATGTTATT 98
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 176 AGGTTATACCGTACGCCCAACGCCAGTGGTGAGCTGAGATTAAAGCACCACGAC 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 CTGGAAATTCATATGCGCAACCTCCTGTAGTATCTAAGATTAAAGCCCACTCAACCTG 158
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 236 CAACACCCCTGGATGCTGCGGATGTTGCAATCATMAAGATAAGTCAGTCAAGTTG 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 CAGAACCTTGTCAGCTGTTCTTGATGCTAGTAAAGAGGAATAGTGTAGATCAGTAC 218
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 296 ATTTTATACGGGCAAGTGTGTGCTCAGAGATTGCTATACCTAAGTGTATACGA 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 ATTTTATTTAAATAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCATGTATATAC 278
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 356 ATATCTAATCCCGAACTAAAGTCCCGTTTGTATACATACATGCTGTGTTTA 415
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 279 CAAAAACATCAGAAATACCTTCTTCAGTAAATGATGATGATGATGAGAGAGGCTCT 338
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 416 TTATGGTGAATAATCATGCTATATGATGATGCTGATTTTCAATTAAGAGATGAG 475
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 339 TCATGGGATCTGGAATAGTATGATGATGATGATGATGATGATGATGATGATGATG 398
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 476 TGTGATTACATACATATATGCTTGGAGCTTACGCTTATTAAGTTAAATTCAGAG 535
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 399 TTCTGTACTTTCATATATGATGATGATGATGATGATGATGATGATGATGATGATG 458
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 536 ACCTTAATGTCCCGTAAATGCCGCTTAAAGATCAAGTCAATGCTGCTGATGATGA 595
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 459 AA-----GCGCTGGCAATGTTGTTGATGACCAAGTTGAAGCTCTAATAATGGTAA 512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 596 AAAATTAATGGCCCACTTTGTGCAATCCGATTAATTAATTAATTAATTAATTAAT 655
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 513 AAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 572
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 656 CCGGTGCTGCTTACCCACATGATGATTAACCCGAACAACTCGGGTCTTTTCATC 715
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 573 CAGGTGGTGAAGTGTATTTGATGATGATGATGATGATGATGATGATGATGATGATG 632
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 716 GTGTATACTAATGTCCGTAATGCTATTTGTCATTTGGC 755
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 633 AAGCATCTCAAAAGTGAAGTGTCTTTTAATCTTGGGC 672
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: April 11, 2003, 08:51:22
Job time : 46.518 secs

Db 721 AATCCTAAAGTGAACCTCTTTGGAGAAAGTGCAGAGCAGCTTC 777

RESULT 4

US-09-880-107-2271
: Sequence 2271, Application US/09880107
: Patent No. US20020142981A1
: GENERAL INFORMATION:
: APPLICANT: Horne, Darci T.
: APPLICANT: Scherf, Uwe
: APPLICANT: Vockley, Joseph G.
: APPLICANT: Gene Logic, Inc.
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
: FILE REFERENCE: 44921-5028-WO
: CURRENT APPLICATION NUMBER: US/09/880,107
: PRIOR FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/237,054
: NUMBER OF SEQ ID NOS: 3950
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2271
: LENGTH: 2381
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474
US-09-880-107-2271

Query Match

3.7%: Score 63.8; DB 10; Length 2381;
Best Local Similarity 55.0%; Pred. No. 2.6e-06;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

Qy 325 GAGAGTTGCTATACCTACCTAGTGTCTATAGCAATATCTAAATCCCGAAGCTAACGTCCTC 384
Db 427 GAAGACTGTTTATATCTAAATGATGATGATCCAGACCTAAAC---AAAAATGCCACT 483
Qy 385 GTTTAGTATACATACATGAGTGGTGGTTTATTCGCTGAAATATCATGTCATATGAT 444
Db 484 GTATTGATATGATGATTTATGAGTGGTGGTTTCAACTGCAACATCATCTTACATGTTAT 543
Qy 445 GTCCTGATTTATTCATTAAGAAAGA---TGTGCTGTTGATTAACATACATATGCTTTG 501
Db 544 GATGGCAAGTTCTGCTGGCTGTAAGAGTTATTTAGTGTCAATGAACATATAGGGTG 603
Qy 502 GGAGCTAGGTTTCTAAGTTTAATTCAGAAAGCTTAATGTCGCCGTTATGCCGCGC 561
Db 604 GGTGCCCTAGGATTTCTTAGCTTT---GCCAGGAATCCTGAGGCTCCAGGGAACATGGGT 660
Qy 562 CTTAAGATCAAGTATGAGCTTGCATTGGATTAAATTAATTTGGCCCACTTTGGTGGC 621
Db 661 TTATTGATCAACAGTCTGCTTCATGAGTGGTTCAAAAAATATATGACCTTTGGTGA 720
Qy 622 AATCCGATTAATTAACAGCTTTGGTGAAGTGGCGGTGCTGCTC 668
Db 721 AATCCTAAAGTGAACCTCTTTGGAGAAAGTGCAGAGCAGCTTC 767

RESULT 5

US-09-748-739A-3
: Sequence 3, Application US/09748739A
: Patent No. US20020119489A1
: GENERAL INFORMATION:
: APPLICANT: Lockridge, Oksana
: APPLICANT: Watkins, Jeffrey D.
: TITLE OF INVENTION: Butyrylcholinesterase Variants and
: FILE REFERENCE: P-IX 4143
: CURRENT APPLICATION NUMBER: US/09/748,739A
: CURRENT FILING DATE: 2000-12-06
: NUMBER OF SEQ ID NOS: 31

: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 2416
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Human Butyrylcholinesterase variant
: NAME/KEY: CDS
: LOCATION: (214)....(1935)
US-09-748-739A-3

Query Match

3.7%: Score 63.8; DB 10; Length 2416;
Best Local Similarity 55.0%; Pred. No. 2.6e-06;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

Qy 325 GAGAGTTGCTATACCTACCTAGTGTCTATAGCAATATCTAAATCCCGAAGCTAACGTCCTC 384
Db 481 GAAGACTGTTTATATCTAAATGATGATGATCCAGACCTAAAC---AAAAATGCCACT 537
Qy 385 GTTTAGTATACATACATGAGTGGTGGTTTATTCGCTGAAATATCATGTCATATGAT 444
Db 538 GTATTGATATGATGATTTATGAGTGGTGGTTTCAACTGCAACATCATCTTACATGTTAT 597
Qy 445 GTCCTGATTTATTCATTAAGAAAGA---TGTGCTGTTGATTAACATACATATGCTTTG 501
Db 598 GATGGCAAGTTCTGCTGGCTGTAAGAGTTATTTAGTGTCAATGATATAGGGTG 657
Qy 502 GGAGCTAGGTTTCTAAGTTTAATTCAGAAAGCTTAATGTCGCCGTTATGCCGCGC 561
Db 658 GGTGCCCTAGGATTTCTTAGCTTT---GCCAGGAATCCTGAGGCTCCAGGGAACATGGGT 714
Qy 562 CTTAAGATCAAGTATGAGCTTGCATTGGATTAAATTAATTTGGCCCACTTTGGTGGC 621
Db 715 TTATTGATCAACAGTCTGCTTCATGAGTGGTTCAAAAAATATATGACCTTTGGTGA 774
Qy 622 AATCCGATTAATTAACAGCTTTGGTGAAGTGGCGGTGCTGCTC 668
Db 775 AATCCTAAAGTGAACCTCTTTGGAGAAAGTGCAGAGCAGCTTC 821

RESULT 6

US-09-748-739A-5
: Sequence 5, Application US/09748739A
: Patent No. US20020119489A1
: GENERAL INFORMATION:
: APPLICANT: Lockridge, Oksana
: APPLICANT: Watkins, Jeffrey D.
: TITLE OF INVENTION: Butyrylcholinesterase Variants and
: FILE REFERENCE: P-IX 4143
: CURRENT APPLICATION NUMBER: US/09/748,739A
: CURRENT FILING DATE: 2000-12-06
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 2416
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Human Butyrylcholinesterase variant
: NAME/KEY: CDS
: LOCATION: (214)....(1935)
US-09-748-739A-5

Query Match

3.7%: Score 63.8; DB 10; Length 2416;
Best Local Similarity 55.0%; Pred. No. 2.6e-06;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

Qy 325 GAGAGTTGCTATACCTACCTAGTGTCTATAGCAATATCTAAATCCCGAAGCTAACGTCCTC 384
Db 481 GAAGACTGTTTATATCTAAATGATGATGATCCAGACCTAAAC---AAAAATGCCACT 537

;; TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
;; FILE REFERENCE: 0342/16548-US2
;; CURRENT APPLICATION NUMBER: US/09/893,519A
;; CURRENT FILING DATE: 2001-06-28
;; PRIOR APPLICATION NUMBER: US 60/215,164
;; PRIOR FILING DATE: 2000-06-29
;; PRIOR APPLICATION NUMBER: US 60/224,457
;; PRIOR FILING DATE: 2000-08-10
;; NUMBER OF SEQ ID NOS: 146
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 112
;; LENGTH: 2444
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: Human Genbank/NM_000055
;; DATABASE ENTRY DATE: 2001-02-03
;; RELEVANT RESIDUES: (1)..(2444)
US-09-893-519A-112

Query Match 3.7%; Score 63.8; DB 9; Length 2444;
Best Local Similarity 55.0%; Pred. No. 2,6e-06;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACCTAGTGTCTATACGAATTAATCTAAATCCGGAACCTAAAGCTCC 384
DB 509 GAAGACTGTTATATCTAATATGATGATCCAGCACCCTAAACC---AAAAATGCCACT 565
QY 385 GTTTTAGTATACATACATGCTGCTGTTTATATCGGTGAATATCATGCTATATGAT 444
DB 566 GTATTGATATGATGATTTATGCTGCTGTTTCAACCTGCAACATCTTACATGTTAT 625
QY 445 GGTCTGATTTTTCATTAATAAAGA---TGTGCTGTTGATTAACATACATATGCTTTG 501
DB 626 GATGCCAATTTCTGCTGCTGCTGGAAGATTTGATGTCATGATGATAGAGG 685
QY 502 GGAGCTAGTGTCTTCTAATTAATTCAGAAGCTTAATGTCGCCGTAATGCCGC 561
DB 686 GGTGCCCTAGTATCTTACTTT---GCCAGGAATCTCGAGGCTCCAGGAACATGGGT 742
QY 562 CTTAAGATCAAGTACGCTTGCATTTGATTAATAAATATGCGCCACTTTGGTGC 621
DB 743 TTAATTGATCAACAGTGTGCTTCAGTGGGTTCAAAAAAATATGACAGCTTTGGTGA 802
QY 622 AATCCGATATATTACATCTTTGTTGTAAGTGGCGTGCCTC 668
DB 803 AATCTTAAAGTGTACTCTCTTTGGAGAAGTGAGGAGCAGCTTC 849

RESULT 10
US-09-974-300-1107
;; Sequence 1107, Application US/09974300
;; Patent No. US20020146721A1
;; GENERAL INFORMATION:
;; APPLICANT: Beika, Randy M.
;; APPLICANT: Clausen, Ib Groth
;; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
;; FILE REFERENCE: 10085,500-US
;; CURRENT APPLICATION NUMBER: US/09/974,300
;; CURRENT FILING DATE: 2001-10-05
;; PRIOR APPLICATION NUMBER: 09/680,598
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 60/279,526
;; PRIOR FILING DATE: 2001-03-27
;; NUMBER OF SEQ ID NOS: 8481
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1107
;; LENGTH: 657
;; TYPE: DNA
;; ORGANISM: Bacillus licheniformis
US-09-974-300-1107

Query Match 3.5%; Score 59.4; DB 10; Length 657;
Best Local Similarity 50.1%; Pred. No. 1.7e-05;
Matches 175; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 377 AACGCCCTTTAGTATACATACATGCTGCTTTATATTCGG---TGAAATCATC 433
DB 30 ATCTGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 89
QY 434 GTGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
DB 90 CGCTTATGACGGGACTACGCTTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 149
QY 494 ATGCTTTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
DB 150 ATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209
QY 554 ATGCGGCTTAAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
DB 210 ATCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
QY 614 TTGCTGCGCATCCCATATATATACATGCTTGTGGAAGTCCGCTGCTGCTACCC 673
DB 270 TTGGGCGAGACCGTATCATATGATGCTTGTGGAAGTCCGCTGCTGCTGCTGCTGCT 329
QY 674 ACTACATGATGCTTAAACCGAACAACCTCGCTGCTTTCATGCTGCTGCTGCT 722
DB 330 CTTCGCTTTTGGCGATGCCGAAGCAAGGCGCTTTTCAACAGCCCAT 378

RESULT 11
US-08-781-986A-43
;; Sequence 43, Application US/08781986A
;; Publication No. US20030054436A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunsch
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5255
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MS-DOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/781,986A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Benson, Bob
;; REGISTRATION NUMBER: 30,446
;; REFERENCE/DOCKET NUMBER: PB248BP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3606 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
US-08-781-986A-43

Query Match 3.3%; Score 56.4; DB 7; Length 3606;
Best Local Similarity 52.1%; Pred. No. 0.00027;

	Matches	176; Conservative	0;	Mismatches	156;	Indels	6;	Gaps	2
QY	325	GAGCATTTGCTAATACCTTAAGTGTCTATAACGAATAATCTAAATCCCGAANCTAACSTCCC							384
Db	2729	GAAAGCTCTTTAATATCAATATAT---TTGGAAACAACATAAATGATCAGACGAGAAGAAACCT							2785
QY	385	GTTTTAGATACATTCAGTAGTGTCGGTGTATTATTCGGGAAAATCATCGTGATATGAT							444
Db	2786	GTCAATCATTATTTTATTTATGTGGTGTGTTTGAATAATGGTCATGTRACAGCCGCAACTCTAT							2845
QY	445	GGTCCTGATTAATTTTCAT--TAAAAAGCATGTGGTGTGATTAACATACATATCGTTG							501
Db	2846	CACCGGCACATTTAGTACAAAAATAACGACATTAATCGTATTATACATGCAATATATCGTTA							2905
QY	502	GGAGCTTAGAGTTTTCTAAGTTTAAATTCAAGAACCTTAATGTGCCGGTAATGCCGCG							561
Db	2906	GGCCGATTAGGATATTTAGACTGTGCATATTTTAAATAAGATTTTCATTCACATTAATGCG							2965
QY	562	CTTAAAGATCAAGTCATAGGCCCTTGATTTGATTTAAAAAATTAATTCGCCCAACTTTGGTGGC							621
Db	2966	CTTTTCAGATCAAATCAAAATGTCTATAAANAATGGCGGCATCAATTTATGTAATCTCGGTGGCG							3025
QY	622	AATCCGATTAATATTACAGTCTTTGGTGAAGATCGCGG							659
Db	3026	GACGCTAATTAACATTACTTTAATGGGTCAAGTGTCCAGG							3063

RESULT 12
US-09-934-323-3
Sequence 3, Application US/09934323
Patent No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: Curfiss, Rory A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
FILE REFERENCE: 10448-081001
CURRENT APPLICATION NUMBER: US/09/934.323
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2508
TYPE: DNA
ORGANISM: Homo sapiens
US-09-934-323-3

Query Match 3.3%, Score 56; DB 10; Length 2508;
Best Local Similarity 53.7%; Pred. Mismatches 100; Gaps 0;
Matches 116; Conservative 0; NoMatches 16; Indels 0;

QY 530 CAGAACCTTAAATGTGCCCGGSTATGCCGGCCTTAAGAATCAAGTCATGGCCTTGCAATT 589
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 671 CCGGGGACCAGGCTCCAAAAGGCACATATGCGCTCTCTGGACACAGATCCAGGCGCTGCGCT 730
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 590 GGATTTAAATAATTAATTCGCGCCCAACTTTGGTGGCAATCCCGCATTAATATTAACAGTCTTTGGTG 649
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 731 GGCTACAGTAAGAAACAATCGCCCACTTTGGGGGGGAGACCCGACGGGTATCACACATCTTTGGTT 790
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 650 AAAGTCCCGGTCGTCCTCTTACCCACATCAATGATGTGTTAAACGAACAACAACTCCGCGTCTTT 709
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 791 CCGGGGACGAGGGGCCCTCGCGGTCAACCTTCTGATCTCCACCAATTCAGAAAGGCGCTGT 850
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 710 TCCATCGTGTAATACTAATATGTCGGGTATGCAATTT 745
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 851 TCACGAAGGCCATCGCCACAGAGTGGCACCGCATTTT 886
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
US-09-934-323-1
Sequence 1, Application US/09934323
Patent No. US20020150910A1

```

: GENERAL INFORMATION:
: APPLICANT: Curtis, Roy A. J
: TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
: TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
: FILE REFERENCE: 10448-081001
: CURRENT APPLICATION NUMBER: US/09/934,323
: CURRENT FILING DATE: 2001-08-21
: PRIOR APPLICATION NUMBER: US 60/226,774
: PRIOR FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 4667
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (420)...(2924)
: US-09-934-323-1

3.3%; Score 56; DB 10; Length 4667;
Best Local Similarity 53.7%; Pred. No. 0.0004;
Matches 116; Conservative 0; Mismatches 100; Indels 0; Gaps 0

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Oy      590   GGATTAAATAATTTGGCGCACTTGTGAGGCACATCCCATATTAATCAGTCCTTGSTG    649
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1150  GCGTAGTGAANAACAATGCCCACCTTTGGGGGCGACCCCAGCGTATACCANTCTTGGTT    1209
           +-----+
Oy      650   AAGTCCGGGTGCTGCTCTTACCCAATCATGATGTAAACGAGAAMAATCGCGCTCTT     709
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1210  CCGGGGCGAAGGGGCTCTCGCGCGTCAACACTTCGTATCCTCTCCACCATTCAGAAGGGCTGT    1269
           +-----+
Oy      710   TCCATCGTGTACTAATGTGTGGGTAATGCTATT       745
           ||||| +---+ || +----+ |||||
Db      1270  TCAGAAAGGCCATCGCCCCAGAGTGGCAGCGCATTT     1305
                                           +-----+
RESULT 14
US-09-418-176-1
; Sequence 1, Application US/09418176
; Publication No. US20030040040a1
; GENERAL INFORMATION:
; APPLICANT: Das, Goutam
; TITLE OF INVENTION: DNA Molecules for Expression of
;                   POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0 , Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/418,176
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/624,398
; FILING DATE: 04-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SB96/00318
; FILING DATE: 12-MAR--1996
; PRIOR APPLICATION DATA:

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GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 2944.03 Seconds

(without alignments)
16933.650 Million cell updates/sec

Title: US-09-776-910-7

Sequence: 1 atgaattcaacgttagttt.....aacatagagattatttttag 1713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
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7: gb_ph:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1713	100.0	1713	6 AR153441	AR153441 Sequence
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4	1703.4	99.4	1713	6 AR153442	AR153442 Sequence
5	1701.8	99.3	1713	6 AR153438	AR153438 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS DEFINITION Sequence 1 from patent US 5843758.
ACCESSION AR062837
VERSION AR062837.1 GI:5990528
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.,Joyce,, Newcomb,R.,David,, Robin,G.,Charlesde,Quetteville,,
Boyce,T.,Mark,, Campbell,P.,Malcolm,, Parker,A.,Gerard,,
Oakesholt,J.,Graham, and Smyth,K.-A.
TITLE Enzyme based bioremediation

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: US 5843758-A 1 01-DEC-1998;
 FEATURES Location/Qualifiers
 source 1..1713
 BASE COUNT 516 a 305 c 370 g 522 t
 ORIGIN

Query Match 100.0%; Score 1713; DB 6; Length 1713;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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 LOCUS DEFINITION
 ACCESSION ARI53441
 VERSION ARI53441.1 GI:15120973
 KEYWORDS
 SOURCE
 ORGANISM
 UNKNOWN.
 UNCLASSIFIED.
 REFERENCE
 1 (bases 1 to 1713)
 Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolm, Robin, G. Charlesde, Quetleville, Claudianos, C., Smyth, K. A., Boyce, T. Mark, Oakeshott, D. Graham, and Brownlie, J. Colin.
 Malathion carboxylesterase
 TITLE JOURNAL
 FEATURES Patent: US 6235515-A 7 22-MAY-2001;
 Location/Qualifiers
 source 1..1713

BASE COUNT 516 a /organism="unknown" 305 c 370 g 522 t
ORIGIN

Query Match 100.0%; Score 1713; DB 6; Length 1713:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
LCU56636
LOCUS 2240 bp mRNA linear INV 10-JAN-2002
DEFINITION Lucilia cuprina alpha esterase (lcaet7) mRNA, implicated in organophosphate resistance, complete cds.
ACCESSION U56636
VERSION U56636.1 GI:1336079
KEYWORDS
SOURCE
ORGANISM
Lucilia cuprina.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Lucilia.
REFERENCE
1 (bases 1 to 2240)
Newcomb R.D., East P.D., Russell R.J. and Oakeshott J.G.
Isolation of alpha cluster esterase genes associated with organophosphate resistance in *Lucilia cuprina*
Insect Mol. Biol. 5 (3), 211-216 (1996)
JOURNAL MEDLINE
96392952
PUBMED
8799740
REFERENCE
2 (bases 1 to 2240)

AUTHORS	Newcomb,R.D., Campbell,P.M., Russell,R.J. and Oakeshot,J.G.
TITLE	cDNA cloning, baculovirus-expression and kinetic properties of the esterase, E3, involved in organophosphorus resistance in Lucilia cuprina
JOURNAL	Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
MEDLINE	97215578
PUBMED	9061925
REFERENCE	3 (bases 1 to 2240)
AUTHORS	Newcomb,R.D., Campbell,P.M., Ollis,D.L., Cheah,E., Russell,R.J. and Oakeshot,J.G.
TITLE	A single amino acid substitution converts a carboxylesterase to an organophosphorus hydrolase and confers insecticide resistance on a blowfly
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997).
MEDLINE	97352821
PUBMED	9207114
REFERENCE	4 (bases 1 to 2240)
AUTHORS	Campbell,P.M., Newcomb,R.D., Russell,R.J. and Oakeshot,J.G.
TITLE	Two different amino acid substitutions in the all-esterase, E3, confer alternative types of organophosphorus insecticide resistance in the sheep blowfly
JOURNAL	Unpublished
REFERENCE	5 (bases 1 to 2240)
AUTHORS	Newcomb,R.D., Campbell,P.M., Russell,R.J. and Oakeshot,J.G.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-1996) Richard D. Newcomb, Molecular Genetics, HortResearch, Private Bag 92 169, Auckland, New Zealand
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0; Gaps	0; Indels	0; Gaps
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QY 181 ATACCGTACGCCCAACCGCCAGTGGTGCAGATTTAAAGCAACCCAGGACACACA		
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QY 241 CCTGGGATGATGCTGCTGATTTGTCATATCAATTAAGATTAAGTCAAGTGAATTT		
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QY 301 ATACCGGCAAGTGTGTGGCTCAGAGATGCTATACCTAAGTGTATACGAATAT		
DB 598 ATACCGGCAAGTGTGTGGCTCAGAGATGCTATACCTAAGTGTATACGAATAT		
QY 361 CTAAATCCCGAAATCAACGTCGCCGTTTAAATACATACATGCTGTGTTTATTATC		
DB 658 CTAAATCCCGAAATCAACGTCGCCGTTTAAATACATACATGCTGTGTTTATTATC		
QY 421 GGTGAATATCATCTGATATGTATGGTCCGTATTTCAATTAAGAGATGGGCTTG		
DB 718 GGTGAATATCATCTGATATGTATGGTCCGTATTTCAATTAAGAGATGGGCTTG		
QY 481 ATTAACATACAAATATGTTTGGAGCTCAGGTTTCTAAGTTTAAATTCAGAACCTT		
DB 778 ATTAACATACAAATATGTTTGGAGCTCAGGTTTCTAAGTTTAAATTCAGAACCTT		
QY 541 AATGTCCCGGTAATATGCCGCTTAAAGATCAAGTATGCGCTTGGTGTGATTAAT		
DB 838 AATGTCCCGGTAATATGCCGCTTAAAGATCAAGTATGCGCTTGGTGTGATTAAT		
QY 601 AATGTGGCAACCTTGGTGCAATCCCGAATATTAATTAACAGTCTTGGTGAAGTCCCGT		
DB 898 AATGTGGCAACCTTGGTGCAATCCCGAATATTAATTAACAGTCTTGGTGAAGTCCCGT		
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DB 958 GCTGCTTACCCACATCATGATGTTAACCGAACAATCTGGGCTTTTCCATGCTGT		
QY 721 ATACTAATGTCGGGTAATGTTATTTGCCATGGGTAATCCCAATGTCAACATCGTGC		
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QY 781 TTACCTTACCCAAATTTGGCGGCTTAAGGTGAGATTAATGATTAAGATGTTTGGAA		
DB 1078 TTACCTTACCCAAATTTGGCGGCTTAAGGTGAGATTAATGATTAAGATGTTTGGAA		
QY 841 TTTCTTATGAAGCCACAGCATTTAATAAATCTGAGAAATAAGTTTAACTGTA		
DB 1138 TTTCTTATGAAGCCACAGCATTTAATAAATCTGAGAAATAAGTTTAACTGTA		
QY 901 GAAGAGGTCAATTAAGTATGTTTCTTTGTCCTTGAAGCATATTCAGAC		

Db 1198 GAAGAGCGTACAAATAGATGCTATCTTCTTTGGTCCCACTGTTGAGCCATATCAGACC 1257
Qy 961 GCTGATTTGTCTTACCCAAACATCCTCGGAAATGTTAAAGCTGTGGGTAATTGCG 1020
Db 1258 GCTGATTTGTCTTACCCAAACATCCTCGGAAATGTTAAAGCTGTGGGTAATTGCG 1317
Qy 1021 ATACCACATATGATGGGTAGACACTTATGAGGTCATTTTTCACCTCAATTCCTTAAG 1080
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Qy 1081 CAATGCTTATGCTTTTAAAGAACTTGTGCAATTTTGTGCCAAGTGAATTG 1140
Db 1378 CAATGCTTATGCTTTTAAAGAACTTGTGCAATTTTGTGCCAAGTGAATTG 1437
Qy 1141 GCTGATGCTGAAGCGACCGCCCAAGAGACTTGGAAATGGTGCATAATTAAGAAAGCT 1200
Db 1438 GCTGATGCTGAAGCGACCGCCCAAGAGACTTGGAAATGGTGCATAATTAAGAAAGCT 1497
Qy 1201 CATGTTACAGAGAGAAACCAACAGCTGATATTTTATGATCTTTGCTCCACATCTAT 1260
Db 1498 CATGTTACAGAGAGAAACCAACAGCTGATATTTTATGATCTTTGCTCCACATCTAT 1557
Qy 1261 TTTCTGTTCCCATGATGCTTTTGTGCAATTTAGCTTTCATACACCTCCGATACACC 1320
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Qy 1321 GTCCTACTGTATGCTTGTGACTTTGATTCGGAAGATCTTATTAATCCTATCGTATTATG 1380
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Qy 1381 CGTAGTGACGCTGTGTTAAGGGTGTATGCTATGCTGATTAACCTATTTCTTCTG 1440
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Qy 1441 AATCAATTTGGCCAAACGATATGCTTAAGAAATCGCGTGAATACAAACATTTGAACGATG 1500
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Qy 1501 ACTGATATGATGATATGATTTGGCAACGCTGTATCCTTTATAGCAATGAATTTGAAGT 1560
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Qy 1561 ATGCAAAATGTTCTCGTGATCCAAATTAAGAAATCCGACGAAGTATACAGTGTGAT 1620
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Qy 1621 ATTAGTACGAATTTGAATGATGATGCTGCTGAATGATTAAGATTAACAATGGGAA 1680
Db 1918 ATTAGTACGAATTTGAATGATGATGCTGCTGAATGATTAAGATTAACAATGGGAA 1977
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Db 1978 TCGATGTTGAAAAACATAGAGATTTATTATG 2010

RESULT 4
AR153442 1713 bp DNA linear PAT 08-AUG-2001
LOCUS AR153442 Sequence 9 from patent US 6235515.
DEFINITION AR153442
ACCESSION AR153442.1 GI:15120974
VERSION AR153442.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Roblin, G. Charlesde, Ouetleville., Claudinon, C., Smyth, K. A.,
Boyce, T. Mark., Oakeshort, J. Graham. and Brownlie, D. Colin.
TITLE Malachon carboxylesterase
JOURNAL Patent: US 6235515-A 9 22-MAY-2001;
FEATURES location/Qualifiers
source 1..1713

BASE COUNT 515 a /organism="unknown"
ORIGIN 305 c 370 g 523 t
Query Match 99.4%; Score 1703.4; DB 6; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 1 ATGATTTTCAACGTTAGCTTATGAGAAATTAATAATGAAATTAATGATTTGAAT 60
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Qy 361 CTAATATCCGAACTAAACGTCCTGTTTAACTATACATACATGCTGCTTTATATTC 420
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Qy 481 ATTAACATACATATGCTTTTGGAGCTCTAGCTTTTCTAAGTTTAATTAAGAACTT 540
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Qy 541 AATGTCGGGCTAATGCGGCTTAAGATCAAGTATGCGCTTGTGATTAATAAT 600
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Qy 601 AATGCGGCAACTTGTGTTGGCAATCCGATATTAATTAAGTCTTGTGAAGTCCGGT 660
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Qy 901 GAAGAGCTACAAATTAAGTATGCTTTTGTGCTCCACTGTTGAGCCATATACAGC 960
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Qy 961 GCTGATTTGTCTTACCCAAACATCCTCGGAATGTTAAACCTGTTGGGTAATTCG 1020

|||||
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 Db 1621 ATTATGACAGATTTGAATGATGATGCTGAAATGATGATGATGATGATGATGATGATG 1680
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 Db 1681 TCGATGTTGAAACATAGAGATTTATTTAG 1713

RESULT 5
 ARI53438 1713 bp DNA linear PAT 08-AUG-2001
 LOCUS ARI53438
 DEFINITION Sequence 1 from patent US 623515.
 ACCESSION ARI53438
 VERSION ARI53438.1 GI:15120970
 KEYWORDS
 ORGANISM Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolm, Robin, G. Charles, Queteleville, Claudianos, C., Smyth, R. A., Boyce, T. Mark, Oakeshott, J. Graham, and Brownlie, J. Colin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 623515-A 1 22-MAY-2001;
 FEATURES location/Qualifiers
 source 1..1713
 /organism="unknown"

BASE COUNT 515 a 304 c 370 g 524 t
 ORIGIN

Query Match 99.3%; Score 1701.8; DB 6; Length 1713;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGATTTCAACGTTAGTTGATGAGAAATTAATAAGAAATTAATGATGATGATGATGATGATG 60
 Db 1 ATGATTTCAACGTTAGTTGATGAGAAATTAATAAGAAATTAATGATGATGATGATGATGATG 60
 QY 61 AAGTTTAACTATGTTTAACCAATGAACGGGTGAGTCAAACTGATGATGATGATGATGATG 120
 Db 61 AAGTTTAACTATGTTTAACCAATGAACGGGTGAGTCAAACTGATGATGATGATGATGATG 120
 QY 121 AAGTGAAGGGGTTAAAGTTAACTGATGATGATGATGATGATGATGATGATGATGATGATG 180
 Db 121 AAGTGAAGGGGTTAAAGTTAACTGATGATGATGATGATGATGATGATGATGATGATGATG 180
 QY 181 ATACCGTACGCCAACCGGCAAGTGGTGAAGGATGATGATGATGATGATGATGATGATGATG 240
 Db 181 ATACCGTACGCCAACCGGCAAGTGGTGAAGGATGATGATGATGATGATGATGATGATGATG 240
 QY 241 CCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 Db 241 CCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 301 ATACCGGCAAAAGTGTGTGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATG 360
 Db 301 ATACCGGCAAAAGTGTGTGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATG 360
 QY 361 CTAATCCCGAAATTAACGTCCTGTTTATGATGATGATGATGATGATGATGATGATGATGATG 420
 Db 361 CTAATCCCGAAATTAACGTCCTGTTTATGATGATGATGATGATGATGATGATGATGATGATG 420
 QY 421 GGTGAATATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 421 GGTGAATATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 481 ATTATCATGATATGCTGTTGGAGCTCTAGTGTGTTTAAAGTTAAATTCAGAAAGCTT 540
 Db 481 ATTATCATGATATGCTGTTGGAGCTCTAGTGTGTTTAAAGTTAAATTCAGAAAGCTT 540
 QY 541 AATGTGCCCGGTAATGCGGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATG 600
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 QY 601 AATGGCCCAACTTGTGTCGCAATCCGATATATTTACAGCTTGTGTAAGGATGATGATGATG 660
 Db 601 AATGGCCCAACTTGTGTCGCAATCCGATATATTTACAGCTTGTGTAAGGATGATGATGATG 660
 QY 661 GCTGCTTACCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 Db 661 GCTGCTTACCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 QY 721 ATACTATGTCGCGTATGCTATTTGTCAGTGGCTAATCCCAATGATGATGATGATGATGATG 780
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 QY 781 TTCACTTACCCCAATTTGCGGCTTAAGGATGATGATGATGATGATGATGATGATGATGATG 840
 Db 781 TTCACTTACCCCAATTTGCGGCTTAAGGATGATGATGATGATGATGATGATGATGATGATG 840
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 Db 841 TTCTTATGAAGCCAGCCAGATTTAATTAACCTGAGAAAGTTTAACTGATGATGATGATGATG 900
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 Db 901 GAAGAGCTACAAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 QY 961 GCTGATGCTTACCAACATGCTCGGAAATGATGATGATGATGATGATGATGATGATGATGATG 1020
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[illegible]

QY 1081 CAATGCTATGCTTGTAAAGAACTTGTCAATTTTGTGCCAAGTAATG 1140
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DB 1141 GGTGATGCTAAGCAGCCGCCAGAGACCTTGGAAATGGTCTAAATTAAGAGCT 1200
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QY 1261 TTCTGTTCCCATGATGCTTTGTTCATTAAGTTCAATCAACCCGGGTACACCC 1320
DB 1261 TTCTGTTCCCATGATGCTTTGTTCATTAAGTTCAATCAACCCGGGTACACCC 1320
QY 1321 GTCTACTTGTATGCTTGCAGCTTGTATTCGAGATCTTAATCCCTATGATTAATG 1380
DB 1321 GTCTACTTGTATGCTTGCAGCTTGTATTCGAGATCTTAATCCCTATGATTAATG 1380
QY 1381 CGTAGTGAGCTGCTTTAAGGCTTTAAGTATGCTGATTAATTAACCTATTTCTTGG 1440
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QY 1441 AATCAATTTGGCCAAAGCATGCTTAAGAAATCCGCTGAATACAAATTAAGACATG 1500
DB 1441 AATCAATTTGGCCAAAGCATGCTTAAGAAATCCGCTGAATACAAATTAAGACATG 1500
QY 1501 ACTGATATGATGATCAATTTGCCACCACTGTATCTTAATCCCTATGATTAATG 1560
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DB 1621 ATTGATGATGATTAAGAAATGATGATGCTGAATGAATGAATTAAGATTAAGATG 1680
QY 1681 TCGATGTTGAAAAAATGATGATGATTTTATG 1713
DB 1681 TCGATGTTGAAAAAATGATGATGATTTTATG 1713

RESULT 7
ARI53440 1713 bp DNA linear PAT 08-AUG-2001
LOCUS Definition Sequence 5 from patent US 6235515.
ACCESSION ARI53440
VERSION ARI53440.1 GI:15120972
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1713)
Russell, R. Joyce, R. Newcomb, R. David, Campbell, P. Malcolm, Robin, G. Charles, Queteville, Claudianos, C., Smith, K. A., Boyce, J. Mark, Oakeshott, J. Graham, and Brownlie, J. Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 5 22-MAY-2001;
FEATURES Location/Qualifiers
source 1..1713
BASE COUNT 516 a 305 c 369 g 523 t
ORIGIN

Query Match 99.2%; Score 1698.6; DB 6; Length 1713;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAATGAGATTAATGCAATTGAAAT 60
QY 61 AAGTTTAACTATGCTTTAACTACCAATGAAGAGGAGTGAAGCAATGATATGCT 120
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DB 1021 ATACCACTATGAT 1080
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Db 1141 GCTGATGCGAAGCGACCGCCCGGACAGACCTTGGAAATGCGTGCCTAAATTTAAAAAGCT 1200
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Oy 1381 GCTAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
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RESULT 8
AR062838 1713 bp DNA linear PAT 29-SEP-1999
LOCUS AR062838
DEFINITION Sequence 2 from patent US 5843758.
ACCESSION AR062838
VERSION AR062838.1 GI:5990529
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN

Query Match 98.2%; Score 1683; DB 6; Length 1713;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1683; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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Db 1 ATGAATTTCAACGTTAGTTTGATGAGAAATTAATTAATGATTAATGATTAATGATTAATGAT 60

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QY	661	GCNCCCTPACCCATCTACATGATGTAAACGAAACAACACCGGGCTTTTCCATCGTGT	720
Db	877	GGGGCTPAAACCCATTTACATGATGATPACCGAACACACCGGTTTATTTCCATGTGT	936
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Db	937	ATCATGATGTCCGGTATTTCCATGTGCTCATATGGGCCCTACAGAAATCCAAAGTGTGTGG	996
QY	781	TTCACTTAGCCAAATTTGGCCGGCTTAAAGGTGAGGATTAATGATPAGGATTTTGGAA	840
Db	997	CTCACACATGGCCAAACCTGTGTGCTTAAAGGGAGAGACAATGAAGAAAGATPCTCTGAA	1056
QY	841	TTTTTTTAAAGCAAGCCACAGAGATTAATATAAACTTGAGGAAAAATTTTAACCTGA	900
Db	1057	TTCTTAATGAAGACCAATCCCTTATGATTTGATTAAGAGAGACCACAGTTTTGACACCC	1116
QY	901	GAGAGCGTACAAATTAAGTGCATGTTCCTTTTGTCCAGCTGTGTAGGCATATCAGAC	960
Db	1117	GAAAGAAATGCAAAATATAGTCATGTTCCCTTTTGGACCCACATGTAGAACATACCA	1176
QY	961	GCTGATTTGTCTTACCCAAACATCCCGGGGAAATGGTAAACATGCTGGGGTAAATCG	1022
Db	1177	GCCGACGTGTGTGATACCCAAACCAATCAGAGAAATGTAAAGAGCCCTGGGGAAATTCG	1233
QY	1021	ATACCCACTATGATGGGTAACTTCATATAGAGGTCTATTTTCTACTTCATTTCTTAAG	1080
Db	1237	ATACCCACTATGATGAGCAATPACCTCTCAGAAAGTTTCTTTCAATCAATTTGCAAA	1296
QY	1081	CAAAATGGCTATGCTGTGTAAGAAATTTGGAAACCTGTGTCAATTTTGTGCCAAGTAA	1144
Db	1297	CAAAATCCGGAGGTGTGTAAGAAAGTTGGAATCCTGTGTAAATTAATGTGCTTGGGAAGTT	1356
QY	1141	GCTGATCTGTAAGCACACCGCCACAGAGACCTTGGAAATGGGTCTAAATTTAAAGAGCT	1200
Db	1357	GCTGACAGTGAACGCACTGTGCCGGGAAACCTGTGAAGGGTGCATTTGAAAGAGCC	1416
QY	1201	CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTTGCTCTCACATCTAT	1266
Db	1417	CATGTGATGGGAAACACCTACTCTGGAATAATTTATGAGACCTTTCCTCATATTTCTAT	1476
QY	1261	TTTCGTGTTCCCATGCATTCGTTTGTTCGATTAACGTTTCAATCACACCTCCGTTACCC	1320
Db	1477	TTTCCTCTCCCATGCAATTCGCTTCCTACATTTCCGCTTACACACACAGCTGGCACTCC	1536
QY	1321	GTCATCTTATGCTGTGCACTTGTGATGGGAAGATCTTAATPACCTATCGATTAATG	1386
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QY	1381	CGTGTGAGAGTGTGTTAAGGGTGTAGTCATGCAATGATGAATTAACCTATTTCTTGG	1444
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QY	1441	AATCAATTTGGCCAAACCTATGACCTTAAAGATCGCTGAATACAAAACATTTAAAGTATG	1500
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QY	1561	ATGGAATAATGTTTCCTGGATTCCAATTAAGAAATTCGAGAGTATATCAAGTGTGAT	1622
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QY	1621	ATATAGTACGAATTTGAATATGATTTGTGCTCGAATGGATTAAGATTAACATATGGGA	1680
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RESULT 10	AF139082	2175 bp	mRNA	linear	INV 20-OCT-2000
LOCUS	AF139082				
DEFINITION	Haemacobia irritans irritans alpha E7 esterase (ae7) mRNA, complete cds.				
ACCESSION	AF139082				
VERSION	AF139082.1				
KEYWORDS	GI:6502938				
SOURCE	Haemacobia irritans irritans.				
ORGANISM	Haemacobia irritans irritans.				
REFERENCE	Neukarya: Metazoa: Arthropoda: Hexapoda; Insecta: Pterygota; Neoptera: Endopterygota; Diptera: Brachycera; Muscomorpha; Muscoidae; Muscidae; Haemacobia.				
AUTHORS	1 (bases 1 to 2175)				
TITLE	Guerrero, F.D.				
JOURNAL	Cloning of a horn fly cDNA, HialphaE7, encoding an esterase whose transcript concentration is elevated in diazinon-resistant flies				
MEDLINE	Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)				
PUBMED	2045807				
REFERENCE	10989298				
AUTHORS	2 (bases 1 to 2175)				
TITLE	Guerrero, F.D.				
JOURNAL	Direct Submission				
FEATURES	Submitted (30-MAR-1999) USDA-ARS, Knippling-Bushland U.S. Livestock Insects Research Laboratory, 2700 Fredericksburg Rd., Kerrville, TX 78028, USA				
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ORIGIN					
Query Match	56.0%; Score 959.4; DB 3; Length 2175;				
Best Local Similarity	72.5%; Pred. No. 1e-203;				
Matches 1242; Conservative	0; Mismatches 471; Indels 0; Gaps 0;				
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 DB 1962 AGTGTTCATATGAAAGCGGAAATTTGTTAG 1994
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 ARI53445
 LOCUS ARI53445 1710 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 14 from patent US 6235515.
 ACCESSION ARI53445
 VERSION ARI53445.1 GI:15120977
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1710)
 AUTHORS Russell, R. Joyce, R. Newcomb, R. David, Campbell, P. Malcolm, Robin, G. Charles, Queteville, Claudianos, C., Smyth, K. A., Boyce, T. Mark, Oakeshott, J. Graham, and Brownlie, J. Colin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 14 22-MAY-2001;
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 Query Match 55.8%; Score 956.6; DB 6; Length 1710;
 Best Local Similarity 73.4%; Pred. No. 4,4e-203; Indels 0; Gaps 0;
 Matches 1223; Conservative 0; Mismatches 444;

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 ACCESSION
 VERSION
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 ORGANISM
 SOURCE
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 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1710)
 AUTHORS
 Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
 Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
 Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J.,
 Nuno, J., Pacle, J., Paragas, V., Park, S., Phouanavong, S., Wan, K.,
 Yu, C., Lewis, S. E., Rubin, G. M. and Celisner, S.
 DIRECT SUBMISSION
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720
 This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila gene collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a polyA tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unspliced precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our web site
 (<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.

FEATURES
 source
 1..2017
 location/qualifiers
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 /strain="y; cn bw sp"
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RESULT 13
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DEFINITION Drosophila melanogaster RE24825 full insert cDNA.
ACCESSION AY121675
VERSION AY121675.1 GI:21464397
KEYWORDS fruit fly,
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2660)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Abmayyan, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G., Miranda, A., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M., and Colniker, S.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA
COMMENT Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720
 This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (<http://fruitfly.berkeley.edu>) or send email to cdna@fruitfly.berkeley.edu.
FEATURES
SOURCE location/Qualifiers
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 /strain="y; cn bw sp"
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 VVISRGALGSLADELDELDPGNALIKOYVALRPMKRNRCORFGDDPNITFGES
 AGGASTHYMMITDQAKLFKHTIIMSGSALAPMAQTTHIMPTRLQATGTTDAND
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 MRDWMKIPVIGNSPEGLMLPPEVNAKPELCOGDCENLAPDOAHVDEOQRKAF
 GKVKRELYFDRTFRGKRTILEYSDLFYKXFMHGHITLTSRAHHAADLAPFLYRPF
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 IYRELLY"
BASE COUNT 724 a 632 c 650 g 654 t
ORIGIN

Query Match 22.0%; Score 377; DB 3; Length 2660;
 Best Local Similarity 53.8%; Pred. No. 9.4e-74;
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 145 ACTGTGTACGATGATCTCTACTACAGTTTGAAGGCTATACCGTACGCCAACCGCAGTG 204
 606 TCCATCTACACCAACACACTACTACAGCTTCGAGGCGATCCGTTGCCAAGCCCGCGGTG 665
 205 GGTGAGTCGATTTAAAGCAACCCAGGACCAACACCTGGAGTGGTGGTATTTGT 264
 666 GCGAGCTCCCTTCAAAGGCGCCGTGGAGCCAGACACTGTCAGATGTCAAGCGGTGC 725
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 325 GAGATTTCTATACCTAGTGTCTATACGAATATTAATCCGAAACTAAACGTCGC 384
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 385 GTTTAGTATACATACATGCTGTGTATTTATATCGGTGAAGAAATCATCGTATTTAT 444
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Db	1550	TCAGGATCAAGGTCGTGGCCCTCCTCAAGTGGATCAAGAACAAATTGGCGTATGTTTCGGCGAG	1609
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Db	1610	ATCCCAACTGCATACACTGTTTTTGGAGAGATGGCTGGAGGCGCCTCCACTCATCATATGA	1669
Qy	683	TGTTAACCGAACAACCGCGGTCTTTCGATCGTGGTATCTATATGTCGGGTAAATGCTA	742
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Qy	743	TTTTGCCATGGGC---TAATACCCAATGTCAACATCGTGCCTTCACCTATACCAAAATTTGG	799
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Qy	800	CCGGCTTAAGGGTGAAGATATGATTAAGATGTTTTGGAAATTTCTATATGAAGCCAAAC	859
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Qy	920	TCATGTTTCCCTTTTGGTCCCACTGTTGAGCATAATCAGACCCTAATGTGCTTTACCA	979
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Qy	980	AACATCTCGGGAATGATTAAATACGTCTTGGGGTAAATTCGATACCACTATGATGGTA	1039
Db	1970	AGGCTCCAAAGGAGATGATATAMACCGCCGTGGGTAATCCATCCCATGTTTATAGAA	2029
Qy	1040	AACCTCATATGAGGGCTATTTTTCACCTCAATTC-----	1075
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Qy	1158	CGCCCCAGAGACCTTGGAAATTTGGGTCTTAAATTAATAAGCTCATGTTACAGAGAAAC	1217
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Qy	1218	ACCAACAGCTGATTAATTTATGAT-----	1242
Db	2270	AAGACCCCAATTAATTAATACATGATGTAAAGTGCCTGCACATTAAGTGTACATATCAT	2329
Qy	1243	-----CTTGGCTGCACATCTAATTTCTGGTTCCCATGCACTTT	1282
Db	2330	AAGCTGTAATTTATTTTTCAGCTCTGTTCATTTACTACTTCTGTGTTCCGGCCCTGAAGG	2389
Qy	1283	TGTTGCAATTAAGCTTTCAATCACAACCTCCGGTACACCCGCTACTTGTATGGCTTCGACT	1342
Db	2390	TGGTCCATTCGCCGACGCGTATGCGGGCTGGAGACTCCAAATATTTCATATGATATGACT	2449
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QY	1583	CAATTAAAGAAATCCGACAGCAATATACAGAGTGTGGAATTAATTAAGCAGCAATTTGAAGAAATGA	1642
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QY	1643	TTGATGTGCTCCGAAATGGATTAAGATTTAAACAATGGGAATCGATGTTTGAAGAAACATAGAG	1702
Db	2750	TGCAATCTCGTAGAGGCGCCCAATTTGAAGGCTGTGGAGAGCGCTGTATATGACCAACAAG	2809
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Db	2810	ATTATTTGT 2818	
RESULT 15	AC015272/c	AC015272	57335 bp
LOCUS	AC015272/c	AC015272	DNA
DEFINITION	Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***	AC015272	linear HTG 16-NOV-1999
ACCESSION	AC015272	AC015272	
VERSION	AC015272.1	GI:6436063	
KEYWORDS	HTG: HTGS_PHASE2.		
SOURCE	Drosophila melanogaster.		
ORGANISM	Drosophila melanogaster.		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prexygota;		
AUTHORS	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
TITLE	Ephyridoidae; Drosophilidae; Drosophila.		
JOURNAL	1 (bases 1 to 57335)		
COMMENT	Adams, M. and Venter, J. C.		
FEATURES	Direct Submission		
source	Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA		
BASE COUNT	17106 a 11816 c 11532 g 16881 t		
ORIGIN	1. 57335		
Query Match	21.6%; Score 370.6; DB 2; Length 57335;		
Best Local Similarity	54.5%; Pred. No. 1.8e-72;		
Matches 1052; Conservative	0; Mismatches 614; Indels 263; Gaps 5;		
QY	46	AAATCATTTGAAATTAAGTTTAACTATGCTTTAACTACCAATGAACGGTGTAGCT	105
Db	36481	AGAACATTCGACATTAAGTCCAGCATGATGCCAGTGGACCAATGAACAGTTTCCGC	36422
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QY	166	TACAGTTTGAAGGTATACCCGACCCCAACCCGACGAGGGGTGAGACTGAGATTTAAACA	225
Db	36361	TTTACCTTCGAGAGGTATCCCTGACCCCAAGCTCCGAGGGGGAATTCGCGTTTAAAGGC	36302
QY	226	CCCCAGCAGCAACACCTCGGATGATGTGCGTGAATTTTGCAATCATTAAGATAAGTCA	285
Db	36301	CCTCAGAGGCCATTCCTCGTGGAGGAGTTCGCCAGCTCAGACGACCGCAAGATTAAGGC	36242
QY	286	GTGCAAGTTGATTTTATTAACGGGCAAGTGTGTGCTCAGAGCAAGTGTCTATACCTAAGT	345
Db	36241	GTCCAGGTGCAATGCTCTCGATTAAGTAGAGGCTCCGAGGACCTGCTATCTATCAAT	36182
QY	346	GCTCTATACGAATAAT-----	360
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Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG,

XX
DR WPI: 1995-263870/34.
P-PSDB: AAR78142.
XX
PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX
PS Claim 5: Page 12-17: 38pp: English.
XX
CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA
CC library was amplified using cluster-specific esterase primers.
CC Isolated clone lc743, a probable full-length cDNA, was expressed
CC using a baculovirus vector in insect cells and shown to encode
CC an OP-susceptible E3 esterase, useful in bioremediation.
XX
XX Sequence 1713 BP: 516 A: 305 C: 370 G: 522 T: 0 other:
S0
Query Match 100.0%; Score 1713; DB 16; Length 1713;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGAATTTCAACGTTAGTTGATGAGCAATTAATGCAAGTTAAATGCAATGAAAT 60
OY 61 AAGTTTAACTATCGTTTAACTACCAATGAAACGCTGAGTGAATGCAATGCAATG 120
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OY 121 AAGTGAAGGCTTAAACGTTTAACTGCTGATGATGCTGATGCTGATGCTGATG 180
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DB 841 TTTCTTATGAAGCCCAACGCTGATGATGATGATGATGATGATGATGATGATG 900
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OY 961 GCTGATGCTGCTTACCAACATCTGCGGAAATGTTAAAGCTGCTGCTGCTG 1020
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OY 1021 ATACCCGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
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DB 1441 AATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
OY 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
DB 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
OY 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
DB 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
OY 1621 ATTAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
DB 1621 ATTAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
OY 1681 TCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1713
DB 1681 TCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1713
RESULT 2
AAT68596 standard: DNA: 1713 BP.
ID AAT68596;
AC AAT68596;
AT 08-AUG-1997 (first entry)
DT

XX LC-alpha-E7 malathion susceptible esterase clone Lc743.
XX Malathion carboxylesterase; organophosphate; insecticide;
KW pesticide; remediation; bioremediation; decontamination; esterase;
KW ss.
XX Lucilia cuprina.
XX
FH Key Location/Qualifiers
FT primer_bind complement (1..26)
FT /tag- a
FT /note= "Lc743 5' primer"
FT primer_bind 1686..1713
FT /tag- b
FT /note= "Lc743 3' primer"
FT mutation 752
FT /tag- c
FT /note= "base 752 is T in resistant clones
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FT /tag- d
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XX 23-NOV-1995; 95AU-0006751.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;
PI Newcomb RD, Oakeshott JG, Roblin GC, Russell RJ, Smyth K;
XX WPI: 1997-298113/27.
DR P-PSDB; AAM17765.
XX
XX DNA encoding enzyme that degrades organophosphate pesticides -
PT useful for decontamination of soil, water, food etc
XX
XX Claim 4; Fig 1; 52pp; English.
XX
XX DNA molecule Lc743 (AAT68596) codes for an esterase (AAM17765) from
CC a malathion susceptible strain of Lucilia cuprina. Comparison
CC with a consensus sequence from derived from clones of the
CC Lc-alpha-E7 resistant allele (see also AAM17768) indicated only one
CC replacement site difference, a Trp to Leu substitution at amino
CC acid position 251 (nucleotide position 752). This mutation is an
CC excellent candidate for the malathion resistance mutation. The
CC resistant enzyme acts as a malathion carboxylesterase and can be
CC formulated for use in degrading environmental carboxylester or
CC dimethyl general organophosphates.
XX
XX Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other:
Query Match 100.0%; Score 1713; DB 18; Length 1713;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATTCACGTTAGTTGATGAGAAATTAAATGAGATTAATGATTCGAAT 60
DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAAATGAGATTAATGATTCGAAT 60
QY 61 AAGTTTAACTATCGTTTAACCTACCAATGAACGGGTAGTGAAGTGAATATGCG 120
DB 61 AAGTTTAACTATCGTTTAACCTACCAATGAACGGGTAGTGAAGTGAATATGCG 120
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DB 121 AAGTGAAGCGTTAAAGCTTAACTGTACGATGATCTTACTACAGTTTGAAGGT 180
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DB 241 CCTGGATGGTGGCGGATGTTGCAATCATAAAGTCAAGTCAAGTTGATTTT 300
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DB 301 ATACGGGCAAAAGTGTGTGCTCAGAGAGTTGTCTATACCTAAGTCTATACGAATAT 360
QY 361 CTAATCCCGAAACTAAACCTCCGTTTACTATATACATAGGTGGTGTATATATC 420
DB 361 CTAATCCCGAAACTAAACCTCCGTTTACTATATACATAGGTGGTGTATATATC 420
QY 421 GGTGAATATCATCGTATATGATGATGCTGATTTTCAATTAAGATGATGTTG 480
DB 421 GGTGAATATCATCGTATATGATGATGCTGATTTTCAATTAAGATGATGTTG 480
QY 481 ATTAACATACATATATCGTTGGAGCTCTAGATTTTCTAAGTTTAAATTCAGAACCTT 540
DB 481 ATTAACATACATATATCGTTGGAGCTCTAGATTTTCTAAGTTTAAATTCAGAACCTT 540
QY 541 AATGCGCCGGTAAATGCGGCTTAAGATCAAGTCATGCGCTTGATTAATAAT 600
DB 541 AATGCGCCGGTAAATGCGGCTTAAGATCAAGTCATGCGCTTGATTAATAAT 600
QY 601 AATGCGCCGGTAAATGCGGCTTAAGATCAAGTCATGCGCTTGATTAATAAT 660
DB 601 AATGCGCCGGTAAATGCGGCTTAAGATCAAGTCATGCGCTTGATTAATAAT 660
QY 661 GCTGCTCTACCACTACATGATGTTTAACGCAACAACTCGCGTCTTTCATCGTGT 720
DB 661 GCTGCTCTACCACTACATGATGTTTAACGCAACAACTCGCGTCTTTCATCGTGT 720
QY 721 ATACTAATGTGGGTAAATGCTATTTTGTCCATGCGCTAATACCAATGTCATGCGC 780
DB 721 ATACTAATGTGGGTAAATGCTATTTTGTCCATGCGCTAATACCAATGTCATGCGC 780
QY 781 TTCACCTTAGCCCAATTTGGCGGCTATAGAGGTGATGATTAAGATGTTTGGAA 840
DB 781 TTCACCTTAGCCCAATTTGGCGGCTATAGAGGTGATGATTAAGATGTTTGGAA 840
QY 841 TTTCTTATGAAGCCACAGCAGATTTAATAAACTTGAAGAAAAAGTTTAACTCTA 900
DB 841 TTTCTTATGAAGCCACAGCAGATTTAATAAACTTGAAGAAAAAGTTTAACTCTA 900
QY 901 GAGAGCGTACAAATTAAGGTATGTTTCTTTGGTCCACTGTTGAGCCATATAGACC 960
DB 901 GAGAGCGTACAAATTAAGGTATGTTTCTTTGGTCCACTGTTGAGCCATATAGACC 960
QY 961 GGTGATTTGTCTTACCCAAACATCTCGGGAAGATGTTAAACGCTGGGGTAATTCG 1020
DB 961 GGTGATTTGTCTTACCCAAACATCTCGGGAAGATGTTAAACGCTGGGGTAATTCG 1020
QY 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080

OY 1081 CAATGCTATGCTTGTAAAGAAATGGAACCTGTTGCAATTTTGTGCCAAGTGAATG 1140
 |||||||
 DB 1081 CAATGCTATGCTTGTAAAGAAATGGAACCTGTTGCAATTTTGTGCCAAGTGAATG 1140
 OY 1141 GGTGATGCTGAACGACCGCCCGACAGACCTTGGAAATGGGTGCTAAATTAATAAGCT 1200
 |||||||
 DB 1141 GGTGATGCTGAACGACCGCCCGACAGACCTTGGAAATGGGTGCTAAATTAATAAGCT 1200
 OY 1201 CATGTTACAGGGAACACACAGCTGATTAATTTATGATCTTTGCTGCATCAT 1260
 |||||||
 DB 1201 CATGTTACAGGGAACACACAGCTGATTAATTTATGATCTTTGCTGCATCAT 1260
 OY 1261 TTCTGTTCCCATGCAATGCTTTGTTGCAATTAACCTTCAATCACACCGCGGTACACC 1320
 |||||||
 DB 1261 TTCTGTTCCCATGCAATGCTTTGTTGCAATTAACCTTCAATCACACCGCGGTACACC 1320
 OY 1321 GTCTACTGATGCTTGCCTTGCCTTGAATGCGAAGATCTTATTAATCCCTATGCTAT 1380
 |||||||
 DB 1321 GTCTACTGATGCTTGCCTTGCCTTGAATGCGAAGATCTTATTAATCCCTATGCTAT 1380
 OY 1381 CGTAGTGACGTGTGTTAAGGCTGTAGTACATGCTGATTAACCTATTTCTCTGG 1440
 |||||||
 DB 1381 CGTAGTGACGTGTGTTAAGGCTGTAGTACATGCTGATTAACCTATTTCTCTGG 1440
 OY 1441 AATCAATTGGCCAAACGATGCTTAAGAAATCGCGTGAATACAAACCAATTTGAACGTATG 1500
 |||||||
 DB 1441 AATCAATTGGCCAAACGATGCTTAAGAAATCGCGTGAATACAAACCAATTTGAACGTATG 1500
 OY 1501 ACTGCTATGATGATTAATTTGCAACACCTGCTAATCTTATGCAATGAATTTGAAGT 1560
 |||||||
 DB 1501 ACTGCTATGATGATTAATTTGCAACACCTGCTAATCTTATGCAATGAATTTGAAGT 1560
 OY 1561 ATGGAATGATGCTTCTGCGATCCATTAAGAAATCGCAAGATTAACAGTCTTGAAT 1620
 |||||||
 DB 1561 ATGGAATGATGCTTCTGCGATCCATTAAGAAATCGCAAGATTAACAGTCTTGAAT 1620
 OY 1621 ATTAGTACGAATTTGAATTAATTTGATGCTGCTGAATGATTAACATGAGTGA 1680
 |||||||
 DB 1621 ATTAGTACGAATTTGAATTAATTTGATGCTGCTGAATGATTAACATGAGTGA 1680
 OY 1681 TCGATGTTGAAACATAGAGATTTATTTAG 1713
 |||||||
 DB 1681 TCGATGTTGAAACATAGAGATTTATTTAG 1713
 |||||||
 RESULT 3
 ID AAO91566 standard; cdna; 1713 bp.
 XX AAO91566
 AC AAO91566;
 DT 22-DEC-1995 (first entry)
 XX
 DE OP-resistant esterase Lc7L103con.
 XX
 KW Esterase; E3; bioremediation; organophosphate; carbamate;
 insecticide; pesticide; water decontamination; meat decontamination;
 ss.
 XX
 OS Lucilia cuprina.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..1713
 FT /*tag= a
 XX
 PN WO9519440-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 13-JAN-1995; 95WO-AU00016.
 XX
 PR 13-JAN-1994; 94AU-000347.

XX
 PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 DR WPI: 1995-263870/34.
 XX
 PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organophosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Example 4; Page 12-17; 38pp; English.
 XX
 CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC OP-susceptible esterase E3 of *L. cuprina*) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (UC7L103 A-D, AAO91562-65) that encoded diazinon-resistant
 CC esterases; a consensus sequence is given in AAO91566.
 CC
 XX
 SO Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other:
 Query Match 98.2%; Score 1682.6; DB 16; Length 1713;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 1694; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAAGTAAATGCAATTTGAAAT 60
 DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAAGTAAATGCAATTTGAAAT 60
 OY 61 AAGTTTAACTATGCTTAACTACCAATGAACGGTGTACTGAACCTGAATTTGGC 120
 DB 61 AAGTTTAACTATGCTTAACTACCAATGAACGGTGTACTGAACCTGAATTTGGC 120
 OY 121 AAGTGAAGGCGTTAAACGTTTAACTGCTGATGATGATTTAAAGCAACCCGACCAACA 240
 DB 121 AAGTGAAGGCGTTAAACGTTTAACTGCTGATGATGATTTAAAGCAACCCGACCAACA 240
 OY 181 ATACGCTACGCCCAACCGCCAGTGGTGAAGATTTAAAGCAACCCGACCAACA 240
 DB 181 ATACGCTACGCCCAACCGCCAGTGGTGAAGATTTAAAGCAACCCGACCAACA 240
 OY 241 CCCTGGATGCTGTGCTGATGTTGCAATCAATGAATGATGCTGATTTATATC 300
 DB 241 CCCTGGATGCTGTGCTGATGTTGCAATCAATGAATGATGCTGATTTATATC 300
 OY 301 ATACGCGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTCTATACGATTAAT 360
 DB 301 ATACGCGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTCTATACGATTAAT 360
 OY 361 CTAAATCCGCAAACTAAACGCTCCGTTTATGATACATGATGATGATTTATATC 420
 DB 361 CTAAATCCGCAAACTAAACGCTCCGTTTATGATACATGATGATGATTTATATC 420
 OY 421 GGTGAATATCATGCTGATATGATGCTGATTTATTTATTTAAAGATGCTGTTG 480
 DB 421 GGTGAATATCATGCTGATATGATGCTGATTTATTTATTTAAAGATGCTGTTG 480
 OY 481 ATTAACATACATATGCTTTGGAGCTCTGAGCTTTCTAATTAATTCAGAACCTT 540
 DB 481 ATTAACATACATATGCTTTGGAGCTCTGAGCTTTCTAATTAATTCAGAACCTT 540
 OY 541 AATGCGCCGCTAATGCGGCTTAAGATCAATGATGATGCTGATTTAAAT 600
 DB 541 AATGCGCCGCTAATGCGGCTTAAGATCAATGATGATGCTGATTTAAAT 600
 OY 601 AATGCGCAACTTTGTTGCAATCCGATTAATTTACATGCTTTGTTGAAGTGGCGGT 660
 DB 601 AATGCGCAACTTTGTTGCAATCCGATTAATTTACATGCTTTGTTGAAGTGGCGGT 660
 OY 661 GCTGCTTACCACTACATATGATTTAAGCAACAACTGCGGCTTTTCATGCTGGT 720
 DB 661 GCTGCTTACCACTACATATGATTTAAGCAACAACTGCGGCTTTTCATGCTGGT 720

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OY 721 ATACATATGCGGGGATGCTATTTGTCATGGGCTATACCAATGCAACATGCGC 780
DB 721 ATACTAATGTGGGTAATGCTATTTGTCATGGGCTAATACCAATGCAACATGCGC 780
OY 781 TTCACCTTAGCCAAATTTGGCGCTATTAAGGCTGAGCATTAATGATTAAGATTTTGGAA 840
DB 781 TTCACCTTAGCCAAATTTGGCGCTATTAAGGCTGAGCATTAATGATTAAGATTTTGGAG 840
OY 841 TTTCTTATGAAGCCCAAGCCACAGATTTAATAAACTTGAGGAAAAAGTTTAACTCTA 900
DB 841 TTTCTTATGAAGCCCAAGCCACAGATTTAATAAACTTGAGGAAAAAGTTTAACTCTA 900
OY 901 GAAGGCGGTACAAATTAAGTATGTTTCCCTTTGGTCCCACTGTTGACCCATACAGACC 960
DB 901 GAAGGCGGTACAAATTAAGTATGTTTCCCTTTGGTCCCACTGTTGACCCATACAGACC 960
OY 961 GCTGATTTGCTTACCACCAATCCTCGGGAATGTTAAACCTGTTGGGGTAATTCG 1020
DB 961 GCTGATTTGCTTACCACCAATCCTCGGGAATGTTAAACCTGTTGGGGTAATTCG 1020
OY 1021 ATACCCTATGATGGGTACACCTTCATATGAGGGTCTATTTTCACTTCAATTCCTAAG 1080
DB 1021 ATACCCTATGATGGGTACACCTTCATATGAGGGTCTATTTTCACTTCAATTCCTAAG 1080
OY 1081 CAATAGCCTATGCTTGAAGGAATGGAACCTGTCATATTTTGTCCCAAGTCAATTCG 1140
DB 1081 CAATAGCCTATGCTTGAAGGAATGGAACCTGTCATATTTTGTCCCAAGTCAATTCG 1140
OY 1141 GCTGATGCTGAAGCGACCGCCCGAGAGACCTTGGAATGGGTCTAAATTTAAAGAGCT 1200
DB 1141 GCTGATGCTGAAGCGACCGCCCGAGAGACCTTGGAATGGGTCTAAATTTAAAGAGCT 1200
OY 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATGATGATCTTGTCTCACATCTAT 1260
DB 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATGATGATCTTGTCTCACATCTAT 1260
OY 1261 TTCGCGTCCCGCATGCTGTTGTCATTAAGTTCATGCTTCATGACCTCCGCTGACCC 1320
DB 1261 TTCGCGTCCCGCATGCTGTTGTCATTAAGTTCATGCTTCATGACCTCCGCTGACCC 1320
OY 1321 GTCTACTTGTATCGCTTGCCTGACTTGTGAGTGGAGATCTTATTAATCCCTATCGATTATG 1380
DB 1321 GTCTACTTGTATCGCTTGCCTGACTTGTGAGTGGAGATCTTATTAATCCCTATCGATTATG 1380
OY 1381 CGTAGTGAAGCTGCTGTTAAGGGTGTAGTCACTGATGATGAATTAACCTATTTCTTGG 1440
DB 1381 CGTAGTGAAGCTGCTGTTAAGGGTGTAGTCACTGATGATGAATTAACCTATTTCTTGG 1440
OY 1441 AATCAATTTGGCCAAACGTAATGCTTAAGATCGGCTGAATCAAAACAAATGAAGCTATG 1500
DB 1441 AATCAATTTGGCCAAACGTAATGCTTAAGATCGGCTGAATCAAAACAAATGAAGCTATG 1500
OY 1501 ACTGCTATATGATGATCAATTTTGCACCACTGTAATCCTTATAGCAATGAATTTAAGGT 1560
DB 1501 ACTGCTATATGATGATCAATTTTGCACCACTGTAATCCTTATAGCAATGAATTTAAGGT 1560
OY 1561 ATGGAATATGTTTCTCTGGGATCCATTTAAGAAATCCGACGAGATTAACAAGTCTTGAAT 1620
DB 1561 ATGGAATATGTTTCTCTGGGATCCATTTAAGAAATCCGACGAGATTAACAAGTCTTGAAT 1620
OY 1621 ATTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 ATTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
OY 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713

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RESULT 4
-AA091564
ID AA091564 standard; cDNA; 1713 BP.

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XX AA091564;
AC 22-DEC-1995 (first entry)
DT
XX
XX
DE OP-resistant esterase Lc7L103c allele.
XX
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW Insecticide; pesticide; water decontamination; meat decontamination;
KW ss.
XX
OS Lucilia cuprina.
XX
EH
EH Key Location/Qualifiers
FT CDS 1..1713
FT /tag= a
XX
XX W09519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95WO-A000016.
XX
XX 13-JAN-1994; 94AU-0003347.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI: 1995-263870/34.
XX
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX eliminate residues of organo:phosphate and carbamate pesticides from
XX water, meat etc.
XX
XX Example 4; Page 12-17; 38pp; English.
XX
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX resistant strain, Llandillo 103. 4 Isolated clones were
XX sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
XX esterases. The esterases, or cells expressing them, are used
XX in bioremediation.
XX
XX Sequence 1713 BP; 512 A; 308 C; 368 G; 525 T; 0 other;
XX
XX Query Match 98.0%; Score 1679.4; DB 16; Length 1713;
XX Best Local Similarity 98.8%; Pred. No. 0;
XX Matches 1692; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY 1 ATGAATTTCAACGTTAGTTTGAAGGAGAAATTAATGAAGATTAATGCAATTAAT 60
DB 1 ATGAATTTCAACGTTAGTTTGAAGGAGAAATTAATGAAGATTAATGCAATTAAT 60
OY 61 AAGTTTAACTATGCTTAACTACCAATGAAGGAGTGAAGTGAAGTGAATATGAGC 120
DB 61 AAGTTTAACTATGCTTAACTACCAATGAAGGAGTGAAGTGAAGTGAATATGAGC 120
OY 121 AAAGTGAAGGCGTTAAAGCTTTAACTGTTGATGATGATGATGATGATGATGATGATGAT 180
DB 121 AAAGTGAAGGCGTTAAAGCTTTAACTGTTGATGATGATGATGATGATGATGATGATGAT 180
OY 181 ATACCGTACGCCCAACCGCCAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240
DB 181 ATACCGTACGCCCAACCGCCAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240
OY 241 CCCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
DB 241 CCCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
OY 301 ATACGGGCAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360
DB 301 ATACGGGCAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360

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Db 301 ATTCAGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGCTCTATACGAATAT 360
 Qy 361 CTAATCCCGCAAACTAAACGTCGCCGTTTCTATATACATACATGGGGGTTTATATC 420
 Db 361 CTAATCCCGCAAACTAAACGTCGCCGTTTCTATATACATACATGGGGGTTTATATC 420
 Qy 421 GGTGAAAATCATGCTGATATGATGCTGATATTTTCAATTTAAAGATGTGTG 480
 Db 421 GGTGAAAATCATGCTGATATGATGCTGATATTTTCAATTTAAAGATGTGTG 480
 Qy 481 ATTAACATACATATGCTTTGGGAGCTCTAGGTTTCTAGTTTAAATTCGAAGACCTT 540
 Db 481 ATTAACATACATATGCTTTGGGAGCTCTAGGTTTCTAGTTTAAATTCGAAGACCTT 540
 Qy 541 AATGTCGCCGTAATGCGCGCTTAAGATCAATGCGCTGCGTTGGATTTAAAT 600
 Db 541 AATGTCGCCGTAATGCGCGCTTAAGATCAATGCGCTGCGTTGGATTTAAAT 600
 Qy 601 AATGTCGCCGTAATGCGCGCTTAAGATCAATGCGCTGCGTTGGATTTAAAT 660
 Db 601 AATGTCGCCGTAATGCGCGCTTAAGATCAATGCGCTGCGTTGGATTTAAAT 660
 Qy 661 GCTGCTCTACCCACATGATGTTAAGCAACCAACGCGGCTCTTCCATCGTGT 720
 Db 661 GCTGCTCTACCCACATGATGTTAAGCAACCAACGCGGCTCTTCCATCGTGT 720
 Qy 721 ATACTAATGTGCGGTAATGCTATTTGTCTCATGCGCTAATACCAATGCTCAACATCGTGC 780
 Db 721 ATACTAATGTGCGGTAATGCTATTTGTCTCATGCGCTAATACCAATGCTCAACATCGTGC 780
 Qy 781 TTGACCTTACCAAAATTTGGCGGCTAATAGGAGATATGATTAAGATGTTTGGAA 840
 Db 781 TTGACCTTACCAAAATTTGGCGGCTAATAGGAGATATGATTAAGATGTTTGGAA 840
 Qy 841 TTTCTTATGAAGCAAGCAGAGATTAATTAACCTTGAAGAAAAGTTTAACTCTA 900
 Db 841 TTTCTTATGAAGCAAGCAGAGATTAATTAACCTTGAAGAAAAGTTTAACTCTA 900
 Qy 901 GAAGAGCGTCAAAATAGGTCATGTTTCTTTTGTCCACTGTTGAGCCATATCAGACC 960
 Db 901 GAAGAGCGTCAAAATAGGTCATGTTTCTTTTGTCCACTGTTGAGCCATATCAGACC 960
 Qy 961 GCTGATTTGTCTTACCAAAACATCCTCGGGAATGTTTAAACCTGCTGGGTAAATTCG 1020
 Db 961 GCTGATTTGTCTTACCAAAACATCCTCGGGAATGTTTAAACCTGCTGGGTAAATTCG 1020
 Qy 1021 ATACCCACTATGATGCTTAACACTTATGAGGCTCTATTTTCACTCAATCTTAAG 1080
 Db 1021 ATACCCACTATGATGCTTAACACTTATGAGGCTCTATTTTCACTCAATCTTAAG 1080
 Qy 1081 CAATGCTCTATGCTTTTAAAGAACTTGTCAATTTTGTCCAAAGTGAATG 1140
 Db 1081 CAATGCTCTATGCTTTTAAAGAACTTGTCAATTTTGTCCAAAGTGAATG 1140
 Qy 1141 GGTGATGCTGAAGCAGCCGCCAGAGACCTTGAAGAAAGGCTCTAAATTAAGAGGCT 1200
 Db 1141 GGTGATGCTGAAGCAGCCGCCAGAGACCTTGAAGAAAGGCTCTAAATTAAGAGGCT 1200
 Qy 1201 CATGTTACAGGAAACACCAACAGCTGATATTTATGATCTTGTCTCACTAT 1260
 Db 1201 CATGTTACAGGAAACACCAACAGCTGATATTTATGATCTTGTCTCACTAT 1260
 Qy 1261 TTTCTGTTCCCATGATGCTTTTGGCAATTAACGTTTAAACACCTCGGCTACACC 1320
 Db 1261 TTTCTGTTCCCATGATGCTTTTGGCAATTAACGTTTAAACACCTCGGCTACACC 1320
 Qy 1321 GTCTACTGTTATGCTTGCATTTTGAATGGAAGATCTTATTAATCCCTATGAT 1380
 Db 1321 GTCTACTGTTATGCTTGCATTTTGAATGGAAGATCTTATTAATCCCTATGAT 1380
 Qy 1381 GCTAGTGAAGCTGTGTTAAGGCTGTACTCATGCTGATGAATTAACCTATTTCTG 1440
 Db 1381 GCTAGTGAAGCTGTGTTAAGGCTGTACTCATGCTGATGAATTAACCTATTTCTG 1440

Qy 1441 AATCAATTTGGCCAAACGATATGCTTAAAGAAATCCGCTGAATACAAACATTTGAACGTATG 1500
 Db 1441 AATCAATTTGGCCAAACGATATGCTTAAAGAAATCCGCTGAATACAAACATTTGAACGTATG 1500
 Qy 1501 ACTGATATGATGATACATTTTGGCCACCATGTAATCCTATATGCAATGAATGAAGT 1560
 Db 1501 ACTGATATGATGATACATTTTGGCCACCATGTAATCCTATATGCAATGAATGAAGT 1560
 Qy 1561 ATGGAATAATGTTTCTGCGGATTCGAATTTAGAAAATCCGACGAAGTATACAGTGTGAAT 1620
 Db 1561 ATGGAATAATGTTTCTGCGGATTCGAATTTAGAAAATCCGACGAAGTATACAGTGTGAAT 1620
 Qy 1621 ATTAGTGACGATTTGAAAATGATGATGCTGCGGAAATGATTAAGATTAACATGGA 1680
 Db 1621 ATTAGTGACGATTTGAAAATGATGATGCTGCGGAAATGATTAAGATTAACATGGA 1680
 Qy 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
 Db 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
 RESULT 5
 AA091565
 ID AA091565 standard; cDNA: 1713 BP.
 XX
 AC AA091565;
 XX
 DT 22-DEC-1995 (first entry)
 XX
 DE OP-resistant esterase Lc7L103D allele.
 XX
 KM Esterase; E3: bio remediation; organophosphate; carbamate;
 KM insecticide; pesticide; water decontamination; meat decontamination;
 KW SS.
 XX
 OS Lucilia cuprina.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1713
 FT /tag- a
 XX
 PN W09519440-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 13-JAN-1995; 95MO-AU00016.
 XX
 PR 13-JAN-1994; 94AU-0003347.
 XX
 PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 XX
 DR WPI: 1995-263870/34.
 XX
 PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Example 4; Page 12-17; 38pp; English.
 XX
 CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E3 (encoding
 CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
 CC resistant strain, Ilanillo 103. 4 isolated clones were
 CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used
 CC in bioremediation.
 XX
 SQ Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other;
 Query Match 98.0%; Score 1679.4; DB 16; Length 1713;

PR 13-JAN-1994: 94AU-0003347.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX Boyce TM, Campbell PM, Newcomb RD, Oakshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 XX WPI. 1995-263870/34.
 DR
 XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 XX Example 4; Page 12-17; 38pp; English.
 XX RT-PCR was used to clone a cDNA allele of *lc-alpha-E7* (encoding
 CC Op-susceptible esterase E3 of *L. cuprina*) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (LC7L103 A-D, A091562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used
 CC in bioremediation.
 CC
 XX Sequence 1713 BP; 513 A; 308 C; 368 G; 524 T; 0 other:
 XX
 XX
 Query Match 97.9%; Score 1677.8; DB 16; Length 1713;
 Best Local Similarly 98.7%; Pred. No. 0;
 Matches 1691; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Db 661 GCTGCTCTACCCACTACATGATGTTAACGAAACACCGCGCTTTCCATGCTGCT 720
 Oy 721 ATACTAATGTGCGGTAAATGCTATTTTGCATAGGGGTAATACCAATGTCAACATGTGCC 780
 Db 721 ATACTAATGTGCGGTAAATGCTATTTTGCATAGGGGTAATACCAATGTCAACATGTGCC 780
 Oy 781 TTCACCTTAGCCAAATGGCCGCTAATAGGGTGAAGATATGATTAAGATCTTTGGAA 840
 Db 781 TTCACCTTAGCCAAATGGCTATAGGGTGAAGATATGATTAAGATCTTTGGAA 840
 Oy 841 TTTCTTATGAAGCCAAACCCACAGATTTAATAAATCTGAGAAACCTTTTAACTCTA 900
 Db 841 TTTCTTATGAAGCCAAACCCACAGATTTAATAAATCTGAGAAACCTTTTAACTCTA 900
 Oy 901 GAAGAGCGTACAAATTAAGTATGTTTCTTTTGGTCCACTGTTAGCCATATCGAGCC 960
 Db 901 GAAGAGCGTACAAATTAAGTATGTTTCTTTTGGTCCACTGTTAGCCATATCGAGCC 960
 Oy 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGGTTAAACCTGTTGGGTAAATTCG 1020
 Db 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGGTTAAACATGCTTGGGGTAATTCG 1020
 Oy 1021 ATACCCACTATGATGGGTATACACTTCATATGAGGGTCTATTTTCACTTCAATTCCTAAG 1080
 Db 1021 ATACCCACTATGATGGGTATACACTTCATATGAGGGTCTATTTTCACTTCAATTCCTAAG 1080
 Oy 1081 CAATGCGCTATGCTTGTATGGAATTTGAACCTTGTGCAATTTTGTGCAAGTGAATTCG 1140
 Db 1081 CAATGCGCTATGCTTGTATGGAATTTGAACCTTGTGCAATTTTGTGCAAGTGAATTCG 1140
 Oy 1141 GCTATGCTGAGACGACGCGCCGACGAGACCTTGAATGGTGTCTTAAATTAAGAGCT 1200
 Db 1141 GCTATGCTGAGACGACGCGCCGACGAGACCTTGAATGGTGTCTTAAATTAAGAGCT 1200
 Oy 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTATGATCTTGTCTTCAATCTAT 1260
 Db 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTATGATCTTGTCTTCAATCTAT 1260
 Oy 1261 TTTCTGTTCCCATGATCATCTTGTATGCAATTTACGTTTCAATCAGACCTGCTACACC 1320
 Db 1261 TTTCTGTTCCCATGATCATCTTGTATGCAATTTACGTTTCAATCAGACCTGCTACACC 1320
 Oy 1321 GTCTACTTGTATGCTTGTGAGCTTGTGAGAGATCTTATTAATCCATATGCTATATAG 1380
 Db 1321 GTCTACTTGTATGCTTGTGAGCTTGTGAGAGATCTTATTAATCCATATGCTATATAG 1380
 Oy 1381 CGTAGTGACGCTGCTTAAAGGCTTATGCTATGCTGATGTAATTAACCTATTTCTCTGG 1440
 Db 1381 CGTAGTGACGCTGCTTAAAGGCTTATGCTATGCTGATGTAATTAACCTATTTCTCTGG 1440
 Oy 1441 AATCAATTTGCCAAACGATATGCTTAAAGATCGCTGATTAACAAACATTTGAACGTATG 1500
 Db 1441 AATCAATTTGCCAAACGATATGCTTAAAGATCGCTGATTAACAAACATTTGAACGTATG 1500
 Oy 1501 ACTGCTATGATGATACAAATTTGCCACACCTGATATCTTATAGCAATGAATGAAGT 1560
 Db 1501 ACTGCTATGATGATACAAATTTGCCACACCTGATATCTTATAGCAATGAATGAAGT 1560
 Oy 1561 ATGGAATTTGCTTCTGAGATCAATTAAGAATTCGAGCAATATACAGTGTGTAAT 1620
 Db 1561 ATGGAATTTGCTTCTGAGATCAATTAAGAATTCGAGCAATATACAGTGTGTAAT 1620
 Oy 1621 ATTAGTGAAGATTAAGAAATGATGATGCTTGAATGATTAAGATTAAGATTAAGTGA 1680
 Db 1621 ATTAGTGAAGATTAAGAAATGATGATGCTTGAATGATTAAGATTAAGATTAAGTGA 1680
 Oy 1681 TCGATGTTTGAAGAAACATAGATTAATTTTAA 1713
 Db 1681 TCGATGTTTGAAGAAACATAGATTAATTTTAA 1713
 RESULT 7

AA091562
ID AA091562 standard; cDNA: 1713 BP.
XX
AC AA091562;
XX
XX 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103a allele.
XX
XX Esterase; E3; bioremediation; organophosphate; carbamate;
KW Insecticide; pesticide; water decontamination; meat decontamination;
ss.
XX
XX Lucilia cuprina.
XX
XX
FH key Location/Qualifiers
FT 1..1713
CD CDS /*tag= a
XX
XX MO9519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95WO-AU00016.
XX
XX 13-JAN-1994; 94AU-000347.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI: 1995-263870/34.
XX
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX
XX
XX Example 4; Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Ilandillo 103. 4 isolated clones were
CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
CC in bioremediation.
XX
XX
SQ Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;
Query Match 97.9%; Score 1676.2; DB 16; Length 1713;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1690; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 301 ATACGGCGAAAGTGTGGCTCAGAGATTGTCTATACCTAAGTCTATACGAATAAT 360
DB 301 ATTACAGCGAAAGTGTGGCTCAGAGATTGTCTATACCTAAGTCTATACGAATAAT 360
QY 361 CTAAATCCCGAAACTAAACGTCGCCGTTTATATACATACAGTGTGGTTTATATAC 420
DB 361 CTAAATCCCGAAACTAAACGTCGCCGTTTATATACATACAGTGTGGTTTATATAC 420
QY 421 GGTGAAATCATCGTATATATGTGTCTGATTTTCATTAAAAAGATGTGTG 480
DB 421 GGTGAAATCATCGTATATATGTGTCTGATTTTCATTAAAAAGATGTGTG 480
QY 481 ATTACATACAAATATCGTTGGAGCTCAGTGTCTAAGTTTAAATTCAGAACCTT 540
DB 481 ATTACATACAAATATCGTTGGAGCTCAGTGTCTAAGTTTAAATTCAGAACCTT 540
QY 541 AATGTGCCCGGTAAATGCCGCTTAAAGATCAAGTCAATGCGTGTGATTAATAAT 600
DB 541 AATGTGCCCGGTAAATGCCGCTTAAAGATCAAGTCAATGCGTGTGATTAATAAT 600
QY 601 AATGTGCCCGGTAAATGCCGCTTAAAGATCAAGTCAATGCGTGTGATTAATAAT 660
DB 601 AATGTGCCCGGTAAATGCCGCTTAAAGATCAAGTCAATGCGTGTGATTAATAAT 660
QY 661 GCTGCTCTACCCACTACATGATGTTAAACCGAACAACGCGGCTTTCCATGCTGT 720
DB 661 GCTGCTCTACCCACTACATGATGTTAAACCGAACAACGCGGCTTTCCATGCTGT 720
QY 721 ATACTAATGTGCGGTAATGCTATTTTGTCCATGCGGCTTAAATCCCAATGTCACATGCTGC 780
DB 721 ATACTAATGTGCGGTAATGCTATTTTGTCCATGCGGCTTAAATCCCAATGTCACATGCTGC 780
QY 781 TTCACCTTAGCCAAATTTGGCGGCTATTAAGGTGAGATTAATGATTAAGATTTTGGAA 840
DB 781 TTCACCTTAGCCAAATTTGGCGGCTATTAAGGTGAGATTAATGATTAAGATTTTGGAA 840
QY 841 TTTCTTATGAAGCCAGACAGATTTAAATTAAGTGAAGAAAGTTTAACTCTA 900
DB 841 TTTCTTATGAAGCCAGACAGATTTAAATTAAGTGAAGAAAGTTTAACTCTA 900
QY 901 GAAGAGCGTACCAATTAAGTCAATGTTTCCCTTTGCTCCACTGTTGAGCCATATCAGACC 960
DB 901 GAAGAGCGTACCAATTAAGTCAATGTTTCCCTTTGCTCCACTGTTGAGCCATATCAGACC 960
QY 961 GCTGATTTGCTTTTACCAACATCTCTGGGAAATGTTTAAATGCTTTGGGTAATTCG 1020
DB 961 GCTGATTTGCTTTTACCAACATCTCTGGGAAATGTTTAAATGCTTTGGGTAATTCG 1020
QY 1021 ATACCCACTATGATGGGTAAACCTCATATGAGGGTCTATTTTCACTTCAATTCCTTAG 1080
DB 1021 ATACCCACTATGATGGGTAAACCTCATATGAGGGTCTATTTTCACTTCAATTCCTTAG 1080
QY 1081 CAATATGCTATGCTTTTAAAGAAATTTGAACCTTTGTCATTTTGTGCAAGTGAATTCG 1140
DB 1081 CAATATGCTATGCTTTTAAAGAAATTTGAACCTTTGTCATTTTGTGCAAGTGAATTCG 1140
QY 1141 GCTGATTTGCTTTTACCAACATCTCTGGGAAATGTTTAAATGCTTTGGGTAATTCG 1200
DB 1141 GCTGATTTGCTTTTACCAACATCTCTGGGAAATGTTTAAATGCTTTGGGTAATTCG 1200
QY 1201 CATGTTACAGGAAACCAACACCTGATATTTTATGAGATCTTGTCTCACATCTAT 1260
DB 1201 CATGTTACAGGAAACCAACACCTGATATTTTATGAGATCTTGTCTCACATCTAT 1260
QY 1261 TTTCTGTTTCCCATGATGTTTGAATTTGCAATTTTCAATCAACACCTCCGCTACACC 1320
DB 1261 TTTCTGTTTCCCATGATGTTTGAATTTGCAATTTTCAATCAACACCTCCGCTACACC 1320
QY 1321 GTCTACTGTATGCTTGTGACTTTGATTCGAGATCTTATTAATTCCTATGATATG 1380
DB 1321 GTCTACTGTATGCTTGTGACTTTGATTCGAGATCTTATTAATTCCTATGATATG 1380
QY 1381 CGTACTGACGCTGTGTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTTTCG 1440

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Db 1381 CCTAGGAGACGTGTGTAAAGGCTTTAGTCATGCTGATGAATTAACCTATTTCTCTGG 1440
Qy 1441 AATTCATTTGGCCAAACGTTAGTCCCTAAGAAATGCCGATACAAAACATTTAGACGTATG 1500
Db 1441 AATCAATTTGGCCAAACGTTAGTCCCTAAGAAATGCCGATACAAAACATTTAGACGTATG 1500
Qy 1501 ACTGATATATGATACAAATTTGGCCACCTGATATCTTATAGCAATGAATTAAGAGT 1560
Db 1501 ACTGATATATGATACAAATTTGGCCACCTGATATCTTATAGCAATGAATTAAGAGT 1560
Qy 1561 ATGGAATAATGTTCTCTGGATCCCAATTAAGAAATCCGACAGATATACAGTCTTTGAAT 1620
Db 1561 ATGGAATAATGTTCTCTGGATCCCAATTAAGAAATCCGACAGATATACAGTCTTTGAAT 1620
Qy 1621 ATTAGTACCAATTTGAATAATGATGATGTCCTGAATGATTAAGATTAACAATGGGAA 1680
Db 1621 ATTAGTACCAATTTGAATAATGATGATGTCCTGAATGATTAAGATTAACAATGGGAA 1680
Qy 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713

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RESULT 8

AAT68597 standard; DNA; 1710 BP.

AAT68597:

08-AUG-1997 (first entry)

Md-alpha-E7 gene.

Malathion carboxylesterase; organophosphate; insecticide;
pesticide; remediation; bioremediation; decontamination; ds.

Musca domestica Rutgers strain.

Key Location/Qualifiers
752
mutation

/tag= a
/note= "Trp-251 TGG codon is altered to a Ser
codon in resistant mutants"

WO9719176-A1.

29-MAY-1997.

22-NOV-1996; 96WO-AU00746.

23-NOV-1995; 95AU-0006751.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Boyce T, Brownlie JC, Campbell PM, Claudianos C;

Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

WPI; 1997-298113/27.

P-PSDB: AAW17767.

DNA encoding enzyme that degrades organophosphate pesticides -

useful for decontamination of soil, water, food etc

Claim 6; Fig 3; 52pp: English.

A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7
coding sequence of the Musca domestica Rutgers strain. It was
isolated by amplification of genomic DNA using alpha-esterase
consensus primers (see also AAT68598-99) and use of a 534 bp
amplicon to screen a genomic library of M. domestica. A
mutation of the gene, resulting in substn. of serine for tryptophan
at amino acid position 251 (see also AAW1767), confers malathion

CC resistance. The resistant enzyme acts as a malathion
CC carboxylesterase and can be formulated for use in degrading
CC environmental carboxylester or dimethyl general organophosphates.

SQ Sequence 1710 BP; 498 A; 369 C; 394 G; 449 T; 0 other;

Query Match

55.8%; Score 956.6; DB 18; Length 1710;

Best Local Similarity 73.4%; Pred. No. 5e-254; Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

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Qy 44 TTTAATGATTTGAATAATAGTTTAACTATGTTTAACTACCAATGAACGGTGTAG 103
Db 44 TTTAATGATTTGAATAATAGTTTAACTATGTTTAACTACCAATGAACGGTGTAG 103
Qy 104 CTGAACATGATATGCAAAAGTGAAGGCGTTAAAGCTTAACTGATGTAACGATGATTC 163
Db 104 TCGATATGATATGCAAAAGTGAAGGCGTTAAAGCTTAAAGCTGATGATGATTC 163
Qy 164 ACTACAGTTTGAAGGTATACCGTACGACCCACGCGCAGTGGGTGAGTGAATTTAAG 223
Db 164 ACTACAGTTTGAAGGTATACCGTACGACCCACGCGCAGTGGGTGAGTGAATTTAAG 223
Qy 224 CACCCGAGGACCAACACCCCTGGGATGCTGGGATGCTGATGATTCATCAATTAAGT 283
Db 224 CACCCGAGGACCAACACCCCTGGGATGCTGGGATGCTGATGATTCATCAATTAAGT 283
Qy 284 CAGTGAAGTTGATTTTATACGCGCAAGTGTGTGCTCAGAGATTTGCTATACCTAA 343
Db 284 CAGTGAAGTTGATTTTATACGCGCAAGTGTGTGCTCAGAGATTTGCTATACCTAA 343
Qy 344 GTGCTATACGAATTAATCTAATATCCGAACTAAGCTCCGTTTATGATACATACATG 403
Db 344 GTGCTATACGAATTAATCTAATATCCGAACTAAGCTCCGTTTATGATACATACATG 403
Qy 404 GTGGTGGTTTATATACGCGGAAATCATGCTATATGATGCTGATTTATTCATTA 463
Db 404 GTGGTGGTTTATATACGCGGAAATCATGCTATATGATGCTGATTTATTCATTA 463
Qy 464 AAAAGATGTTGTTGATTAATACATCAATATGTTGGAGCTCAGTTTCTAAGTT 523
Db 464 AAAAGATGTTGTTGATTAATACATCAATATGTTGGAGCTCAGTTTCTAAGTT 523
Qy 524 TAAATTCAGAGACCTTAATATGTCGCGGTATATCCGCGCTTAAAGATCAAGTATGCG 583
Db 524 TAAATTCAGAGACCTTAATATGTCGCGGTATATCCGCGCTTAAAGATCAAGTATGCG 583
Qy 584 TGGCTGATTAATAAATATGTCGCAACTTTGTGCGCAATCCGCAATATATTAAGTCT 643
Db 584 TGGCTGATTAATAAATATGTCGCAACTTTGTGCGCAATCCGCAATATATTAAGTCT 643
Qy 644 TTGGTGAAGTGGCGGTGCTGCTACCCATACATGATGTTAACCAGCAAACTCGCG 703
Db 644 TTGGTGAAGTGGCGGTGCTGCTACCCATACATGATGTTAACCAGCAAACTCGCG 703
Qy 704 GTCTTTCCATGCTGGTATACCTAATGTGCGGTATATGCTATTTGTCATGGGCTAATACC 763
Db 704 GTCTTTCCATGCTGGTATACCTAATGTGCGGTATATGCTATTTGTCATGGGCTAATACC 763
Qy 764 AATGTCACATCGTGCCTTACCTTAACCAATTTGGCCGCGCTTAAGGAGGAGATTAATG 823
Db 764 AATGTCACATCGTGCCTTACCTTAACCAATTTGGCCGCGCTTAAGGAGGAGATTAATG 823
Qy 824 ATAGGATGTTTGAATTTCTTATGAAGAACCAAGCCACAGATTTAATAAACTTGAAG 883
Db 824 ATAGGATGTTTGAATTTCTTATGAAGAACCAAGCCACAGATTTAATAAACTTGAAG 883
Qy 884 AAAAGTTTAACTCTAGAGAGCGTTACAATTAAGTATGTTCTTTTGGTCCACTG 943
Db 884 AAAAGTTTAACTCTAGAGAGCGTTACAATTAAGTATGTTCTTTTGGTCCACTG 943
Qy 944 TTGAGCATATACAGACCGCTGATGTTGCTTATCCCAAACTCTCGGGAAATGCTTAA 1003
Db 944 TTGAGCATATACAGACCGCTGATGTTGCTTATCCCAAACTCTCGGGAAATGCTTAA 1003

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QY 1004 CTGCTTGGGTAATTCGATACCATATGATGGTAACACTTTCATATGAGGCTATTTT 1063
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1004 GCGCTGGGAAATTCGATACCATATGATGGTAACACTTTCATATGAGGCTATTTT 1063
QY 1064 TCACCTCAATTCCTTAAGCAAAATGCTTGTGTTAAGCAATGGAACCTTGCTCAAT 1123
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1064 CCAATTCATATTCGCAAAACAAATTCGAGAGTGTAAAGAGTGAATCTCTGTGAAT 1123
QY 1124 TTGTGCCAAGTAATGCTGTGATGCTGAACGACCGCCGAGAGCTTGAAGATGGGTG 1183
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1124 ATGTGCTTGGAGTGTGCTGACAGTGAACGAGTCCCGGAAACCTGTGAGAGGGCTG 1183
QY 1184 CTAATTTAAAGAGCTGATTCACGAGAGAAACACAAACAGCTGATATTTTATGATC 1243
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1184 CCATTGTGAAGAGCCCATGATGATGGGAAACACACTACTCTGATATATTTATGAGC 1243
QY 1244 TTGTGCTCACATCTATTTCTGTGTTCCCATGATGCTGTTGTGCAATTTACGTTCAATC 1303
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1244 TTGTGCTCATATTTCTATTTCTCTCTCCCATGATGCTGTTGTGCAATTTACGTTCAAC 1303
QY 1304 ACACCTCCGGTACACCCGCTACTGCTATGCTGCTGACTTTGATTCGGAAGATCTTATTA 1363
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1304 ACACAGCTGGCAGCTCCATTTATTTGTATGCTTTGATTCGATTCGGAAGAAATATTA 1363
QY 1364 ATCCCTATGATTTATGCTGATGAGCGTGTAAAGGGTGTGATGCTGATGAT 1423
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1364 ACCCTATGATTTATGCTGATGAGCGTGTAAAGGGTGTGATGCTGATGATGAGC 1423
QY 1424 TAACCTATTTCTTGTGAATCAATTTGCCCAACGATGCTTAAAGATGCGTGAATACA 1483
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Db 1424 TAACCTATCTCTTGTGAACATTTTGTGAAGAGCGCTGCCAAGAGAAAGCCGCAATACA 1483
QY 1484 AAACATTTGAACGATGATGCTGATATGATGATCAATTTGCCACCACTGCTTATTA 1543
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1484 AAACATTTGAACGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1543
QY 1544 GCAATGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1603
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1544 GCAATGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1603
QY 1604 TATACAGTGTGTTGAATTTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1663
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1604 TCTATAAATGTTAATATATCGGCGATGATGAAATGATGATGATGATGATGATGATGATGAT 1663
QY 1664 AGATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710
   || || || || || || || || || || || || || || || || || || || || || ||
Db 1664 AATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710

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RESULT 9

ABLO2067

ID ABL02067 standard; cDNA; 2001 BP.

AC ABL02067;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 683;

KW Drosophila: developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ss.

OS Drosophila melanogaster.

PN WO2001/1042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

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XX (PEKE ) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
XX P-PSDB; ABB57964.
DR New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT Claim 1; SEQ ID NO 683; 21bp + Sequence listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
XX sequences (AB101840-AB116175) and the encoded proteins
XX (ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 2001 BP; 502 A; 488 C; 521 G; 490 T; 0 other:
XX
Query Match 39.6%; Score 678.8; DB 23; Length 2001;
Best Local Similarity 62.7%; Pred. No. 3.4e-177;
Matches 1074; Conservative 0; Mismatches 637; Indels 3; Gaps 1;
QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGAGATTAATGCTTGAAT 60
   || || || || || || || || || || || || || || || || || || || || || ||
Db 95 ATGAATTAAGAACCTGCTGTTGTGAGCGCTTGTGAGCGCTTGAACCAATCAGAT 154
QY 61 AAGTTTAACTATGTTTAACTACCAATGAACGGTGTGCTGAATCAATATATGAC 120
   || || || || || || || || || || || || || || || || || || || || || ||
Db 155 AAGTCCAGAGTATGCGCAGTCGACATGAACAGTTGTGCGCAGCAGAGTACGCG 214
QY 121 AAAGTGAAGGGCTTAAAGCTTAACTGTATGATGATGATGATGATGATGATGATGATGATGAT 180
   || || || || || || || || || || || || || || || || || || || || || ||
Db 215 CAAGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 274
QY 181 ATACCTGACGCCAACCGCAGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
   || || || || || || || || || || || || || || || || || || || || || ||
Db 275 ATCCCGTACGCCACCTCCGCTGGGGAGTGGCGTTTAAAGGCCCTCAGAGGCCCAT 334
QY 241 CCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
   || || || || || || || || || || || || || || || || || || || || || ||
Db 335 CCTGAGAGGAGTTCGCCACTGCAAGCCGGAAGATGAAGCCCTCAGAGTCAAGTTC 394
QY 301 ATACGGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
   || || || || || || || || || || || || || || || || || || || || || ||
Db 395 GCTTCGATGAAGTGAAGGCTCCGAGGATCCCTATATCTATGATGATGATGATGATGATGATGAT 454
QY 361 CTAATTCGCCAATCAACGCTCCGTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 420
   || || || || || || || || || || || || || || || || || || || || || ||
Db 455 GTGAAGCCCGACAAAGGCTCCCGGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 514
QY 421 GGTGAATAATCATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
   || || || || || || || || || || || || || || || || || || || || || ||
Db 515 GCGGAGGCCAATGCGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
QY 481 ATTAACATCAATATGTTGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
   || || || || || || || || || || || || || || || || || || || || || ||
Db 575 GTCAGATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 634
QY 541 AATGTCGCCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
   || || || || || || || || || || || || || || || || || || || || || ||
Db 635 AATGTACCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 694
QY 601 AATGCGCCACACTGTTGGTGGCAATCCCGATATATTTAGAGTCTTGGTGAAGTGCCGCT 660

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Db 695 AATTTGGCTAGTTTCGGCGAGATCCCACTGCATCTGTTTGTGAGAGATGCTGGA 754
Qy 661 GCTGCCCTACCCACTACATGATGTTTAAAGCAAACTCGGCTCTTTTCCATCGTGGT 720
Db 755 GGGCGCTCCACTACTACTACATGATGCTAACCGATCAGACCAGGCGCTTTTCAATCGGCG 814
Qy 721 ATACTAATGTGGGTAATGCTATTTGTCCATGGGC--TAATACCCCAATGTCACATCGT 777
Db 815 ATCTTCAGATCGGCGCATGTCATTTGCTTGGGCTACAGAGCGCATTAATACCCTAAT 874
Qy 778 GCTTACCTTACCCAAATTTGCGGCTATAGGGTGAAGATATGATTAAGATGTTTG 837
Db 875 CCTACAGGATACCAAGTGGTGTGCTACAGGGGAGACACACAGATGTGCTG 934
Qy 838 GAATTTCTTATGAAAGCCACAGGATTTAATAACTTGAAGAAAGATTTAACT 897
Db 935 GACTTCTTGACAGACGTAAGGCAAGATCTTATTCGGCTGAGGAAATGTCCTGACA 994
Qy 898 CTAGAAAGAGCTACAATAAGTCAATGTTTCTTTTGGTCCACTGTGAGCCATATCAG 957
Db 995 CTGAGAGAAAGCATGAAGAAGATATGTTTCTTTGGCCATCCCTGGAACATCTCC 1054
Qy 958 ACCGCTGATTTGCTTACCCAAACATCCCGGGAATGTTTAACTGTTGGGTAAT 1017
Db 1055 ACCGCCGAATGTGTATATCCAGCTCCAAAGAGATGATGAAGACCGCTTGAGCTAAC 1114
Qy 1018 TCGATACCCACTATGATGGGTAACACTTCAATATGAGGGTCTATTTTCACTTCAATCTT 1077
Db 1115 TCCATCCCATGTTTATAGAAACACTTGTGAGAGGGCTGCTGGGTCCAGAGTA 1174
Qy 1078 AAGCAATGCTTGTGTTGTAAGAAATGGAACCTGTCTCAATTTTGCCAACTGA 1137
Db 1175 AAGCTTATCCCGAGGTGCTGACAGCTGATGTCGACACACTTCTTCCCAAGAA 1234
Qy 1138 TTGGCTGATGCTGAAGCAGCCGCCAGAGACCTTGAATGGGTACTAAATTAAGA 1197
Db 1235 TTGCTGGCCACGAGGCCAGTAAGAAACTGATTCGTGGAGTGCACAGATTCAGAT 1294
Qy 1198 GCTCATGTTACAGAGAAACACCACAGCTGATTAATTTATGAGCTTGTCTCAATC 1257
Db 1295 GTTCATCGCACTGCTCAGAAAGCACCAGATTAATACATGATCTGTTGATTTAG 1354
Qy 1258 TATTTTGTGTTCCCATGATGCTTTGTGCAATACGTTTCAATACACCTCCGTA 1317
Db 1355 TACTTGTGTTCCGCGCTGAGGGGTGTCATTCGCCAGCGCTGAGAGCT 1414
Qy 1318 CCCGCTACCTGATGCTTGCATTTGATGCGAAGATCTTATTAATCCCTATGCTATT 1377
Db 1415 CCAGTATATTTCTATGATATGATCTTCACTCCGAGAGCTCATTTTTCGTACCGCAT 1474
Qy 1378 ATGCGTAGTGAAGTGTGTTAAGGTTTAAAGTATGATGATGAATTAACCTATTTCTTC 1437
Db 1475 ATGCGGTGAGACGGGCTGCAAGGGGTCAGAGCATGCCGAGATTTGAGTACCAATTC 1534
Qy 1438 TGAATCATTTGGCCAAACGATATGCTAAAGAAATCGCTGATTAACAAACATTTGACGT 1497
Db 1535 ACCAGGCTCTGCTCGCGGTGCGGAAGAAAGTCGAGATCGGAACATCGAACCA 1594
Qy 1498 ATGACTGTATATGATATCAATTTGGCACCACTGATATCTTATGCAANTGAATTTGA 1557
Db 1595 ACCGTGCGATCTGACACCAAGTTTGTGCGCAGGGTAATCCCTACAGCAGAAAGATCAAC 1654
Qy 1558 GGTATGGAATATGTTCTGAGGATCAATTAAGAAATCCGAGCAAGTATACAGTGTGG 1617
Db 1655 GGTATGACACTGTCACATTTGATTCAGTTTGCAGAAATCGAGAGGTATCAAAAGTCCCTC 1714
Qy 1618 AATATTAGTGAAGATTTGAATATGATGATGCTGGAATGATTAAGATTAAGCAATGG 1677
Db 1715 AACATGAGTACCTGAGTTCATGATCGATCGAGTGGCCCAATTTGAAGGCTCG 1774
Qy 1678 GAATGATGTTGAAGAAACATAGATTTATTTT 1711

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Db 1775 GAGAGCCTTATGACGACAAACAAGATTTATTTCT 1808
RESULT 10
ID ABL02081 standard; cDNA; 1704 BP.
XX
AC ABL02081;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide seq ID NO 725.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmacological; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PMD, Myers EW;
XX
DR WPI: 2001-656860/75.
XX
DR P-PSDB: ABB57978.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 725; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB12072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 1704 BP; 417 A; 445 C; 460 G; 382 T; 0 other;
Query Match 22.2%; Score 380.2; DB 23; Length 1704;
Best Local Similarity 54.0%; Pred. No. 1.1e-94;
Matches 878; Conservative 0; Mismatches 728; Indels 21; Gaps 4;
Qy 85 ACCAATGAACGGTCTGCTACCTGAATGATATGCAAGTGAAGGCGTTAAAGCTTTA 144
Db 64 AGCAATGACAAAGTCTATCCCGACACGGTCTACGAAAGGTAAAGGGTGAAGTGGCAG 123
Qy 145 ACTGTGTACGATGATCTTCTACTACAGTTTGAAGGATATACCTAGCCCAACCGCATG 204
Db 124 TCCATCTAGGCAACAACACTACTACAGCTTGAAGGGATCCGTTGGCAAGCGCGGTG 183
Qy 205 GGTGACCTGAGATTTAAAGCACCACGACCAACACCTGGAGTGTGCTGATTTGT 264
Db 184 GCGAGGCTCTCCCTTCAAGGCGCCGCGGAGCCAGACACTGTGATGATCAAGCGGTGC 243
Qy 265 TGCATCATTAAGATTAAGTCAAGTGAATTTTATTAACGGGCAAGTGTGTGCTCA 324
Db 244 ACACATGTTGCGCGCAAGCCCTGCGAGATCAACATCGTTCTGAAGCAGGTGCAAGGACG 303

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XX Sequence 6175 BP: 1732 A; 1242 C; 1350 G; 1851 T; 0 other:
 Query Match 21.6%; Score 370.6; DB 23; Length 6175;
 Best Local Similarity 54.5%; Pred. No. 8,76-92;
 Matches 1052; Conservative 0; Mismatches 614; Indels 263; Gaps 5;

46 AATGATGAAATTAAGTATTTAACTATGCTTTAACTACCAATGAAGGCTGTAGCT 105
 3054 AGACCATGACGATTAAGTCCAGACATGCCAGTCAACCAAGAAAGTGTGGCC 3113
 106 GAACTGATATGCAAGTGAAGGCGTTAAAGCTTAACGTGTGATGATATCCATC 165
 3114 GACACGAGTACGCGACAGTGAAGGCTATCAAGCGTCTATCTCTACAGATGTCCTAC 3173
 166 TACAGTTTGAAGGCTATACGCTACGCCAACCGCCAGTGGGTGAGCTGATTTAAAGCA 225
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 226 CCCGACGACCAACACCTGGGATGCTGCTGATGTTGCAATCATTAAGATTAAGTCA 285
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 286 GTGCAAGTGAATTTATTAAGCGCAAGTGTGGCTCAGAGGATGTCTATACCTAAGT 345
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 346 GTCTATAGCAATTAAT----- 360
 3354 GTGTACACCAACATGATGATTAATCTTAATCTGTGATCAATTAACATCGTTAAAC 3413
 361 -----CTAATCCCAACATAACG 380
 3414 GTAATACCTTTAAACATTTTATTTGTGTACATTTTATGAGGACCCGACAGGCTCG 3473
 381 TCCCGTTTATGATACATCATGCTGCTTTATTTACGATGAATCAATCGTATAT 440
 3474 CCGGCTATGCTTGGATTCACGAGAGGCTTCATTTACGCGAGGCCAATCGGAGATG 3533
 441 GTATGCTGCTGATTTATTTCTTAAAGAGTGTGCTGATTAACATCAATCAATCGTT 500
 3534 GTATGCGCCGATTTACTTTATGAAGAGATGTTGTTCTGTCAGATACAGTACCTG 3593
 501 GGGAGCTCT----- 509
 3594 TGGGCTTTGGGTAATCTACTGTGTGCGTATGCGCAATATTTGACTAACAATTAATGA 3653
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 860 CACAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 919

Db 4014 CCAAGATCTTAATCCGCTGAGAGAAATGCTCCTGACACTGAGGAGCAATGAACAGA 4073
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 4134 ACCCTCAAGAGATGATGTAAGAGCCGCTGAGTACTCATCCCATGTTATTAAGAA 4193
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 1643 TTTGATGCTGGAATGATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1702
 4914 TCGATCTGCTGAGATGCTGAGATTTGAAGGTCTGGAGAGGCTCTATGACGACCAAG 4973
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RESULT 12
 ID ABL02099
 standard: cdna: 1665 BP.
 ID ABL02099
 AC ABL02099;
 XX

DT 26-MAR-2002 (first entry)
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 779.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical; gene; ss.
XX Drosophila melanogaster.
OS
XX W0200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
PA
PI Venter JC, Adams M, Li PWD, Myers EW.
XX WPI; 2001-656860/75.
DR P-PSDB; ABB57996.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 779; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB16175), expressed DNA
CC sequences (AB16173-AB16172).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1665 BP; 397 A; 446 C; 468 G; 354 T; 0 other;
SQ
Query Match 21.4%; Score 366.6; DB 23; Length 1665;
Best Local Similarity 52.3%; Pred. No. 6.3e-91;
Matches 860; Conservative 0; Mismatches 774; Indels 9; Gaps 2;
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DB 5 TCGACTTTAAGTCCACACAGACGATACAGSAGCCAGGAAAGACTGTCTGACACCA 64
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DB 65 CCTAGCGACCCATCAAGGGGTGTTAAAGAGAGTCCATCTAGGCGCAGCTCTACTTCACT 124
QY 173 TTGAGGATACCGGTACCGCCACCGCAGTGGTGAAGTGAAGTTTAAAGCCCGCAGC 232
DB 125 TCGAGCGGATCCCTTCCCAAAACCGGCGGTGGGAGCTACGCTACAGAGCTCCCGCAGC 184
QY 233 GACCAACACCCCTGGAGTGTGCGTGAATGTTGCAATCAATAAGATGACAGTCAAG 292
DB 185 CCGCGGAGGTCTGAGCGSAGTCAAGAGCTGACCTCCAGGATCCCAAGCACCTGCGAGA 244
QY 293 TTGATTTTATACGGGCAAGTGTGTGCTCAGAGATTTGCTATACCTAAGTGTCTATA 352
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QY 473 TGTGTGATTAACATATACATATCTTTGGAGCTCTAGAGTTTCTAAGTTTAAATTCAG 532
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QY 533 AAGACCTTAATGTGCGCGGTAAAGCGGCTTAAAGATCAAGTCATGCGCTTGGTGA 592
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 ID ABL02103 standard; cDNA; 1593 BP.
 XX
 AC ABL02103:
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 791.
 XX
 KW Drosophila: developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.

XX
 PI Venter JC, Adams M, Li PWD, Myers EM.
 XX
 DR WPI: 2001-656860/75.
 XX
 DR P-PSDB; ABB58000.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Claim 1; SEQ ID NO 791; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB101840-AB116175).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://ipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 1593 BP; 417 A; 394 C; 405 G; 377 T; 0 other:
 Query Match 18.7%; Score 320.4; DB 23; Length 1593;
 Best Local Similarity 52.7%; Pred. No. 3; e-78;
 Matches 829; Conservative 0; Mismatches 711; Indels 32; Gaps 5;
 QY 111 TGAATATGCAAAATGAAAGGCGTTAAAGCTTAACTGTGATGATGATCTTACTACAG 170
 Db 6 TGACGCGGCTCTGCGGGAGTGAAGAAACAACTCGGGAGGAAGAACTTCTACAG 65
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1663.49 Seconds
(without alignments)
16677.553 Million cell updates/sec

Title: US-09-776-910-7

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Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_esthum:*
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6: em_estpl:*
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8: em_hic:*
9: gb_estl:*
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11: gb_hic:*
12: gb_estc3:*
13: gb_estc4:*
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15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
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20: em_gss_pln:*
21: em_gss_vrt:*
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23: em_gss_man:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	284	15.6	649	9	AI388926	GH19977.5
3	265.2	15.5	688	9	AI403569	GH23036.5
4	236.6	15.0	671	9	AI517692	GH28740.5
5	234.4	14.9	569	13	BI609541	RH14337.5
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7	250	14.6	674	13	BI628316	RH56682.5
8	249.4	14.6	676	13	BI635372	BI635372
9	248.4	14.5	673	13	BI614181	BI614181
10	246.8	14.4	672	13	BI614443	BI614443
11	246.4	14.4	670	13	BI233202	BI233202
12	245	14.3	648	9	AI113763	AI113763
13	245	14.3	648	9	AI403098	AI403098
14	243.4	14.2	646	9	AI109901	AI109901
15	243.4	14.2	646	9	AI293416	AI293416
16	241	14.1	526	9	AI108080	AI108080
17	239.8	14.0	516	9	AI108156	AI108156
18	239.2	13.9	658	13	BI654586	BI654586
19	238.4	13.9	656	13	BI619037	BI619037
20	236.8	13.8	656	13	BI614821	BI614821
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22	236.2	13.8	656	13	BI621302	BI621302
23	233.8	13.6	630	9	AI403830	AI403830
24	233.2	13.6	628	9	AI109573	AI109573
25	231.4	13.5	619	9	AI516869	AI516869
26	231	13.5	638	13	BI564361	BI564361
27	230.8	13.5	628	9	AI513346	AI513346
28	230	13.4	614	12	BG641228	BG641228
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33	228	13.3	633	13	BI370683	BI370683
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45	217.8	12.7	612	13	BI631806	BI631806

ALIGNMENTS

RESULT 1
AI062034 778 bp mRNA linear EST 19-APR-2001
LOCUS
DEFINITION
GH01076.5prime GH Drosophila melanogaster head pot2 Drosophila
melanogaster cDNA clone GH01076 5prime similar to U51050;
Drosophila melanogaster alpha esterase (aet) gene, partial cds,
mRNA sequence.

ACCESSION
AI062034
VERSION
AI062034.1 GI:3337873
KEYWORDS
EST.
SOURCE
fruit fly.
ORGANISM
Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 778)

REFERENCE
Harvey,D., Broksstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP

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Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, estfruitfly@berkeley.edu
Plate: 10 row: G column: 4

FEATURES
High quality sequence stop: 363.
Location/Qualifiers

[illegible]

Plate: RH.143 row: D column: 1
High quality sequence stop: 447.
Location/Qualifiers
1..569

Query Match	14.96;	Score	0
Best Local Similarity	65.58;	Pred. NO. 1.9e-58;	Indels 0;
Matches 3/2;	Conservative	0;	Mismatches 196;
			Gaps 76

[illegible]

D6
1 GCCTACGCGTGTAGCTGAATGGCAAGTGAAAGCGTTA 136

77 CATTACTACCATGAACGGGTGTCGTGAACCTGAATATGCCAAGTGAAAGCGTTA 136

Db
61 GCCAGTGCACCAATGAAACACATTGTCCGCCGACACGGAGTACGGCCAAAGTGACGGGATAC 127

QY | 137 AACGTTACTGTGTACGAATGATCTTCACTCAGCCCGTAACTGGAGGGTATCCCGTACGCCACGC 18

107 CCCCAGTGGGTGAGCTGAGATTTAAAGCACCCACGACCAACACCCCTGGATGTTGTC 25

Db 181 CTCGCTGGGGAGTTCGGGTTAAGCCCTCAGAGGCCCATTCCTGGGAGCGATC 31

257 GTGATTCGTGCATCACTAAGCATACGCGCAGCCAGTGGAGTTG
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |

DB 241 GCGACGCGAGCTGGTCTATACCTAAGTGTCTATACGAATATCTAAATCCGAACTA 37

212 CTTCCTCAGAGGATTGTTCTATACCTAAGTGTCTATACGAATATCTAAATCCGAACTA 38

301 AGGGCTCGAGGACTGGCCTTATCTCATGTGTACACCAACATGTGAAGCCCGACAAAG

377 AACGTCCCGTTTACTATACACACAGGAGGCGGCGCAATCGGG 4

D6 361 CACGCGCCGCAATTTTCTCATTAAAGCATGTGGTGATTACATAAATATC
437 AATATGATGTCCTGATTATTTGCATTAAAGCATGTGGTGATTACATAAATATC

Db 421 AATGGTATGGCCCGATTACTTTNGAAGAAGATGTTGTTCTCGATACGATACAGTACC

497 GTTGGGAGCTCTAGGTTTCTAAAGTAAATGACCGAATG 5

401 GNCATCGCTT
584 CCGGCTTAAAGATCAAGTCATGGCCTT

Db 541 CTGGCCCTCAAGGATCAGGTGCTGGCCCT 568

RESULT 6

B1639480		660 bp	mRNA	linear
LOCUS				
B1639486				
CD32067	5nrime SD Drosophila melanogaster Schneider L2 cell			
CD32067	5 similar t			

alpha-Est7: FBan000112 GO: [carboxyesterase (GO:0004091);
pot2 diacylglycerol kinase (GO:0004091)] located on: 3R 84D5-84D5:: 05

accession , mRNA sequence.
BI639486

VERSION	KEYWORDS	EST.	GI:15541696
SOURCE	ORGANISM	EST.	
		fruit fly.	
		Drosophila melanogaster	
		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
		Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
		Ephyridiidae; Drosophilidae; Drosophila.	
REFERENCE		1 (bases 1 to 660)	
AUTHORS		Lawley,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,	
		Levits,S. and Rubin,G.M.	
TITLE		BDGP/HHMI Drosophila EST Project	
JOURNAL		Unpublished (2001)	
COMMENT		Contact: Stapleton, M.	
		BDGP	
		Lawrence Berkeley National Lab	
		One Cyclotron Rd, Berkeley, CA 94720, USA	
		Fax: 510 486 6798	
		Email: http://www.fruitfly.org/EST , estfruitfly.berkeley.edu	
		Plate: SD 220 row: F column: 7	
		High quality sequence stop: 346.	
FEATURES		Location/Qualifiers	
source		1..660	
		/organism="Drosophila melanogaster"	
		/db_xref="taxon:7227"	
		/clone="SD22067"	
		/clone.lib="SD Drosophila melanogaster Schneider L2 cell	
		/culture.por2"	
		/lab.host="DH5-alpha"	
		/note="Vector: por2; Site:1: EcoRI; Site:2: XhoI; Sized	
		fractionated cDNAs were directly ligated into por2.	
		Plasmid cDNA library."	
BASE COUNT		169 a 170 c 176 g 145 t	
ORIGIN			
Query Match		14.6%; Score 250.2; DB 13; Length 660;	
Best Local Similarity		64.4%; Pred. No. 2.8e-57;	
Matches		391: Conservative 0; Mismatches 213; Indels 3; Gaps 1.	
535	GACCTTAATGTGCGCGGTAATCCGGCCTTAAAGATCAAGTCATGGCCTTGGTGATT	594	
Db	9 GAGCTAAATGTATCCAGGAATATGCTGGCTCAAGATCAGTCTGGCCTCAAGTGGATC	68	
595	AAAAATTAATGCGCAACTTTTGTTGGCAATCCCGATTAATTATACAGTCTTGGTGAAGT	654	
Db	69 AAGAACAATTTGCGGTAGTTTCCGGCGAGATCCCACTGCATCATCTTTTGGAGAGAGT	128	
655	GCGGCTGCGCCTTACCCACATCAATGATGTTAACCAGAACAACTCGCGGTCTTTTCCAT	714	
Db	129 GCTGAGAGGCGCTCCACTACATCAATGATGATTAACCGATCAACCCAAAGGCTCTTTCT	188	
715	GCTGTATATCTAATCTCGGGTAATCTTATTTTTCATGAGC--TAAATACCAATGTCAA	771	
Db	189 CCGGCAATCTTGCATAGTCGGGCAAGTGCATTTTCTTGGGCTTACACGGCGCATTTACC	248	
772	CATGCTGCCCTTACCTTAAACCAATTTGGCGGCTATAAGGTGAGATTAATGATAAGAT	831	
Db	249 CATATATCCCTACAGATAGCCCAAGCTGGTGGCTCAAGCGGAGACAAACGAAGAT	308	
832	GTTTGGAAATTTCTATGAAAGCCAAAGCCACAGATTTAATAAATCTGAGGAAAAAGTT	891	
Db	309 GGTCTGAGATTTCTTACAGAACGTAAGGCAAGGATCTTATTCGCTGAGGAAAAATGTG	368	
892	TTAATCTTAAAGAGACGTAACAATTAAGGTCATGTTTCTTGGTCCCACTTTGAGCCA	951	
Db	369 CTGACACTGAGAGAACGATAGAAAGATTAATGTTTGGCTTTGGCCCACTCGGAGACA	428	
952	TATCAGACCGCTGATTTGTCTTACCCAAACACTCTCGGGAATGTTAAACTGCTTGG	1011	
Db	429 TTCTCCAGCCCGAATGTGTGATATTCCAAGCTCCCAAGAGATGATGAAGACCGCTGG	488	
1012	GCTAATTCGATACCCACATATGATGGTAACTTCAATAGAGAGTCTATTTTTCACCTTA	1071	
Db	489 AATACTCATCCATGTTTATAGAAACCTTGTAAGAGGCGCTGCTGGGTTC	548	

QY	1072	ATTCCTAAGCAAAAGCCGATCGTTGTATAGAAATGGAACCTGTGCTCATTTTGCCCA	1131
Db	549	GAGGTAAGAGCTTATCCCGCAGGTGCTGCAGACGCTTGATGCTGCACACTTTCATTC	608
QY	1132	AGTGAAT	1138
Db	609	AAAGATT	615
RESULT 7			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 367; Conservative			
1	ATGATTTTCACAGCTAGTTCATGTGATGAGAAATTAATAAGATGAAATTAATGCACTTGAAT	60	
Db	111	ATGAAATTAAGAACCTTCGGCTTGTGTGGAGCGCTTGCGCGCTTCAAAAACCATCGAGCAT	170
QY	61	AAGTTTAACTATCGTTTAACTATCCATGCAATGAAGCGTGTAGCTGAACACTAATATGCGC	120
Db	171	AAAGTCGACGATATCGCGACATGACCAATGAAGAAAGTTGTGCGGACACGGAGATGCGC	230
QY	121	AAATGGAAGGCGTTAAAGCTTAACTGTGATGCAATGATTCCTACTACAGTTTGAAGGCT	180

Db 231 CAAGTGGAGGGTATCAACGCTATCTCTACAGATGTGCCTACTGAGTTGAGGGT 290
 QY 181 ATACCGTACGCCCAACGCCCACTGGTGTAGCTGAGATTAAAGCACCCAGGACCAACA 240
 Db 291 ATCCGTCAGCCGACCTCCGGTGGGGAGTTCGGTTTAAAGCCCTCAGAGGCCATT 350
 QY 241 CCCCTGGAGTGTGCTCGTATGTTGCAATCATTAAGATACTAGTCAGCATGTTATT 300
 Db 351 CCCCTGGAGGAGTTCGGGACTGACAGCCAGGAGATTAAGCCGCTCAGTGCAGTTTC 410
 QY 301 ATACCGGCAAGTGTGTGCTCAGAGATTGTCTATACCTAAGTGTCTATACGAATAT 360
 Db 411 GCTCTTGATAGCTAGAGGGCTCCGAGACTGCTCTATCTCAATGCTGACACCAAT 470
 QY 361 CTAATCCCGAAGCAATACGTCCTGTTTATGATATACATGATGATGTTTATTATTC 420
 Db 471 GTGAGGCCGACAGAGCTGCGCCGGTTATGTTGATTACAGGAGAGGCTTCATTATC 530
 QY 421 GGTGAATATCATGATATGATGTGCTGATTTATTTTCAATTAAGAGATGTGTTG 480
 Db 531 GCGAGGCCAATCGGGAAATGATAGCCCGGATTAATGATAAGAGATGTTGTTCTC 590
 QY 481 ATTAACATCATATATGCTTTGGAGCTAGCTTTTCTAAGTTTAATTCAAGACCTT 540
 Db 591 GTACAGATACAGTACCTGCTGGGCTTGTGATTTATGAGCTTAAGTCCCGCCAGCTA 650
 QY 541 AATGTGCGCGGTAAATGCGCGCT 563
 Db 651 AATGTACCGAAGATGCTGCT 673

RESULT 8
 BI635372 676 bp mRNA linear EST 10-SEP-2001
 LOCUS SD16705.5prine SP Drosophila melanogaster Schneider L2 cell culture
 DEFINITION Drosophila melanogaster CDNA clone SD16705 5 similar to
 alpha-EST: Fban0001112 GO: [carboxylesterase (GO:0004091)],
 carboxylesterase (GO:0004091) located on: 3R 84D5-84D5; 05/18/2001
 , mRNA sequence.
 ACCESSION BI635372
 VERSION BI635372.1 GI:15537582
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 676)
 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S. and Rubin, G.M.
 BDGP/HMI Drosophila EST Project
 Unpublished (2001)
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
 Plate: SD 167 row: A column: 5
 High quality sequence stop: 641.
 Location/Qualifiers
 1..676
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="SD16705"
 /clone_11b="SD Drosophila melanogaster Schneider L2 cell
 culture pot2"
 /lab_host="DH5-alpha"
 /note="Vector: pot2; Site 1: EcoRI; Site 2: XhoI; Sized
 fractionated cDNAs were directly ligated into pot2.
 Plasmid cDNA library."
 BASE COUNT 155 a 173 c 194 g 154 t
 ORIGIN

Query Match 14.6%; Score 249.4; DB 13; Length 676;
 Best Local Similarity 65.2%; Pred. No. 4.7e-57;
 Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 1 ATGAATTCACAGTTAGTTGATGAGAAATTAATGAGAGATTAATGCAATTGAAAT 60
 Db 114 ATGAATTAAGAACCTCGGGTTTGTGTGGAGCGCTTGGCGGCTTCATAACCATCGAGCAT 173
 QY 61 AGCTTTTAACTACGTTTAACTACCAATGAAGAGGTGTGATGTAAGATGAATATATG 120
 Db 174 AAGTCCAGACATATGCGCAGTCGACCAATGAAGATGTTGCGGACAGAGATGAGGC 233
 QY 121 AAGTGAAGGCGTTAAAGCTTTAACTGATGATGATGATTCCTACTACAGTTTGGGT 180
 Db 234 CAAGTGGAGGGTATCAAGGCTCTATCTCTACGATGTGCTTACTTACAGTTGAGGGT 293
 QY 181 ATACCGTACGCCCAACCGGCACTGGGTGAGCTGAGATTTAAAGCACCCAGGACCAACA 240
 Db 294 ATCCCGTACGCCCACTCCGGTGGGGAGTTCGGTTTAAAGGCCCTCAGAGGCCATT 353
 QY 241 CCCCTGGAGTGTGCTGCTGATGTTGCAATCATTAAGATAAGTACGTAAGTATGATTT 300
 Db 354 CCTGGAGACGAGTTGCGGACTGACAGCCAGCCAGATTAAGCCGCTCAGGTGAGTTG 413
 QY 301 ATACGGGCAAGATGTGCTCAGAGATTGTCTATACCTAAGTGTCTATACGAATAT 360
 Db 414 GCTTCGATAGATGATGAGGGCTCCGAGGACTGCTCTATCTCAATGTGACCAACAAT 473
 QY 361 CTAATCCCGAAGCTTAACGTCCTTTTATGATATCATATACATGATGTTTATTTATTC 420
 Db 474 GTGAAGCCCGAAGAGGCTCCCGTTATGTTTGTGATTCACGAGAGAGGCTTCATTATTC 533
 QY 421 GGTGAATATCATGATATGATGTGCTGATTTTCAATTAAGAGATGTGTTG 480
 Db 534 GCGAGGCCAATCGGGAATGATATGCGCGGATTAATTAAGAGATGTTGTTCTC 593
 QY 481 ATTAACATCATATATGCTTTGGAGCTAGCTTTTCTAAGTTTAATTCAAGACCTT 540
 Db 594 GTACAGATACAGTACCTGCTGGGCTTGTGATTTATGAGCTTAAGTCCCGCCAGCTA 653
 QY 541 AATGTGCGCGGTAAATGCGCGCT 563
 Db 654 AATGTACCGAAGATGCTGCT 676

RESULT 9
 BI614181 673 bp mRNA linear EST 07-SEP-2001
 LOCUS RH43493.5prine RH Drosophila melanogaster normalized Head p1c-1
 DEFINITION Drosophila melanogaster CDNA clone RH43493 5 similar to alpha-EST:
 Fban0001112 GO: [carboxylesterase (GO:0004091)], carboxylesterase
 (GO:0004091) located on: 3R 84D5-84D5; 08/18/2001, mRNA sequence.
 ACCESSION BI614181
 VERSION BI614181.1 GI:15509706
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 673)
 Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
 J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Fritse, E., George
 R., Gonzalez, M., Guerin, H., Harris, N., Li, P., Liao, G., Mitra, S.,
 Mungall, C.J., Nunoo, J., Pacleb, J., Parasas, V., Park, S.,
 Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S. and Rubin
 G.M.
 BDGP/HMI RH Drosophila EST Project
 Unpublished (2001)
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Db 471 GTTAAAGCCGACAGAGCTCCCGGTTATGTTGGATTACAGGAGAGGCTTCATTATC 530

QY 421 GGTGAATATCATGTGATATGATGCTGCTGATTATTTATTAATAAGAGTGTGTTG 480

Db 531 GCGAGAGCCAAATCGGGAATGATGCGCGGATTTACTTATGAAAGAAATGTTGTTTC 590

QY 481 ATTAACATATCATATTCGTTTGGAGCTAGTCTTCTTAAGTTTAATTCAGAAAGCTT 540

Db 591 GTACAGATACATACGACTTGGGCTTTGGATTATGACTTAAGTCCCGGAGCTA 650

QY 541 AATGTCCCGGTATGCGGCC 562

Db 651 AATGTACCAAGAAATGCTGGCC 672

RESULT 11

LOCUS B1233202 670 bp mRNA linear EST 11-JUL-2001

DEFINITION RE29491.Sprime RE Drosophila melanogaster normalized Embryo, pFic-1

ACCESSION Drosophila melanogaster cDNA clone RE29491.5 similar to alpha-Est7;

VERSION Fban0001112 located on: 3R 84D5-84D5.; 04/12/2001, mRNA sequence.

KEYWORDS B1233202

SOURCE B1233202.1 GI:14700784

ORGANISM EST.

Drosophila melanogaster

fruit fly.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 670)

Stapleton, M., Brokslein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Chame, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Mungall, C.J., Nuno, J., Pacled, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celinkier, S. and Rubin, G.M.

BDGP/HHMI RE Drosophila EST Project

UNPUBLISHED (2001)

CONTACT: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu

Plate: RE.294 row: H column: 7

High quality sequence stop: 534.

Location/Qualifiers

1..670

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="RE29491"

/clone_lib="RE Drosophila melanogaster normalized Embryo pFic-1"

/sex="male and female"

/dev_stage="0-24 hours mixed stage embryonic"

/lab_host="DHS-alpha Tona"

/note="Organ: embryo; Vector: pFic1; Site_1: XhoI; Site_2: BamHI. Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

BASE COUNT 152 a 168 c 194 g 155 t 1 others

ORIGIN

Query Match 14.48; Score 246.4; DB 13; Length 670;

Best Local Similarity 64.98; Pred. No. 3.1e-56;

Matches 364; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 1 ATGAATTTCAAGCTTATGATGAGAAATTAATGAAGAGATTAAATGATGAAT 60

Db 110 ATGAATTAAGAACTTCGCTTGTGAGCGCTTGCGGCGCCCTCAAAACCATGAGCAT 169

QY 61 AAGTTTAAACTATCGTTTAACATGAAGAAAGCGTGTAGCTGAAGATGATGGC 120

Db 170 AAGTCCAGACAGTATGCCAGCTGACCAATGAACAGTTGTGCCGACAGGATACGCC 229

QY 121 AAGTGAAGAGCGGTTAAAGCTTTAACTGTGTACGATGATTCCTACTACGTTTACGGT 180

Db 230 CAAGTAGGGGATCAAGGCTATCTCTACGATGTCCTACTCTGCTTCAGAGGCT 289

QY 181 ATACCGTACGCCCAACCGCCAGTGGTGAAGTGAAGTAAAGCAACCCAGGACCAACA 240

Db 290 ATCCGTACGCCCAAGCTCCGGTGGGGAGTTCGGTTTAAAGCCCTCAGAGGCCATT 349

QY 241 CCCTGGATGTGTGTGCTATTTGTCATATCAATGAAGTAAAGTCAAGTCAATGTTT 300

Db 350 CCCTGGAGCGAGTTGCGCAGTCGACGACGCCAGGAGATGAAGCCGCTCAGGTGCA 409

QY 301 ATACGGGCAAGTGTGTGCTCAGAGTTGCTATACCTAAGTGTCTATCAATATAT 360

Db 410 GTCTTCGATTAAGTAGAGGCTCCGAGAGCTCCTATCTAATGTGTACCAACAAT 469

QY 361 GTAAATCCCGAAACTAAACGTCCTCCGTTTATATACATACATAGTGTGTTTATATC 420

Db 470 GTGAAGCCCGACAAAGCTCCCGGTTATGTTGATTCACGAGAGGCTTCATTATC 529

QY 421 GGTGAATATCATGTGATATGATGCTGCTGATATTTATTAATAAGAGTGTGTTG 480

Db 530 GCGAGGCCAATCGGGAATGTATGCGCGGATTAATTAAGAAAGATGTTGTTCTC 589

QY 481 ATTAACATATCAATATTCGTTTGGAGCTGCTAGCTTTCTTAAGTTTAATTCAGAAAGCTT 540

Db 590 GTACAGATACATACGACTTGGGCTTTGGATTATGAGCTTAAGTCCCGCAGCTA 649

QY 541 AATGTCCCGGTAAATGCGGCC 561

Db 650 AATGTACCAAGAAATGCTGGC 670

RESULT 12

LOCUS A1113763 648 bp mRNA linear EST 19-APR-2001

DEFINITION GH10213.Sprime GH Drosophila melanogaster head pot2 Drosophila

melanogaster cDNA clone GH10213 5prime similar to us1050:

Drosophila melanogaster alpha esterase (aef) gene, partial cds,

mRNA sequence.

ACCESSION A1113763

VERSION A1113763.1 GI:3514566

KEYWORDS EST.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 648)

Harvey, D., Brokslein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project

UNPUBLISHED (2001)

CONTACT: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu

Plate: 102 row: B column: 1

High quality sequence stop: 435.

Location/Qualifiers

1..648

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="GH10213"

/clone_lib="GH Drosophila melanogaster head pot2"

/sex="male and female"

/dev_stage="adult"

/lab_host="DHS - alpha"

/note="Organ: head; Vector: pot2; Site_1: EcoRI; Site_2:

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
 Plate: 224 row: F column: 4
 High quality sequence stop: 533.
 Location/Qualifiers
 1. 648
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_id="GH22464"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="DH5 - alpha"
 /note="Organ: head; Vector: pORT2; Site: 1; EcorI: Site-2;
 XhoI: Sized fractionated cDNAs were directly ligated into
 pORT2. Plasmid cDNA library."

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

14.3%; Score 245; DB 9; Length 648;

Query Match
 Best Local Similarity 65.0%; Pred. No. 7.4e-56;
 Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

VERSION	AT109901.1 GI:3478225					
KEYWORDS	EST.					
SOURCE	fruit fly.					
ORGANISM	<i>Drosophila melanogaster</i>					
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					
AUTHORS	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;					
TITLE	Ephydroidae; Drosophilidae; Drosophila.					
JOURNAL	1 (bases 1 to 646)					
COMMENT	Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M. BDGP/HMT Drosophila EST Project Unpublished (2001) Contact: Stapleton, M. BDGP Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu Plates: 92 row: H column: 8 High quality sequence stop: 513. Location/Qualifiers 1..646 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="GH09292" /clone_lib="GH Drosophila melanogaster head por2" /sex="male and female" /dev_stage="adult" /lab_host="DH5 - alpha" /note="Organ. head; Vector: por2; Site_1: EcORI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into por2. Plasmid cDNA library." BASE COUNT 152 a 163 c 182 g 149 t ORIGIN					
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ACCESSION	AI293416		
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KEYWORDS	EST.		
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REFERENCE	1 (bases 1 to 646)		
AUTHORS	Harvey,D., Brokstein,P., Hong,L., Evans-Holim,M., Su,C., Tsang,G.,		
TITLE	Lewis,S., and Rubin,G.M.		
JOURNAL	BDFP/HHMI Drosophila EST Project		
COMMENT	Unpublished (2001)		
	Contact: Stapleton, M.		
	BDFP		
	Lawrence Berkeley National Lab		
	One Cyclotron Rd, Berkeley, CA 94720, USA		
	Fax: 510 486 6798		
	Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu		
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Best Local Similarity	64.8%; Pred.No. 2e-95;		
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Searched: 441362 seqs, 15338381 residues

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Minimum DB seq length: 0
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SUMMARIES

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ALIGNMENTS

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Patent No. 5843758
GENERAL INFORMATION:
APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKESHOTT, John G.
APPLICANT: SMYTH, Kerrie A.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669, 524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 1:
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US-08-669-524-1
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OY 1381 CGTAGTGAACGCTGTTAAGGTTAGTCAATGCTGATGAATTTAACCATTCTTCTG 1440
Db 1381 CGTAGTGAACGCTGTTAAGGTTAGTCAATGCTGATGAATTTAACCATTCTTCTG 1440
OY 1441 AATCAATTTGCCAAACGTTATGCTTAAAGATGCGTGAATACAAACATTTAGCATG 1500
Db 1441 AATCAATTTGCCAAACGTTATGCTTAAAGATGCGTGAATACAAACATTTAGCATG 1500
OY 1501 ACTGATATATGATCAATTTGCCACACCTGTAATCCCTTATAGCAATGAATTTGAAGT 1560
Db 1501 ACTGATATATGATCAATTTGCCACACCTGTAATCCCTTATAGCAATGAATTTGAAGT 1560
OY 1561 ATGAAATGTTTCCGCGATCCAAATTTAAGAAATCGAGAAATGATTAAGTGTGAT 1620
Db 1561 ATGAAATGTTTCCGCGATCCAAATTTAAGAAATCGAGAAATGATTAAGTGTGAT 1620
OY 1621 ATTAGTGAACGATTTGAATGATGCTGCTGAAGGATTAAGATTTAACAATGGA 1680
Db 1621 ATTAGTGAACGATTTGAATGATGCTGCTGAAGGATTAAGATTTAACAATGGA 1680
OY 1681 TCGATGTTTGAAGAAACATGAGATTTATTTT 1713
Db 1681 TCGATGTTTGAAGAAACATGAGATTTATTTT 1713

RESULT 3
US-09-068-960-9
; Sequence 9, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patenclin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-9

Query Match 99.4%; Score 1703.4; DB 4; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 ATGAATTTCAACGTTAGTTTGATGGAGAAATTTAAATGAAGATTAAATGATGAAAT 60
Db 1 ATGAATTTCAACGTTAGTTTGATGGAGAAATTTAAATGAAGATTAAATGATGAAAT 60
OY 61 AAGTTTTTAACTATCGTTTAACTACCAATGAAGGTTGTTAGCTGAAGCTAAATATGTC 120
Db 61 AAGTTTTTAACTATCGTTTAACTACCAATGAAGGTTGTTAGCTGAAGCTAAATATGTC 120

Db	1141	GCTGATGCTGAACGCACCCGCCCCACAGACCTTGGAAATGGGTCGTAAATTAATAAAGGCT	1200
QY	1201	CATGTTACAGGAGAAACACCAACACAGCTGATAATTTATGATGCTTTGGTCACATCTAT	1260
Db	1201	CATGTTACAGGAGAAACACCAACACAGCTGATAATTTATGATGCTTTGGTCACATCTAT	1260
QY	1261	TTCTGTTGTTCCCATGCAATGCTTTGTTGCAATTTAGCTTTTCAATCAACACCTCGGTACACC	1320
Db	1261	TTCTGTTGTTCCCATGCAATGCTTTGTTGCAATTTAGCTTTTCAATCAACACCTCGGTACACC	1320
QY	1321	GTCATCTGTTGCTGCTTGCTGACTTTTGATTCGGGAACATCTATTATCCCTATCGTATTATG	1380
Db	1321	GTCATCTGTTGCTGCTTGCTGACTTTTGATTCGGGAACATCTATTATCCCTATCGTATTATG	1380
QY	1381	CGTAGTGACGACGTGTTGTTAAAGGTGTTAGTATCATGCTGTATGAATTAACCTATTCTCTGG	1440
Db	1381	CGTAGTGACGACGTGTTGTTAAAGGTGTTAGTATCATGCTGTATGAATTAACCTATTCTCTGG	1440
QY	1441	AATCAATTTGGCCAAACGTAATGCCCTAAAGAAATCGCGTGAATCAAAACAAATGAACGTATG	1500
Db	1441	AATCAATTTGGCCAAACGTAATGCCCTAAAGAAATCGCGTGAATCAAAACAAATGAACGTATG	1500
QY	1501	ACTGCTATATGGAATACAAATTTGGCCACACAGTGTATGCTTATACCATTAAGTAATGAAGT	1560
Db	1501	ACTGCTATATGGAATACAAATTTGGCCACACAGTGTATGCTTATACCATTAAGTAATGAAGT	1560
QY	1561	ATGGAATAATGTTTCTCTGGGATCCCAATTAAGAAATCCGACGAAGTATCAAGTCTTTGAAT	1620
Db	1561	ATGGAATAATGTTTCTCTGGGATCCCAATTAAGAAATCCGATGAAGTATCAAGTCTTTGAAT	1620
QY	1621	ATTAGTAGCAATTTGAAATAATGATTGATGCTCGGAATGATTAAGATTAAACAATGGGAA	1680
Db	1621	ATTAGTAGCAATTTGAAATAATGATTGATGCTCGGAATGATTAAGATTAAACAATGGGAG	1680
QY	1681	TCGATGTTTGAATAACATAGAGATTTATTTTATG	1713
Db	1681	TCGATGTTTGAATAACATAGAGATTTATTTTATG	1713
RESULT 4			
US-09-068-960-1			
; Sequence 1, Application US/09068960A			
; Patent No. 6235515			
; GENERAL INFORMATION:			
; APPLICANT: Commonwealth Scientific and Industrial R&sch. Org.			
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE			
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051			
; CURRENT APPLICATION NUMBER: US/09/068,960A			
; CURRENT FILING DATE: 1998-05-20			
; EARLIER APPLICATION NUMBER: PCT/US96/00746			
; EARLIER FILING DATE: 1996-11-22			
; EARLIER APPLICATION NUMBER: AU 6751			
; NUMBER OF SEQ ID NOS: 43			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 1713			
; TYPE: DNA			
; ORGANISM: Lucilia cuprina			
US-09-068-960-1			
Query Match			
Best Local Similarity 99.3%; Score 1701.8; DB 4; Length 1713;			
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
QY	1	ATGAATTTTCACGCTAGTTTGATGGAAGAATTAATAATGGAAGATTAAATGATGTAATAAT	60
Db	1	ATGAATTTTCACGCTAGTTTGATGGAAGAATTAATAATGGAAGATTAAATGATGTAATAAT	60
QY	61	AAGTTTAAACATATCGTTTAACTACCAATGAAGAGGTGCTAGCTGAACATGAATATGCTGC	120
Db	61	AAGTTTAAACATATCGTTTAACTACCAATGAAGAGGTGCTAGCTGAACATGAATATGCTGC	120

QY 121 AAAGTGAAGGCGTTAAACGTTTAACTGTACGATGATTCCTACTACAGTTTGGAGGT 180
DB 121 AAAGTGAAGGCGTTAAACGTTTAACTGTACGATGATTCCTACTACAGTTTGGAGGT 180
QY 181 ATACCGTACGCCCAACGCCGAGTGGAGTGAATTTAAAGCACCCAGCAGCAACA 240
DB 181 ATACCGTACGCCCAACGCCGAGTGGAGTGAATTTAAAGCACCCAGCAGCAACA 240
QY 241 CCTGGATGGTGTGCTGATTTGTGCAATCAATAAAGATGATGCTGCAAGTTGATTT 300
DB 241 CCTGGATGGTGTGCTGATTTGTGCAATCAATAAAGATGATGCTGCAAGTTGATTT 300
QY 301 ATAAAGGCGCAAGTGTGCTGAGAGATGTCTATCTAAGTGTCTATACGAATAT 360
DB 301 ATAAAGGCGCAAGTGTGCTGAGAGATGTCTATCTAAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTGTTTACTATACATACATGCTGTGTTTATATC 420
DB 361 CTAAATCCCGAACTAAACGTCCTGTTTACTATACATACATGCTGTGTTTATATC 420
QY 421 GGTGAAATCANTCGTATATGATGCTGATTTATTCATTAATAAGATGCTGTG 480
DB 421 GGTGAAATCANTCGTATATGATGCTGATTTATTCATTAATAAGATGCTGTG 480
QY 481 ATTAACATACATATCTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAACCTT 540
DB 481 ATTAACATACATATCTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAACCTT 540
QY 541 AATGCGCCGGTAATGCGGCTTAAAGATCAAGTCAATGCGCTGCTGGATTAATAAT 600
DB 541 AATGCGCCGGTAATGCGGCTTAAAGATCAAGTCAATGCGCTGCTGGATTAATAAT 600
QY 601 AATGCGCAACTTGTGGGCAATCCGATATATTAAGTCTTGTGGTGAAGTCCGGT 660
DB 601 AATGCGCAACTTGTGGGCAATCCGATATATTAAGTCTTGTGGTGAAGTCCGGT 660
QY 661 GCTGCTCTACCCACTACATGATGTAAACGAACAACCTCGCGCTTTTCCATGCTGT 720
DB 661 GCTGCTCTACCCACTACATGATGTAAACGAACAACCTCGCGCTTTTCCATGCTGT 720
QY 721 ATACTAAATGCTGGGTAATGCTATTTTGTCCATGAGGCTAATACCAATGTCACATGCTGCC 780
DB 721 ATACTAAATGCTGGGTAATGCTATTTTGTCCATGAGGCTAATACCAATGTCACATGCTGCC 780
QY 781 TTACACTTACGCAATTTGGCGGCTATAAGGCTGAGATATGATTAAGATGTTTGGAA 840
DB 781 TTACACTTACGCAATTTGGCGGCTATAAGGCTGAGATATGATTAAGATGTTTGGAA 840
QY 841 TTTCTTATGAAGCCCAACGAGATTTAAATAACTTGAAGAAAAGTTTAACTGTA 900
DB 841 TTTCTTATGAAGCCCAACGAGATTTAAATAACTTGAAGAAAAGTTTAACTGTA 900
QY 901 GAAGAGCGTACAAATTAAGTCAATGCTTTTGTGCCACTGTTGAGCCATATCAGAC 960
DB 901 GAAGAGCGTACAAATTAAGTCAATGCTTTTGTGCCACTGTTGAGCCATATCAGAC 960
QY 961 GCTGATTTGTCTTACCAACATCTCTGGGAAATGCTTAAACGCTTGGGTAATTCG 1020
DB 961 GCTGATTTGTCTTACCAACATCTCTGGGAAATGCTTAAACGCTTGGGTAATTCG 1020
QY 1021 ATACCATATGATGGGTAACTCATATGAGGCTATTTTTCATTCATTTCTTAAG 1080
DB 1021 ATACCATATGATGGGTAACTCATATGAGGCTATTTTTCATTCATTTCTTAAG 1080
QY 1081 CAATGCTATGCTTTGAAGAAATGGAACCTTGTCAATTTTGTGCCAAGTGAATG 1140
DB 1081 CAATGCTATGCTTTGAAGAAATGGAACCTTGTCAATTTTGTGCCAAGTGAATG 1140
QY 1141 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGGAAATGCTGCTAAATTTAAAGGCT 1200
DB 1141 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGGAAATGCTGCTAAATTTAAAGGCT 1200
QY 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTGCTCACAATCTAT 1260

DB 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTGCTCACAATCTAT 1260
QY 1261 TTTCTGTTCCCATGATCAGCTTTTGTGCAATTTAGCTTTCAATCACACTCCGGTACACC 1320
DB 1261 TTTCTGTTCCCATGATCAGCTTTTGTGCAATTTAGCTTTCAATCACACTCCGGTACACC 1320
QY 1321 GTCATCTGTATGCTGTGACCTTTGATGCGAAGATCTTATTAATCCCTATGCTATTAG 1380
DB 1321 GTCATCTGTATGCTGTGACCTTTGATGCGAAGATCTTATTAATCCCTATGCTATTAG 1380
QY 1381 CGTATGAGCTGTGCTGTTAAGGCTGTTAGTCATGCTGATGATTAATTAACCTATTCTTCG 1440
DB 1381 CGTATGAGCTGTGCTGTTAAGGCTGTTAGTCATGCTGATGATTAATTAACCTATTCTTCG 1440
QY 1441 AATCAATTTGCCAAACGATATGCTTAAAGATGCGTGAATACAAACAAATTAACGATG 1500
DB 1441 AATCAATTTGCCAAACGATATGCTTAAAGATGCGTGAATACAAACAAATTAACGATG 1500
QY 1501 ACTGATATGATGATCAATTTTCCACCTGCTATCTTATGCAATGAATTAAGT 1560
DB 1501 ACTGATATGATGATCAATTTTCCACCTGCTATCTTATGCAATGAATTAAGT 1560
QY 1561 ATGGAATATGTTTCCCTGGGATCCAAATTAAGAAATCCGAGAAATTAAGTGTGAT 1620
DB 1561 ATGGAATATGTTTCCCTGGGATCCAAATTAAGAAATCCGAGAAATTAAGTGTGAT 1620
QY 1621 ATTAGTCAATTTGAATAATGATGATGCTGCTGAATAGATTAACATTAAGGAA 1680
DB 1621 ATTAGTCAATTTGAATAATGATGATGCTGCTGAATAGATTAACATTAAGGAA 1680
QY 1681 TCGATGTTTGAATAACATAGAGATTTATTAG 1713
DB 1681 TCGATGTTTGAATAACATAGAGATTTATTAG 1713

RESULT 5
US-09-068-960-3
Sequence 3, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rarch. Org.
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
EARLIER FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patenlin Ver. 2.0
SEQ ID NO 3
LENGTH: 1713
TYPE: DNA
ORGANISM: Lucilia cuprina
US-09-068-960-3

Query Match 99.3%; Score 1701.8; DB 4; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTTGTGAGAGAAATTTAAATGAGATTAATGCAATGAAT 60
DB 1 ATGAATTTCAACGTTAGTTTGTGAGAGAAATTTAAATGAGATTAATGCAATGAAT 60
QY 61 AAGTTTAAACTATGCTTTTACATCAATGAAGAGGCTGATGCTGAAGTGAATATGCT 120
DB 61 AAGTTTAAACTATGCTTTTACATCAATGAAGAGGCTGATGCTGAAGTGAATATGCT 120
QY 121 AAAGTGAAGGCGTTAAACGTTTAACTGTACGATGATTCCTACTACAGTTTGGAGGT 180
DB 121 AAAGTGAAGGCGTTAAACGTTTAACTGTACGATGATTCCTACTACAGTTTGGAGGT 180

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OY 181 ATACGTTACGACCAACCGCCAGTGGTGTAGCTGAGATTAAAGCACCACCGACCAACA 240
    |||||
DB 181 ATACGTTACGACCAACCGCCAGTGGTGTAGCTGAGATTAAAGCACCACCGACCAACA 240
OY 241 CCTGGGATGCTGTGGTGTATGTCATATCAATAAAGTAAGTCAAGTGTGATTTT 300
    |||||
DB 241 CCTGGGATGCTGTGGTGTATGTCATATCAATAAAGTCAAGTGTGATTTT 300
OY 301 ATACGCGCAAAAGTGTGTGCTCAGAGATTTGTCTATACCTAAGTGTCTATACGAATAT 360
    |||||
DB 301 ATACGCGCAAAAGTGTGTGCTCAGAGATTTGTCTATACCTAAGTGTCTATACGAATAT 360
OY 361 CTAAATCCGAACTAAAGCTCCGCTTTTATATACATACATAGTGTGTGTTATATTC 420
    |||||
DB 361 CTAAATCCGAACTAAAGCTCCGCTTTTATATACATACATAGTGTGTGTTATATTC 420
OY 421 GGTGAAATCATCGTATATGTATGTATGCTCCGATTTATTTTCAAAAAGATGTGTG 480
    |||||
DB 421 GGTGAAATCATCGTATATGTATGTATGCTCCGATTTATTTTCAAAAAGATGTGTG 480
OY 481 ATTACATACATATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT 540
    |||||
DB 481 ATTACATACATATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT 540
OY 541 AATGCGCCGCTAATGCCGCTTAAAGATCAAGTATGCTGCTTGGATTTAAAT 600
    |||||
DB 541 AATGCGCCGCTAATGCCGCTTAAAGATCAAGTATGCTGCTTGGATTTAAAT 600
OY 601 AATGCGCCGCTAATGCCGCTTAAAGATCAAGTATGCTGCTTGGATTTAAAT 660
    |||||
DB 601 AATGCGCCGCTAATGCCGCTTAAAGATCAAGTATGCTGCTTGGATTTAAAT 660
OY 661 GCTGCTCTACACCATATGATGTTAAACCGCAAACTCCGCTTTTCCATGCTGT 720
    |||||
DB 661 GCTGCTCTACACCATATGATGTTAAACCGCAAACTCCGCTTTTCCATGCTGT 720
OY 721 ATACTATGTGCGGTATGCTATTTTGTCCATGCTGCTTAAACCTGCTTAAACCTGCT 780
    |||||
DB 721 ATACTATGTGCGGTATGCTATTTTGTCCATGCTGCTTAAACCTGCTTAAACCTGCT 780
OY 781 TTACCTTATGAGCAAAATGCGGCTATTAAGGATGAGATTAATGAAGATTTTGA 840
    |||||
DB 781 TTACCTTATGAGCAAAATGCGGCTATTAAGGATGAGATTAATGAAGATTTTGA 840
OY 841 TTTCTTATGAAAGCCAGCAGAGATTTAAACTTGAAGAAAGTTTAACTCTA 900
    |||||
DB 841 TTTCTTATGAAAGCCAGCAGAGATTTAAACTTGAAGAAAGTTTAACTCTA 900
OY 901 GAAGAGCGTACAAATTAAGGATTTTCTGCTTGTCCACTGTGAGCCATATCAGACC 960
    |||||
DB 901 GAAGAGCGTACAAATTAAGGATTTTCTGCTTGTCCACTGTGAGCCATATCAGACC 960
OY 961 GCTGATGTGCTTACCCAAATCTCTCGGAAATGCTTAAACCTGCTTGGGTAATTCG 1020
    |||||
DB 961 GCTGATGTGCTTACCCAAATCTCTCGGAAATGCTTAAACCTGCTTGGGTAATTCG 1020
OY 1021 ATACCCAGTATGATGATTAACCTCATATGAGGCTATTTTCTACCTCAATTTTAA 1080
    |||||
DB 1021 ATACCCAGTATGATGATTAACCTCATATGAGGCTATTTTCTACCTCAATTTTAA 1080
OY 1081 CAATGCTATGCTTGTAAAGAAATTTGAACCTGTGCAATTTTGTGCAAGAAATTCG 1140
    |||||
DB 1081 CAATGCTATGCTTGTAAAGAAATTTGAACCTGTGCAATTTTGTGCAAGAAATTCG 1140
OY 1141 GCTGATGCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1200
    |||||
DB 1141 GCTGATGCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1200
OY 1201 CATGTTACAGAGAAACCAACAGCAGTATATTTATGATGCTTGTGCTCATCATAT 1260
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DB 1201 CATGTTACAGAGAAACCAACAGCAGTATATTTATGATGCTTGTGCTCATCATAT 1260
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OY 1261 TTTCTGTTCCCATGCTATGCTTTGTGCAATTAAGCTTTCATACACCCCGGTACACC 1320
    |||||
DB 1261 TTTCTGTTCCCATGCTATGCTTTGTGCAATTAAGCTTTCATACACCCCGGTACACC 1320
OY 1321 GTCTACCTGATGCTGCTTGCAGCTTTGATTTGGAAGATCTTATTAATCCCATGCTATG 1380
    |||||
DB 1321 GTCTACCTGATGCTGCTTGCAGCTTTGATTTGGAAGATCTTATTAATCCCATGCTATG 1380
OY 1381 GCTAGTGAAGCTGCTGTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTG 1440
    |||||
DB 1381 GCTAGTGAAGCTGCTGTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTG 1440
OY 1441 AATCAATTTGCGCAAAAGTATGCTTAAAGATCCGCTAATACAAACAAATGAACTATG 1500
    |||||
DB 1441 AATCAATTTGCGCAAAAGTATGCTTAAAGATCCGCTAATACAAACAAATGAACTATG 1500
OY 1501 ACTGATATGATATCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
    |||||
DB 1501 ACTGATATGATATCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
OY 1561 ATGGAATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
    |||||
DB 1561 ATGGAATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
OY 1621 ATTAGTACCAATTTGAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
    |||||
DB 1621 ATTAGTACCAATTTGAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
OY 1681 TCGATGTTTGAATAACATAGAGATTTATTTAG 1713
    |||||
DB 1681 TCGATGTTTGAATAACATAGAGATTTATTTAG 1713

RESULT 6
US-09-068-960-5
; Sequence 5, Application US/09068960A
; Patent No. 6235515
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-5

Query Match          99.2%; Score 1698.6; DB 4; Length 1713;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-669-524-2

Query Match 98.28; Score 1683; DB 2; Length 1713;
Best Local Similarity 98.28; Pred. No. 0;
Matches 1683; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 1 ATGATTTTCAACGTTAGTTGATGAGAAATTAATGSAAGATTAAATGTCATGAAAT 60
DB 1 ATGATTTTCAACGTTAGTTGATGAGAAATTAATGSAAGATTAAATGTCATGAAAT 60
QY 61 AAGTTTTTAACTATGCTTAACTACCAATGAAGAAAGGTTGAGTGAAGTATGCG 120
DB 61 AAGTTTTTAACTATGCTTAACTACCAATGAAGAAAGGTTGAGTGAAGTATGCG 120
QY 121 AAGTGAAGGCGTTAAACGTTAGTGTAGATGATTCCTACTACAGTTTGAAGGT 180
DB 121 AAGTGAAGGCGTTAAACGTTAGTGTAGATGATTCCTACTACAGTTTGAAGGT 180
QY 181 ATACCGTACGCGCAACCGCGAGTGGTGAAGTAAAGCAGCCGACGACCAACA 240
DB 181 ATACCGTACGCGCAACCGCGAGTGGTGAAGTAAAGCAGCCGACGACCAACA 240
QY 241 CCCGTGATGCTGCTGATTTGCAATCATTAAGATAAGTCAAGTGAATTT 300
DB 241 CCCGTGATGCTGCTGATTTGCAATCATTAAGATAAGTCAAGTGAATTT 300
QY 301 ATACCGGCAAGTGTGGTGCAGAGATTTGCTATACCTAAGTGTCTATACCAAT 360
DB 301 ATACCGGCAAGTGTGGTGCAGAGATTTGCTATACCTAAGTGTCTATACCAAT 360
QY 361 CTAAATCCGCAAACTAAGCGTCCGTTTATGATACATACATGCTGCTGATTTAT 420
DB 361 CTAAATCCGCAAACTAAGCGTCCGTTTATGATACATACATGCTGCTGATTTAT 420
QY 421 GGTGAATATATGCTGATATGATGCTGCTGATTTATTTCAATTAAGATGCTG 480
DB 421 GGTGAATATATGCTGATATGATGCTGCTGATTTATTTCAATTAAGATGCTG 480
QY 481 ATTAACATATATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 ATTAACATATATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 AATGTCGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 AATGTCGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AATGTCGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 AATGTCGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GCTGCGCTACCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 GCTGCGCTACCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 ATACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 ATACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 TTACCTTACGCAATTTGCGCGCTATTAAGGAGATATATATAGATGCTTTGG 840
DB 781 TTACCTTACGCAATTTGCGCGCTATTAAGGAGATATATATAGATGCTTTGG 840
QY 841 TTCTTATGAAAGCGCAAGCGACAGATTTAATAAAGTTGAGGAAAGTTTAACT 900
DB 841 TTCTTATGAAAGCGCAAGCGACAGATTTAATAAAGTTGAGGAAAGTTTAACT 900
QY 901 GAAGAGCGTACAAATAGGCTATGCTTTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 GAAGAGCGTACAAATAGGCTATGCTTTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 GCTGATTTGCTTACCGCAACATCTCGGGAATGTTAAAGCTGCTGCTGCTG 1020
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DB 961 GCTGATTTGCTTACCGCAACATCTCGGGAATGTTAAAGTTGCTGCTGCTG 1020
QY 1021 ATACCGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 ATACCGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1081 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 GCTGATGCTGCAAGCGACCGCGCGAGAGCTTGGAAATGCTGCTGCTGCTGCT 1200
DB 1141 GCTGATGCTGCAAGCGACCGCGCGAGAGCTTGGAAATGCTGCTGCTGCTGCT 1200
QY 1201 CATGCTACAGAGAGAAACCAACAGCTGATATTTATGATCTTCTGCTGCT 1260
DB 1201 CATGCTACAGAGAGAAACCAACAGCTGATATTTATGATCTTCTGCTGCT 1260
QY 1261 TTCTGCTTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 TTCTGCTTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 GTCTACTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 GTCTACTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 CTTAGTGGAGTGGTGTGTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 CTTAGTGGAGTGGTGTGTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 AATCAATTTGGCCAAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 AATCAATTTGGCCAAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 ACTGCTATATGATATACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 ACTGCTATATGATATACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 ATTAAGTACGCAATTTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 ATTAAGTACGCAATTTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713

RESULT 8
US-09-068-960-14
: Sequence 14, Application US/09068960A
: Patent No. 6235515
: GENERAL INFORMATION:
: APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
: TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
: FILE REFERENCE: Attorney Docket No. 6235515 50179-051
: CURRENT FILING DATE: 1998-05-20
: EARLIER APPLICATION NUMBER: PCT/US96/00746
: EARLIER FILING DATE: 1996-11-22
: EARLIER APPLICATION NUMBER: AU 6751
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 14
: LENGTH: 1710
: TYPE: DNA
: ORGANISM: Musca domestica
US-09-068-960-14
```



```

NAME: jerser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1584
US-08-747-221B-51

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Query Match	10.6%	Score 101.2;	DB 3;	Length 1584;
Best Local Similarity	56.48;	Pred. No. 3,8e+43;		
Matches 361;	Conservative	0;	Mismatches 273;	Indels 6;
				Gaps 1

[illegible]

RESULT 10
US-08-747-221B-52/C
; Sequence 52, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
;

APPLICANT: Wtelnieski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, proteins and Uses thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/74/221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

Query Match	10.6%	Score 181.2;	DB 3;	Length 1584;
Best Local Similarity	56.48;	Pred. No. 3,8e+43;		
Matches 361; Conservative	0;	Mismatches 273;	Indels 6;	Gaps 1

Oy	116	ATGGCANAAGTAAAGGGGTGTTAAACGTTTAACTGTTGTACGATGATTCCTACTACATTTTGG	175
Db	1556	AAGGACTTTTAAAGGAAAGAAAGCAATATTAGTAAAGAAAGAAATGTGTTCCATGATTATT	1497
Oy	176	AGGGTATACGGTACGCCCAACCGCCGAGTGGGAGCTAGATTTTAAAGCAACCCACGCGAC	235
Db	1496	CTGGAAATTCATATGATGCCAAACCTCGTAGTGGTACGATCTAAAGTTTAAACCCCTCAACCTGG	1437
Oy	236	CACACCCCTGGAGTGTGCTCGTGAATGTTGCATCATTAAGAGATTAACCTACGTCGCAAGTTG	295
Db	1436	CAGAACCTTGGTACAGGTGTTCTGATGACATAGTAAAGAAAGGAATGTTAGATCAGTAC	1377
Oy	296	ATTTTATACGGGCAAGSTGTGTGGCTCAGAGATGTTCTATACCTAAGTGTCTATACGA	355
Db	1376	ATTTTATTAATAAAATTTTAACTAGGGGCTCAAGATTTGTTTAACTCCATGTTCTATGTAC	1317
Oy	356	ATATCTTAATCCCGAACTAACGTCGCCCTTTAGTATACATCATGATGTTGTTTAA	415
Db	1316	CAAAAACATCAGAGAATCACTTCTTCCAGAAATGATGATGATCATGATGAGAGAGGCTCT	1257
Oy	416	TTTATCGGTAAATCATGCTGATATGTATGTCCTGATATTTTCAATTAATAAAGGATGGG	475
Db	1256	TCATGGGATCTGAAATVATGTATGTATGTGTGCTCTGAAATTTTGAATGATATATGGAATG	1197
Oy	476	TGTTGATTAACATCAATATCGTTTGGAGAGCTAGAGTTCCTTAAGTTTAAATTCAGAG	535
Db	1196	TTTGTGTACTTTCATTTATCATTTAGGTGTTTGGGATTTTGAACCTGGGAAATAGAG	1137
Oy	536	ACCTTAATGTCCCGGTAAATGCCGCTTAAAGATCAAGTCATGCGCTGCGGTGGATTA	595
Db	1136	AA-----GGCGCCGGCAATGTGGTTGATGAGACAGAGTTGAAGCTCTTAATATGGGTAA	1083

TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1584 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-005-051-52

Query Match 10.6%; Score 181.2; DB 4; Length 1584;
 Best Local Similarity 56.4%; Pred. No. 3.8e-43;
 Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

QY 116 ATGGCAAGTGAAGCGTTAAAGCTTAACTGTACATGATCTCTACTACTTTTG 175
 DB 1556 AAGTACTTAAAGAGAAAGAGCAATTAAGTAAAGAAAGAAATGTTCCTACTATT 1497
 QY 176 AGGGTATACCGTACGCCCAACCGCCAGTGGTGAAGTGAATTTAAGACCCGAC 235
 DB 1496 CTGGAAATCCATATGCCAAACCTCTGTAGTGAATTAAGCCACCTCAACCTG 1437
 QY 236 CAACACCTGGGATGGTGGCGATGTGTCATCAATCAATGAATAGTCAAGTTG 295
 DB 1436 CAGAACCTTGTCAGGTGTTCTTCACTAGTAAAGAGGAAATGTGTAGATCAGTAC 1377
 QY 296 ATTTTATACGGGCAAGTGTGGCTCAGAGATGTCTATACCTAAGTGTATACGA 355
 DB 1376 ATTTTATTAATAAATAAAGTGAAGGGCTGAAGATTGTTTACCTCATGTCTATGAC 1317
 QY 356 ATATCTAATCCCAACTAAGCTCCGTTTAACTATACATCAATGCTGTGTTTA 415
 DB 1316 CAAAAACATCAGAAATCACTCTTCCAGTAAATGATGATGAGAGAGGCTTCT 1257
 QY 416 TTATGGTGAATATCATGTGATATGATGCTCTGATTTATTTATTAAGAGATGG 475
 DB 1256 TCATGGGATCTGAAATGATGATGATGATGCTGATATTTGATGATTAAGAAATG 1197
 QY 476 TGTGATTAACATCAATATGCTTTGGAGCTCTAGTCTTCTAAGTTTAAATTCAG 535
 DB 1196 TTCTGGTACTTCAATATTCAGATTTAGTGTGTTGGATTTTGAACCTGGAAATGAG 1137
 QY 536 ACCTAATGTGCCCGTAATATGCGGCTTAAGATCAATGATGCTGTTGGATTA 595
 DB 1136 AA-----GCCCTGGCAATGTTGTTGATGACGAGTGAAGCTTAAATGGGTAA 1083
 QY 596 AAATATGCGCAACTTGTGGGCAATCCCATATATTAAGTCTTTGGTGAAGTG 655
 DB 1082 AAACATATTTGCAATCTTTGGTGGTGAAGCCCAACATGACTATTTTGGAGATCAG 1023
 QY 656 CCGGTGCTGCTTACCCACTACATGATGTTAAGCAACAACTGCGGCTTTTTCATC 715
 DB 1022 CAGTGGTGAAGTGTGATTTGATGATGATGATGATGATGATGATGATGATGATG 963
 QY 716 GTGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 755
 DB 962 AAGCATCTCAACAAGTGAAGTCTTTTAACTCTGGGC 923

RESULT 13
 US-08-747-221B-36

Sequence 36, Application US/08747221B
 Patent No. 6063610
 GENERAL INFORMATION:
 APPLICANT: Silver, Gary W.
 TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESS: Heska Corporation

STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,221B
 FILING DATE: No. 6063610ember 12, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2007 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 11..1594
 US-08-747-221B-36

Query Match 10.6%; Score 181.2; DB 3; Length 2007;
 Best Local Similarity 56.4%; Pred. No. 4.3e-43;
 Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

QY 116 ATGGCAAGTGAAGCGCTTAAAGCTTAACTGTGATGATGATCTCTACTACTTTTG 175
 DB 39 AAGTACTTAAAGAGAAAGAGCAATTAAGTAAAGAAAGAAATGTTCCTACTATT 98
 QY 176 AGGGTATACCGTACGCCCAACCGCCAGTGGTGAAGTGAATTTAAGACCCGAC 235
 DB 99 CAGAACCTTGTCAGGTGTTCTTGTATGCTAAGTAAAGAGGAAATGTGTAGATCAGTAC 218
 QY 236 CAACACCTGGGATGGTGGCTGATTTGCAATCAATGAATGAATGATGATGATGATG 295
 DB 159 CAGAACCTTGTCAGGTGTTCTTGTATGCTAAGTAAAGAGGAAATGTGTAGATCAGTAC 218
 QY 296 ATTTTATACCGGCAAGTGTGGCTCAGAGATTTGCTATACCTAAGTGTCTATACGA 355
 DB 219 ATTTTATTAATAAATAAAGTGAAGGGCTGAAGATTTGTTTAACTCAATGCTATGAT 278
 QY 356 ATATCTAATCCCGAACTAAACGCTCCGTTTAACTAATACATACATGATGATGATG 415
 DB 279 CAAACATCAGAGAAATTCATCTTCCAGTAAATGATGATGATGATGATGATGATG 338
 QY 416 TTATCGGTGAATAATCATCGTATGATGATGATGATGATGATGATGATGATGATG 475
 DB 339 TCATGGATCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATG 398
 QY 476 TGTGATTAACATCAATATGTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAG 535
 DB 399 TTCTGGTACTTCAATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 512
 QY 536 ACCTTAATGCGCGGTAATGCGGCTTAAGATCAAGTCAATGCTGCTTGGATTA 595
 DB 459 AA-----GCCCTGGCAATGTTGGTGAAGCCAGGTTGAACCTTAAATGCGTTAA 512
 QY 596 AAATATATGCGCAACTTGGTGGCAATCCGATATATTAATTAATTAATTAATTAATG 655
 DB 513 AAACAAATATGCAATCTTGGTGGTGAAGCCCAACAAATGATGATGATGATGATGATG 572

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; MOLECULE TYPE: CDNA
; FEATURE:

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

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(Without alignments)
15895.765 Million cell updates/sec

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Perfect score: 1713
Sequence: 1 atgaattcaacgttagtt.....aacatagagattatttag 1713

Scoring table:
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Gapop 10.0, Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PC1_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	87.2	5.1	1691	9 US-10-083-590-13	Sequence 13, Appl
2	77.2	4.5	1611	9 US-09-738-626-1254	Sequence 1254, Ap
3	62.2	3.6	1967	10 US-09-748-739A-1	Sequence 1, Appl1
4	62.2	3.6	2381	10 US-09-880-107-2271	Sequence 2271, Ap
5	62.2	3.6	2416	10 US-09-748-739A-3	Sequence 3, Appl1
6	62.2	3.6	2416	10 US-09-748-739A-5	Sequence 5, Appl1
7	62.2	3.6	2416	10 US-09-748-739A-7	Sequence 7, Appl1
8	62.2	3.6	2416	10 US-09-748-739A-16	Sequence 16, Appl1
9	62.2	3.6	2444	9 US-08-893-519A-112	Sequence 112, App
10	59.9	3.4	2508	10 US-09-934-323-3	Sequence 3, Appl1
11	59.9	3.4	4667	10 US-09-934-323-1	Sequence 1, Appl1
12	57.8	3.4	657	10 US-09-974-300-1107	Sequence 1107, Ap
13	57.8	3.3	2428	9 US-09-418-176-1	Sequence 1, Appl1
14	57.8	3.3	2428	10 US-09-969-347-220	Sequence 220, App
15	56.8	3.3	2191	9 US-08-954-531-1038	Sequence 1038, Ap
16	56.8	3.3	2191	10 US-09-880-107-3854	Sequence 3854, Ap
17	56.8	3.3	2484	10 US-10-102-806-271	Sequence 271, App
18	56.4	3.3	2451	9 US-09-875-353-3	Sequence 3, Appl1
19	56.4	3.3	3502	9 US-09-875-353-1	Sequence 1, Appl1

20	55.4	3.2	1641	10 US-09-895-860-3	Sequence 3, Appl1
21	55.4	3.2	2087	10 US-09-895-860-1	Sequence 1, Appl1
22	55.4	3.2	3824	9 US-10-036-041-22	Sequence 22, Appl
23	55.4	3.2	3824	9 US-10-028-072-541	Sequence 541, App
24	55.4	3.2	3824	9 US-10-035-855-22	Sequence 22, Appl
25	55.4	3.2	3824	9 US-10-121-049-541	Sequence 541, App
26	55.4	3.2	3824	9 US-10-123-904-541	Sequence 541, App
27	55.4	3.2	3824	9 US-10-140-470-541	Sequence 541, App
28	55.4	3.2	3824	9 US-09-931-836-22	Sequence 22, Appl
29	55.4	3.2	3824	9 US-10-175-746-541	Sequence 541, App
30	55.4	3.2	3824	9 US-10-176-918-541	Sequence 541, App
31	55.4	3.2	3824	9 US-10-176-921-541	Sequence 541, App
32	55.4	3.2	3824	9 US-10-227-884-209	Sequence 209, App
33	55.4	3.2	3824	9 US-10-036-214-22	Sequence 22, Appl
34	55.4	3.2	3824	9 US-10-137-865-541	Sequence 541, App
35	55.4	3.2	3824	9 US-10-140-474-541	Sequence 541, App
36	55.4	3.2	3824	9 US-10-035-719-22	Sequence 22, Appl
37	55.4	3.2	3824	9 US-10-142-431-541	Sequence 541, App
38	55.4	3.2	3824	9 US-10-143-114-541	Sequence 541, App
39	55.4	3.2	3824	9 US-10-230-163-209	Sequence 209, App
40	55.4	3.2	3824	9 US-10-140-002-541	Sequence 541, App
41	55.4	3.2	3824	9 US-10-036-160-22	Sequence 22, Appl
42	55.4	3.2	3824	9 US-10-142-419-541	Sequence 541, App
43	55.4	3.2	3824	9 US-10-218-631-209	Sequence 209, App
44	55.4	3.2	3824	9 US-10-230-338-209	Sequence 209, App
45	55.4	3.2	3824	9 US-10-035-958-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1					
US-10-083-590-13					
: Sequence 13, Application US/10083590					
: Publication No. US20030027257A1					
: GENERAL INFORMATION:					
: APPLICANT: IATROU, Kostas					
: APPLICANT: FARRELL, Patrick J.					
: TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF					
: FILE REFERENCE: 028722-207					
: CURRENT APPLICATION NUMBER: US/10/083, 590					
: CURRENT FILING DATE: 2002-02-27					
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/256, 694					
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-24					
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/136, 421					
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20					
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/056, 871					
: PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-21					
: NUMBER OF SEQ ID NOS: 14					
: SOFTWARE: Patentin Ver. 2.0					
: SEQ ID NO 13					
: LENGTH: 1691					
: TYPE: DNA					
: ORGANISM: Heliothis virescens					
US-10-083-590-13					
Query Match					
Best Local Similarity 53.3%; Pred. No. 1.4e-12;					
Matches 210; Conservative 0; Mismatches 178; Indels 6; Gaps 1;					
QY	368	CCGAACCTAAGCGCCGTTTACATACATACATGCTGTTTATATTCGCTGAAA	427		
DB	380	CCACACCTTACGCGCTATCTGCTGTCATACATGCGAGGATTCCTTCGCGCTCCG	439		
QY	428	ATCATGCGATATATGATGCTGCTATATTCATTAAAGCATGCTGTTTATATTCGCTG	487		
DB	440	CCACACGAGGACCTACGAGGACCAATATTTGGCTACCAAGATGCTATCTACGCT	499		
QY	488	TACATATCGTTTGGAGGCTCTAGTTTCTTAAATTCAGAGACCTTATGTC	547		
DB	500	TTAATTCAGATTAAGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	553		

[illegible]

RESULT 2

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1 Sequence 1254, Application US/09738626
2 Publication NO. US20020197605A1
3
4 GENERAL INFORMATION:
5
6 APPLICANT: NAKAGAWA, SATOSHI
7 APPLICANT: MIZOGUCHI, HIROSHI
8 APPLICANT: ANDO, SEIKO
9 APPLICANT: HAYASHI, MIKIRO
10 APPLICANT: OCHIAI, KEIKO
11 APPLICANT: YOKOI, HARUHIKO
12 APPLICANT: TATEISHI, NAOKO
13 APPLICANT: SENOH, AKIHIRO
14 APPLICANT: IKEDA, MASATO
15 APPLICANT: OZAKI, AKIO
16
17 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
18
19 FILE REFERENCE: 249-125
20
21 CURRENT APPLICATION NUMBER: US/09/738, 626
22
23 CURRENT FILING DATE: 2000-12-18
24
25 PRIOR APPLICATION NUMBER: JP 99/377484
26
27 PRIOR FILING DATE: 1999-12-16
28
29 PRIOR APPLICATION NUMBER: JP 00/159162
30
31 PRIOR FILING DATE: 2000-04-07
32
33 PRIOR APPLICATION NUMBER: JP 00/280988
34
35 PRIOR FILING DATE: 2000-08-03
36
37 NUMBER OF SEQ ID NOS: 7059
38
39 SOFTWARE: PatentIn ver. 3.0
40
41 SEQ ID NO 1254
42
43 LENGTH: 1611
44
45 TYPE: DNA
46
47 ORGANISM: Corynebacterium glutamicum
48
49
50 US-09-738-626-1254

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Query Match 4.58; Score 77.2; DB 9; Length 1611;

Matches	277;	Conservative	0;	Mismatches	263;	Indels	12;	Gaps	37
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 Db 78 GGGATTTCCTTACGCGCCAAACACTGCGCGAATAATTCCTTCCGCGACACCCGGCCGC 137
 QY 237 AACACCCCTGGATGTGTGCGTATTTGTGCA--ATCATTAAGATTAAGTCAGTGCAC 293
 Db 138 CAGAGAAATGGGACGCGCGTCGCAATTTGCTCATATTTGCGGGAGTAGACTTCTCAGCCAC 197
 QY 294 TGATTTTTAACGGCAAGTGTGTGCTCAGAGATTGTCATTAACCTAAGTGTCTATAC 353
 Db 198 GTACCTCGACAGATTAAGTATTCGCGGGTTCAGAGACTGCCTTAACCTCATGTGCGCG 257
 QY 354 GAAATATCTAATCCCGAAACTAAAGCCCGCTTTAGTATACATACATGSGTGGATT 413
 Db 258 G-----CCTGATTTCCGAGAAACCTTCCTGTTGTGTGATCTCCAGCGCGCTTCCT 311
 QY 414 TATTATCGGTGA--AAATCATCTGATATTAATGTCCTGATATTTCATTAAGA 470

Db.	312	CATCATGGGCTCAATCAAGCGAAAAAGGGCGTGGCGGGATATTAACTCGTCAACAAACTGAA	371
QY	471	TGTGGTGTGATTATACATATACATATATCGTTTGGGAGCTCTAGTTTTCAGTTTAATATC	530
Db	372	TGTGTTCTACGCTGTCGGTATTATTTCCGCGCTCGGGGCTTTGGGCTATCTAGATATCTGGCTTC	431
QY	531	AGAGAACCTTAAATATGCGCCGGTAAATGCGCGCTTAAAGATCAAGTCATGCGCTTGGCTG	590
Db	432	CGTGGGGAGGATTTGCGTAGCAACCCCGCGCTCAAGATACACTCTCTGGCCCTTGGAGTG	491
QY	591	GATTAAAAATATATTGGCGCACTTTGGTGGCAATCCGATATATTACATCTTTTGGTGA	650
Db	492	GGTCAGCCGTATATTCGAGCAATTCGGTGGGAGTCTTGACACAGTCAACCTCATATGGGCGA	551
QY	651	AAGTGCAGGCTCTCCTCTTACCCACTACATGATGTTAACCGAACAACACTGGCGTCTTTT	710
Db	552	ATCCGCGGGCGCTCGACAGAGTGTTCATCATCATGTGTGTCGCCGCTTCAGAGAGGACTATT	611
QY	711	CCATGCTGGTAT	722
Db	612	CCACGCCGCCAT	623

RESULT 3

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1 Sequence 1 Application US/09748739A
2 Patent No. US20020119489A1
3
4 GENERAL INFORMATION:
5 APPLICANT: Lockridge, Oksana
6 APPLICANT: Watkins, Jeffry D.
7 TITLE OF INVENTION: Butyrylcholinesterase Variants and
8 TITLE OF INVENTION: Methods of Use
9 FILE REFERENCE: P-1X 4143
10 CURRENT APPLICATION NUMBER: US/09/748,739A
11 CURRENT FILING DATE: 2000-12-06
12 NUMBER OF SEQ ID NOS: 31
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 1
15 LENGTH: 1967
16
17 TYPE: DNA
18 ORGANISM: Artificial Sequence
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20 FEATURE:
21 OTHER INFORMATION: Human Butyrylcholinesterase Variant
22 FEATURE:
23 NAME/KEY: CDS
24 LOCATION: (86)...(1891)
25 US-09-748-739A-1

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Query Match	Score	DB	Length
3.68;	62.2;	10;	1967;

Matches	190;	Conservative	0;	Mismatches	148;	Indels	9;	Gaps	3,
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OY	385	GTTTATGATATACATACATAGTGTGTGTTTATATATCGGTAAATCATCTGTATATAT	444
Db	494	GATATGATATGATATTAATGAGTGGTGTTTCAAACTGGAACATCATCTTATACATGTTAT	553
OY	445	GGTCTGTTATTTTCATTAATAAAGA--TGGTGTGTTGATTAAACATACATATCGTTTG	501
Db	554	GATGCAAGTTCTTGCGTCGGGTTGAAAGAGTTATGTAGAGTCTAAATGACATATAGGGTG	613
OY	502	GGAGCTTAGAGTTTCTTAGTTTAATTAATCAACAACCTTAATGTGCGCCGGAATAGCCGGC	561
Db	614	GGTGCCCTTAGGATTCCTTAGCTT--GCCAGGAATATCTGAGGCTCCAGGGAACATGGGT	670
OY	562	CTTAAGACCTCAAGCATCATGCGCTTGCGTTGGATTAAATAATAATTTGCGCAACCTTGTGTC	621
Db	671	TATATTGATCAACAGATGGCTCTTCAGTGGGTTCAAAAAAATATATAGCAGCCTTGTGTGGA	730
OY	622	AATCCGATATATTTACAGTCTTTGGTGAAGAAGTGCGCGGTGTCGCTC	668

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RESULT 4

US-09-880-107-2271
Sequence 2271, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scheff, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 2271
LENGTH: 2381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474
US-09-880-107-2271

Query Match

Best Local Similarity 54.8%; Score 62.2; DB 10; Length 2381;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGATTGCTATACCTAAGTGTCTATACGAATATCTAAATCCCGAACTAAACGTC 384
DB 427 GAAGACGTGTTATCTAAATGATGATTCACACCTAAAC---AAAAATGCCACT 483
QY 385 GTTTAGTATACATACATGCGTGTGTTTATTCGTCGTAATCATCGATATGAT 444
DB 484 GTATTGATATGATTTATGCGTGTGTTTCAAACTGAAACATCATCTTACATGTTAT 543
QY 445 GGTCTGATTTATCATTAATAAGCA---TGTGTTGATTATACATATATCGTTG 501
DB 544 GATGGCAAGTTTCGCTCGGTTGAAAGATTATGAGTCAATGAACTATAGGTG 603
QY 502 GGACCTAGTGTTCCTAAGTTTAAATTCAGAGACCTTAATGCGCGTAAATGCCGC 561
DB 604 GGTCCCTAGGATCTTAGCTT---GCCAGGAATCCTGAGCTCCAGGAGACATGGGT 660
QY 562 CTAAAGTCAAGTCATGCGCTTCGCTTGAATTAATAATATTCGCCAATTTGGTGGC 621
DB 661 TTATTTGATCAACAGTTGCTTCAGTGGGTTCAAAAAAATATAGAGCCCTTTGGTGA 720
QY 622 AATCCCGATATATTAAGTCTTTGTTGAAGTCCGCTGCTGCTC 668
DB 721 AATCTAAAGTAACTCTCTTTGGAGAAAGTCAGAGACGCTTC 767

RESULT 5

US-09-748-739A-3
Sequence 3, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3
LENGTH: 2416
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
NAME/KEY: CDS
LOCATION: (214)...(1935)
US-09-748-739A-3

Query Match

Best Local Similarity 54.8%; Score 62.2; DB 10; Length 2416;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGATTGCTATACCTAAGTGTCTATACGAATATCTAAATCCCGAACTAAACGTC 384
DB 481 GAAGACGTGTTATCTAAATGATGATTCACACCTAAAC---AAAAATGCCACT 537
QY 385 GTTTAGTATACATACATGCGTGTGTTTATTCGTCGTAATCATCGATATGAT 444
DB 538 GTATTGATATGATTTATGCGTGTGTTTCAAACTGAAACATCATCTTACATGTTAT 597
QY 445 GGTCTGATTTATCATTAATAAGCA---TGTGTTGATTATACATATATCGTTG 501
DB 598 GATGGCAAGTTTCGCTCGGTTGAAAGATTATGAGTCAATGAACTATAGGTG 657
QY 502 GGACCTAGTGTTCCTAAGTTTAAATTCAGAGACCTTAATGCGCGTAAATGCCGC 561
DB 658 GGTCCCTAGGATCTTAGCTT---GCCAGGAATCCTGAGCTCCAGGAGACATGGGT 714
QY 562 CTAAAGTCAAGTCATGCGCTTCGCTTGAATTAATAATATTCGCCAATTTGGTGGC 621
DB 715 TTATTTGATCAACAGTTGCTTCAGTGGGTTCAAAAAAATATAGAGCCCTTTGGTGA 774
QY 622 AATCCCGATATATTAAGTCTTTGTTGAAGTCCGCTGCTGCTC 668
DB 775 AATCTAAAGTAACTCTCTTTGGAGAAAGTCAGAGACGCTTC 821

RESULT 6

US-09-748-739A-5
Sequence 5, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2416
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
NAME/KEY: CDS
LOCATION: (214)...(1935)
US-09-748-739A-5

Query Match

Best Local Similarity 54.8%; Score 62.2; DB 10; Length 2416;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGATTGCTATACCTAAGTGTCTATACGAATATCTAAATCCCGAACTAAACGTC 384
DB 481 GAAGACGTGTTATCTAAATGATGATTCACACCTAAAC---AAAAATGCCACT 537

Query Match	3.48;	Score 59;	DB 10;	Length 2508;
Best Local Similarity	53.28;	Pred. No. 3.9e-05;		
Matches 125;	Conservative 0;	Mismatches 110;	Indels 0;	Gaps 0

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RESULT 12
US-09-974-300-1107
; Sequence 1107, Application US/09974300
; Patent No. US2002014671A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Gorth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085,500-US

```

CURRENT APPLICATION NUMBER: US/09/974.300
 CURRENT FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 09/680.598
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/279.526
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 8481
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 1107
 LENGTH: 657
 TYPE: DNA
 ORGANISM: Bacillus licheniformis
 US-09-974-300-1107

Query Match 3.4%; Score 57.8; DB 10; Length 657;
 Best Local Similarity 49.9%; Pred. No. 3.8e-05;
 Matches 174; Conservative 0; Mismatches 172; Indels 3; Gaps 1;

OY 377 AACGTCCTTTTATATACATACATGCTGCTTTTATATCG--TGAATAATCATC 433
 DB 30 ATCTGCTCTTATGCTGATTCATGCGGCGCTTTTATCGCGCGGAGTGAAC 89
 OY 434 GTGATATGCTGCTGATTTATTAATAAAGATGCTGCTGATTAACATCAAT 493
 DB 90 CGCTTATGACGGGACTACCTGCAAGCAGGAAAGTGATCGTACCATCAAT 149
 OY 494 ATCTGTTGGAGCTTACGCTTTCTAAGTTTAAATTCAGACCTTAATGCTCCGGTA 553
 DB 150 ATGCGCTCGGTCGCTGCTTTTTCATCTATCTCAATGATGATCTCTACAGAGCA 209
 OY 554 ATGCGGCTTAAAGATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
 DB 210 ATCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
 OY 614 TTGCTGCAATCCGATATATTACAGCTTTGCTGCTGCTGCTGCTGCTGCTGCT 673
 DB 270 TTGCGGAGACCGTACATTCATGCTTTTGGAGAGTGGCGGATCGATGAGCATCG 329
 OY 674 ACTACATGATGTAAACGCAACAACTGCGGCTTTTCCATCGTGTAT 722
 DB 330 CTGCTTTTGGCGATGCCAAGCAAGGCGCTTTTTCACAGGCGCAT 378

RESULT 13
 US-09-418-176-1
 Sequence 1, Application US/09418176
 Publication No. US20030040040A1

GENERAL INFORMATION:
 APPLICANT: Das, Goutam
 TITLE OF INVENTION: DNA molecules for Expression of
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: White & Case
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10036-2787
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/418.176
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/624.398
 FILING DATE: 04-APR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/SE96/00318

FILING DATE: 12-MAR-1996
 PRIOR APPLICATION DATA: SE 9501939-4
 APPLICATION NUMBER: 24-MAY-1995
 FILING DATE: 24-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Thelma A. Chen Cleland
 REGISTRATION NUMBER: 40,948
 REFERENCE/DOCKET NUMBER: 1103326-0206
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 819-8200
 TELEFAX: (212) 554-8113
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2428 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: mammary gland
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 82..2319
 OTHER INFORMATION: /product= "bile-salt-stimulated
 OTHER INFORMATION: lipase"
 FEATURE:
 NAME/KEY: exon
 LOCATION: 985..1173
 FEATURE:
 NAME/KEY: exon
 LOCATION: 1174..1377
 FEATURE:
 NAME/KEY: exon
 LOCATION: 1378..1575
 FEATURE:
 NAME/KEY: exon
 LOCATION: 1576..2415
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 151..2316
 FEATURE:
 NAME/KEY: polyA_signal
 LOCATION: 2397..2402
 FEATURE:
 NAME/KEY: repeat_region
 LOCATION: 1756..2283
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 NAME/KEY: 5'UTR
 LOCATION: 1..81
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 NAME/KEY: repeat_unit
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 NAME/KEY: repeat_unit
 LOCATION: 1888..1920
 FEATURE:
 NAME/KEY: repeat_unit
 LOCATION: 1921..1953
 FEATURE:
 NAME/KEY: repeat_unit
 LOCATION: 1954..1986

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FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1987..2019
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 2020..2052
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LOCATION: 2053..2085
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NAME/KEY: repeat_unit
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LOCATION: 2185..2217
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 2218..2250
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 2251..2283
PUBLICATION INFORMATION:
AUTHORS: Nilsson, Jeanette
AUTHORS: Blackberg, Lars
AUTHORS: Carlsson, Peter
AUTHORS: Enerback, Sven
AUTHORS: Herneli, Olle
AUTHORS: Bjursell, Gunnar
TITLE: cDNA cloning of human-milk
TITLE: bile-salt-stimulated lipase and evidence for its
TITLE: identity to pancreatic carboxylic ester hydrolase
JOURNAL: Eur. J. Biochem.
VOLUME: 192
PAGES: 543-550
DATE: Sept.-1990
US-09-418-176-1

Query Match
Best Local Similarity 53.3%; Score 57; DB 9; Length 2428;
Matches 120; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 530 CAGAAGACCTTAATGTGCGGCGGTATGCGGCGCTTAAGATCAAGTCAATGCGCTT 589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 608 CTGGGAGCGCAATCTGCCAGTACATGCTTCCGGATCAGACATGCGCATTCCTT 667
QY 590 GGATTAAATAATGCGGCAACTTTGGTGCATCCGATTAATTAATTAATGCTTTG 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 668 GGGTGAAGAGAAATATCCGCGCTTCGGGGGGGACCCCAACAATCAACGCTTCC 727
QY 650 AAAGTGGCGGTGCTGCTTACCACTACATGATTTAAGCAACAAACTGCGGCTTT 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 728 AGTCTGCGGAGGTGCGGCGCTTCTCTGCAAGACCTCTCCCTTACAAAGGCGCT 787
QY 710 TCCATCGTGTATCTAATGTCGGGTATGCTATTTGTCATGGG 754
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 788 TCCGGCGAGCATCAGCCAGAGCGGCGGCTGCGCTGATGCTCGG 832

RESULT 14
US-09-969-347-220
Sequence 220, Application US/09969347
Patent No. US20020115085A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-69
```

```
CURRENT APPLICATION NUMBER: US/09/969,347
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,598
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,604
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
SOFTWARE: PatentIn version 3.0
SEQ ID NO 220
LENGTH: 2428
TYPE: DNA
ORGANISM: Homo sapiens
US-09-969-347-220

Query Match
Best Local Similarity 53.3%; Score 57; DB 10; Length 2428;
Matches 120; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 530 CAGAAGACCTTAATGTGCGGCGGTATGCGGCGCTTAAGATCAAGTCAATGCGCTT 589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 608 CTGGGAGCGCAATCTGCCAGTACATGCTTCCGGATCAGACATGCGCATTCCTT 667
QY 590 GGATTAAATAATGCGGCAACTTTGGTGCATCCGATTAATTAATTAATGCTTTG 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 668 GGGTGAAGAGAAATATCCGCGCTTCGGGGGGGACCCCAACAATCAACGCTTCC 727
QY 650 AAAGTGGCGGTGCTGCTTACCACTACATGATTTAAGCAACAAACTGCGGCTTT 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 728 AGTCTGCGGAGGTGCGGCGCTTCTCTGCAAGACCTCTCCCTTACAAAGGCGCT 787
QY 710 TCCATCGTGTATCTAATGTCGGGTATGCTATTTGTCATGGG 754
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 788 TCCGGCGAGCATCAGCCAGAGCGGCGGCTGCGCTGATGCTCGG 832

RESULT 15
US-09-954-531-1038
Sequence 1038, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1038
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-531-1038

Query Match
Best Local Similarity 53.2%; Score 56.8; DB 9; Length 2191;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGATGCTATACCTAAGTGTCTATACGAATTAATTAATCCGAA---ACTAA 378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 436 TCTGAGCATCTCTATCTCAGCATTAACAGCGGCGCCATAGCATGAAGGCTTAAC 495
QY 379 CGTCCGCTTTAGTATACATACATGCTGTTTATTATTCGGTGAATAATCATCTGAT 438
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Db 496 CTGCCGCTGATGCTGTGATCCACGCTGGCTTGTG--GCATGGCTTCCTTGT 553
OY 439 ATGTATGCTCCTGATTAATTCATTAATAAGATGGTGTGATTACATACATATCGT 498
Db 554 ATGATGCTTCATGCTGCTGCT-TGGAGAACGTGTGTGTCATCATCCAGTACCGC 612
OY 499 TTGGGAGCTCTAGCTTTCTAAGTTAAATTCAGAACCTTAATGTGCCCGTAATGCC 558
Db 613 CTGGGTGCTCCTGGCTT-----CTTCAGCACTGGAGACAGCAACCGCAACTGG 666
OY 559 GGCTTAAGATCAAGTCATGGCTTGCCTTGATTAATAATTAATGCGCAACTTGGT 618
Db 667 GGCTACCTGGACCAAGTGGCTGACCTAGCTGGGTCAGAGAAATATCGCCACTTGG 726
OY 619 GGCATCCCGATATATATACAGTCTTTGGTGAAGTCCGCTGCTCTACCCACTAC 678
Db 727 GGCACCCCTGACCGTGTACCATTTTGGGAGACTGCGGGTGGACAGATGTGTCTCG 786
OY 679 ATGATGTTAACCGAACAACTCGCGCTTTTCCATCGTGTAT 722
Db 787 CTGTGTGTGCTCCCATATCCCAAGAGACTCTTCCAGGAGCCAT 830
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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:08:22 ; Search time 44.0154 seconds
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Title: US-09-776-910-8
Perfect score: 3073
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3073	100.0	570	16	AA178142
2	3073	100.0	570	18	AA17765
3	3060	99.6	570	18	AA17766
4	3060	99.6	570	18	AA17768
5	2345	76.3	570	18	AA17767
6	2006.5	65.3	572	22	AB17850
7	1412.5	46.0	567	22	AB17857
8	1408.5	45.8	554	22	AB17866
9	1389.5	45.2	572	22	AB17867
10	1324.5	43.1	554	22	AB17861

11	1302.5	42.4	566	22	AB17863	Drosophila melanog
12	1295.5	42.2	565	22	AB17746	Drosophila melanog
13	1238	40.3	542	22	AB17790	Drosophila melanog
14	1228.5	40.0	530	22	AB17868	Drosophila melanog
15	1184	38.5	602	23	AA17598	Drosophila cell cy
16	1073	34.9	541	22	AB17789	Drosophila melanog
17	1022.5	33.3	568	22	AB17831	Drosophila melanog
18	955.5	31.1	528	19	AA17862	C. felis ester
19	856	27.9	528	22	AA17862	C. felis ester
20	856	27.9	528	22	AA17862	C. felis ester
21	846	27.5	513	19	AA17863	C. felis ester
22	785.5	25.6	530	19	AA17865	C. felis ester
23	785.5	25.6	530	19	AA17867	C. felis ester
24	785.5	25.6	530	22	AA17864	C. felis ester
25	785.5	25.6	530	19	AA17863	C. felis ester
26	785.5	25.6	530	19	AA17863	C. felis ester
27	785.5	25.6	530	22	AA17864	C. felis ester
28	779.5	25.4	550	19	AA17865	C. felis ester
29	779.5	25.4	550	19	AA17865	C. felis ester
30	779.5	25.4	550	22	AA17863	C. felis ester
31	771.5	25.1	505	19	AA17861	C. felis ester
32	771.5	25.1	505	19	AA17862	C. felis ester
33	771.5	25.1	505	22	AA17865	C. felis ester
34	764	24.9	576	22	AB17915	Drosophila melanog
35	759.5	24.7	495	19	AA17869	C. felis ester
36	757.5	24.7	562	22	AB17868	Drosophila melanog
37	754.5	24.6	530	19	AA17866	C. felis ester
38	754.5	24.6	530	19	AA17867	C. felis ester
39	711.5	23.2	575	23	AB17958	Carboxylesterase c
40	710	23.1	584	23	AB17676	Carboxylesterase d
41	673.5	21.9	527	22	AB17835	Drosophila melanog
42	623	20.3	570	19	AA17860	C. felis ester
43	623	20.3	570	19	AA17860	C. felis ester
44	623	20.3	570	22	AA17861	C. felis ester
45	623	20.3	595	19	AA17859	C. felis ester

ALIGNMENTS

RESULT 1	
AA178142	
ID	AA178142 standard; Protein: 570 AA.
XX	
AC	AA178142;
XX	
DT	22-DEC-1995 (first entry)
XX	
DE	OP-sensitive esterase E3.
XX	
KW	Esterase; E3; bioremediation; organophosphate; carbamate;
KW	Insecticide; pesticide; water decontamination; meat decontamination.
XX	
OS	Lucilia cuprina.
XX	
PN	W09519440-A1.
XX	
PD	20-JUL-1995.
XX	
PF	13-JAN-1995; 95WO-AU00016.
XX	
PR	13-JAN-1994; 94AU-0003347.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
XX	
PI	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI	Parker AG, Robin GC, Russell RJ, Smyth K;
XX	
DR	WPI: 1995-263870/34.
DR	N-PSDB: AAQ91561.
XX	
PT	Pure E3 esterase from Lucilia cuprina and related DNA - used to eliminate residues of organo:phosphate and carbamate pesticides from

PT water, meat etc.
 PS Example 3: Page 12-17; 38pp; English.
 XX CDNA from organophosphate (OP)-sensitive L. cuprina pupa cDNA
 CC library was amplified using cluster-specific esterase primers.
 CC Isolated clone Lc743, a probable full-length cDNA, was expressed
 CC using a baculovirus vector in insect cells and shown to encode
 CC an OP-susceptible E3 esterase useful in bioremediation.
 CC
 XX
 SQ Sequence 570 AA:
 Query Match 100.0%; Score 3073; DB 16; Length 570;
 Best Local Similarity 100.0%; Pred. No. 7.8e-306; Indels 0; Gaps 0;
 Matches 570; Conservative 0; Mismatches 0;
 QY 1 MNEVNSLMEKLLKWKIKCIENKFLNRYLTNETVVAETEKYKGVKRLTYDDSYSEFG 60
 DB 1 MNEVNSLMEKLLKWKIKCIENKFLNRYLTNETVVAETEKYKGVKRLTYDDSYSEFG 60
 QY 61 IRYAOPVVELRFRKAPORPTPMDGVRDCCNKKDSQVDFITGKVCSEDCILYSVTNN 120
 DB 61 IRYAOPVVELRFRKAPORPTPMDGVRDCCNKKDSQVDFITGKVCSEDCILYSVTNN 120
 QY 121 LNPETRKRPVLYITHGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNEEDL 180
 DB 121 LNPETRKRPVLYITHGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNEEDL 180
 QY 121 LNPETRKRPVLYITHGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNEEDL 180
 DB 121 LNPETRKRPVLYITHGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNEEDL 180
 QY 181 NVPGNAGLKDQVVALRWIKNKCANFGNPNITVFGESAGASTHYMMLTEOTRGFLFHRG 240
 DB 181 NVPGNAGLKDQVVALRWIKNKCANFGNPNITVFGESAGASTHYMMLTEOTRGFLFHRG 240
 QY 241 ILMGNAICPMANTOCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEKVLT 300
 DB 241 ILMGNAICPMANTOCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEKVLT 300
 QY 301 EERTNKVMPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMKGNTSYEGLEFSTSILK 360
 DB 301 EERTNKVMPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMKGNTSYEGLEFSTSILK 360
 QY 361 QMPMLVKLETCVNFVPSLADAEKTAPELLEMGAKIKKAHYTGEPADNFMDCSHIT 420
 DB 361 QMPMLVKLETCVNFVPSLADAEKTAPELLEMGAKIKKAHYTGEPADNFMDCSHIT 420
 QY 421 FWFPNHRLLQRLFNHTSGTPVLYLRFDPSDDLINPYRIMRSGRGVYSHADELTYFEW 480
 DB 421 FWFPNHRLLQRLFNHTSGTPVLYLRFDPSDDLINPYRIMRSGRGVYSHADELTYFEW 480
 QY 481 NQLAKRMPKESREYKTIERTMTGIMIOFATGPNYSNEIEGMENVSWDPYIKKSDEVYKCLN 540
 DB 481 NQLAKRMPKESREYKTIERTMTGIMIOFATGPNYSNEIEGMENVSWDPYIKKSDEVYKCLN 540
 QY 541 ISDELKMDVPEMDKIKOMESMFEKHRDLF 570
 DB 541 ISDELKMDVPEMDKIKOMESMFEKHRDLF 570
 RESULT 2
 AAM17765
 ID AAM17765 standard; Protein: 570 AA.
 XX AAM17765;
 AC
 XX 08-AUG-1997 (first entry)
 DT
 XX LC-alpha-E7 malathion susceptible clone Lc743 esterase E3.
 DE
 XX Malathion carboxylesterase; organophosphate; insecticide;
 KW pesticide; remediation; bioremediation; decontamination; esterase.
 XX Lucilia cuprina.
 OS
 XX
 FH Key Location/Qualifiers

FT Misc-difference 251
 FT /note= "amino acid 251 is Leu in resistant
 FT mutants"
 XX W09719176-A1.
 XX 29-MAY-1997.
 XX 22-NOV-1996; 96NO-AU00746.
 XX 23-NOV-1995; 95AU-0006751.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;
 PI Newcomb RD, Oakeshott JG, Robin GC, Russell KO, Smyth K;
 XX WPI: 1997-298113/27.
 XX N-PSDB: AAT68596.
 DR DNA encoding enzyme that degrades organophosphate pesticides
 XX useful for decontamination of soil, water, food etc
 PS Disclosure: Fig 1: 52pp; English.
 XX Esterase E3 (AAM17765) from a malathion susceptible strain of
 CC Lucilia cuprina differs from an esterase enzyme (see also
 CC AAM17768) from malathion resistant RM8 strains by a Trp for Leu
 CC substn. at amino acid position 251, owing to a mutation in the
 CC encoding DNA sequence (see also AAT68596). The resistant enzyme,
 CC termed malathion carboxylesterase, can be formulated for use in
 CC degrading environmental carboxylester or dimethyl general
 CC organophosphates.
 CC
 SQ Sequence 570 AA:
 Query Match 100.0%; Score 3073; DB 18; Length 570;
 Best Local Similarity 100.0%; Pred. No. 7.8e-306; Indels 0; Gaps 0;
 Matches 570; Conservative 0; Mismatches 0;
 QY 1 MNEVNSLMEKLLKWKIKCIENKFLNRYLTNETVVAETEKYKGVKRLTYDDSYSEFG 60
 DB 1 MNEVNSLMEKLLKWKIKCIENKFLNRYLTNETVVAETEKYKGVKRLTYDDSYSEFG 60
 QY 61 IRYAOPVVELRFRKAPORPTPMDGVRDCCNKKDSQVDFITGKVCSEDCILYSVTNN 120
 DB 61 IRYAOPVVELRFRKAPORPTPMDGVRDCCNKKDSQVDFITGKVCSEDCILYSVTNN 120
 QY 121 LNPETRKRPVLYITHGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNEEDL 180
 DB 121 LNPETRKRPVLYITHGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNEEDL 180
 QY 121 LNPETRKRPVLYITHGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNEEDL 180
 DB 121 LNPETRKRPVLYITHGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNEEDL 180
 QY 181 NVPGNAGLKDQVVALRWIKNKCANFGNPNITVFGESAGASTHYMMLTEOTRGFLFHRG 240
 DB 181 NVPGNAGLKDQVVALRWIKNKCANFGNPNITVFGESAGASTHYMMLTEOTRGFLFHRG 240
 QY 241 ILMGNAICPMANTOCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEKVLT 300
 DB 241 ILMGNAICPMANTOCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEKVLT 300
 QY 301 EERTNKVMPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMKGNTSYEGLEFSTSILK 360
 DB 301 EERTNKVMPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMKGNTSYEGLEFSTSILK 360
 QY 361 QMPMLVKLETCVNFVPSLADAEKTAPELLEMGAKIKKAHYTGEPADNFMDCSHIT 420
 DB 361 QMPMLVKLETCVNFVPSLADAEKTAPELLEMGAKIKKAHYTGEPADNFMDCSHIT 420
 QY 421 FWFPNHRLLQRLFNHTSGTPVLYLRFDPSDDLINPYRIMRSGRGVYSHADELTYFEW 480
 DB 421 FWFPNHRLLQRLFNHTSGTPVLYLRFDPSDDLINPYRIMRSGRGVYSHADELTYFEW 480
 QY 481 NQLAKRMPKESREYKTIERTMTGIMIOFATGPNYSNEIEGMENVSWDPYIKKSDEVYKCLN 540
 DB 481 NQLAKRMPKESREYKTIERTMTGIMIOFATGPNYSNEIEGMENVSWDPYIKKSDEVYKCLN 540

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Db      481  NQLAKRMPKESREKXTERMTGIWFATGNPNYSNEIEGMENVSMDPIKKSDEYKCLN 540
QY      541  ISDELKMTDVPMDIKIKOMESMEFEKHDLF 570
Db      541  ISDELKMTDVPMDIKIKOMESMEFEKHDLF 570

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RESULT 3

```

AAW17766
ID      AAW17766 standard; Protein; 570 AA.
AC      XX
AAW17766;
XX      08-AUG-1997 (first entry)
DE      Malathion carboxylesterase.
XX      Malathion carboxylesterase: organophosphate; insecticide;
KM      pesticide; remediation; bioremediation; decontamination; esterase;
KW      Lucilia cuprina.
XX      Synthetic.
XX      Key Location/Qualifiers
FH      MISC-difference 251
FT      /label=Leu, Ser, Ala, Ile, Val, Thr, Cys, Met, Gly
FT      /note="pref. Leu or Ser"
XX      WO9719176-A1.
XX      29-MAY-1997.
XX      22-NOV-1996; 96WO-AU00746.
XX      23-NOV-1995; 95AU-0006751.
XX      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX      Boyce T, Brownlie JC, Campbell PM, Claudianos C;
PI      Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
DR      WPI; 1997-298113/27.
XX      DNA encoding enzyme that degrades organophosphate pesticides -
PT      useful for decontamination of soil, water, food etc
XX      Claim 1; Fig 1; 52pp; English.
XX      A malathion carboxylesterase (AAW17766) differs from the esterase
CC      (AAW17765) of a malathion susceptible clone of Lucilia cuprina by
CC      a substn. of the tryptophan residue at amino acid position 251.
CC      The enzyme is capable of hydrolysing carboxylester and/or
CC      dimethylloxon organophosphates and can be formulated for use in
CC      bioremediation strategies for treating soil or water.
XX      SQ      Sequence 570 AA:
Query Match 99.6%; Score 3060; DB 18; Length 570;
Best Local Similarity 99.8%; Pred. No. 1,7e-304;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1  MNFVNSLMERKIKKIKENKFLNRLTNETVVAETREYGVKVKRLTVYDDSYSEEG 60
Db      1  MNFVNSLMERKIKKIKENKFLNRLTNETVVAETREYGVKVKRLTVYDDSYSEEG 60
QY      61  IIPYAOPVGELEFRKAPRPTFMDCVNDCCNHHKDSVOYDFTTGVCSGSEDCLYSVYTN 120
Db      61  IIPYAOPVGELEFRKAPRPTFMDCVNDCCNHHKDSVOYDFTTGVCSGSEDCLYSVYTN 120
QY      121  LNPTKRPVLVYIHGGGFTIGENHRDMYGPDYFIKKDVVLINIOYRLGALGFLSLNSED 180
Db      121  LNPTKRPVLVYIHGGGFTIGENHRDMYGPDYFIKKDVVLINIOYRLGALGFLSLNSED 180

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QY      181  NVPGNAGLKDOVMALRMKNNKNCANFGNPDNITVFGESAGASTHYMLTROTGLFHRG 240
Db      181  NVPGNAGLKDOVMALRMKNNKNCANFGNPDNITVFGESAGASTHYMLTROTGLFHRG 240
QY      241  ILMGNAICPWPANTOCQHRAFTLAKLAGYKGEDNDKDLFEFLMAKAPODLILKEKVLTL 300
Db      241  ILMGNAICPXPANTOCQHRAFTLAKLAGYKGEDNDKDLFEFLMAKAPODLILKEKVLTL 300
QY      301  EERTNKVMEPPGPTVEPYQTADCVLPKHPRMVKVTAMGNSIPTMGNTSYGLEFTSTLK 360
Db      301  EERTNKVMEPPGPTVEPYQTADCVLPKHPRMVKVTAMGNSIPTMGNTSYGLEFTSTLK 360
QY      361  QMPVLVELETCVNFVPSLADARTAPETLEMGAKIKKAVVTGPTPADNFMDCSHY 420
Db      361  QMPVLVELETCVNFVPSLADARTAPETLEMGAKIKKAVVTGPTPADNFMDCSHY 420
QY      421  FWFPMHRLQLRFNHTSGTPYLYLRFDPDSDDLNPYRIMSGRGVKVSHADELTYFFW 480
Db      421  FWFPMHRLQLRFNHTSGTPYLYLRFDPDSDDLNPYRIMSGRGVKVSHADELTYFFW 480
QY      481  NQLAKRMPKESREKXTERMTGIWFATGNPNYSNEIEGMENVSMDPIKKSDEYKCLN 540
Db      481  NQLAKRMPKESREKXTERMTGIWFATGNPNYSNEIEGMENVSMDPIKKSDEYKCLN 540
QY      541  ISDELKMTDVPMDIKIKOMESMEFEKHDLF 570
Db      541  ISDELKMTDVPMDIKIKOMESMEFEKHDLF 570

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RESULT 4

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AAW17768
ID      AAW17768 standard; Protein; 570 AA.
AC      XX
AAW17768;
XX      08-AUG-1997 (first entry)
DE      Malathion carboxylesterase RM8Con.
XX      Malathion carboxylesterase: organophosphate; insecticide;
KM      pesticide; remediation; bioremediation; decontamination; esterase;
KW      Lucilia cuprina.
XX      Lucilia cuprina.
XX      OS      Lucilia cuprina.
XX      29-MAY-1997.
XX      22-NOV-1996; 96WO-AU00746.
XX      23-NOV-1995; 95AU-0006751.
XX      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX      Boyce T, Brownlie JC, Campbell PM, Claudianos C;
PI      Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
DR      WPI; 1997-298113/27.
XX      DNA encoding enzyme that degrades organophosphate pesticides -
PT      useful for decontamination of soil, water, food etc
XX      Claim 6; Fig 1; 52pp; English.
XX      A malathion carboxylesterase (AAW17768), designated RM-8Con, differs
CC      from the esterase (AAW17765) of a malathion susceptible clone of
CC      Lucilia cuprina by a substn. of the tryptophan residue at amino
CC      acid position 251 by a leucine residue. This mutation is situated
CC      at the base of the active site gorge, 6.5 Angstroms from the active
CC      site serine. The RM8Con amino acid sequence is a consensus deduced
CC      from the DNA sequences of 3 resistant clones (RM8 A-C) and their

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CC comparison to reference susceptible clone LC743 (AAT68596) of
 CC Lc-alpha-E7. The enzyme is capable of hydrolysing carboxylester
 CC and/or dimethylloxon organophosphates and can be formulated for use
 CC in biofumigation strategies for treatment of soil or water.

XX Sequence 570 AA:

Query Match 99.6%; Score 3060; DB 18; Length 570;
 Best Local Similarity 99.8%; Pred. No. 1.7e-304;
 Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MNFNVSLMEKLEKWKIKICJENKFLNLTNETVVAETEGYKGVKRLTYDDSYSEEG 60
DB 1 MNFNVSLMEKLEKWKIKICJENKFLNLTNETVVAETEGYKGVKRLTYDDSYSEEG 60
OY 61 IRYAOPVGELEFRKAPQRPPTPMDGVDCCNHDKSVQVDFITGKVCSEDCLYLSVTNN 120
DB 61 IRYAOPVGELEFRKAPQRPPTPMDGVDCCNHDKSVQVDFITGKVCSEDCLYLSVTNN 120
OY 121 LNPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLINIOYRLGALGFLSINSEDL 180
DB 121 LNPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLINIOYRLGALGFLSINSEDL 180
OY 181 NYPGNAGLDQYVALRMKIKNNCANFGNPDNITVGEASASTHYMMLTEOTRGLFHRG 240
DB 181 NYPGNAGLDQYVALRMKIKNNCANFGNPDNITVGEASASTHYMMLTEOTRGLFHRG 240
OY 241 ILMSCNAICPMANTOCQAHAFILAKIAGKGEDNDKDVLEFLMKAKPDLIKLEEKVLT 300
DB 241 ILMSCNAICPMANTOCQAHAFILAKIAGKGEDNDKDVLEFLMKAKPDLIKLEEKVLT 300
OY 301 EERTNKVMEFPFGTVPYOTADCVLPKHREWKITAMGNSIPTMGNTSYEGLEFSTSLK 360
DB 301 EERTNKVMEFPFGTVPYOTADCVLPKHREWKITAMGNSIPTMGNTSYEGLEFSTSLK 360
OY 361 QMPLVKELETQVNFVPSSELADETAPELLEMGAKIKAAHYGETPTADNEMDLCSHY 420
DB 361 QMPLVKELETQVNFVPSSELADETAPELLEMGAKIKAAHYGETPTADNEMDLCSHY 420
OY 421 FWEPMHRLQLRNHTSGRPVLYLRFPDSEDLINRYRIMRSRGYKGVSHADELYTFEW 480
DB 421 FWEPMHRLQLRNHTSGRPVLYLRFPDSEDLINRYRIMRSRGYKGVSHADELYTFEW 480
OY 481 NOLAKRMPKESREYKTIERTMTGIMIOFATGNDPYSNEIEGEMENVSDPIKSDVYKCLN 540
DB 481 NOLAKRMPKESREYKTIERTMTGIMIOFATGNDPYSNEIEGEMENVSDPIKSDVYKCLN 540
OY 541 ISDELKMIIDVPEMDKIKQWESMEKRDLP 570
DB 541 ISDELKMIIDVPEMDKIKQWESMEKRDLP 570

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RESULT 5
 AAM17767
 ID AAM17767 standard; Protein: 570 AA.

XX AAM17767;

XX 08-AUG-1997 (first entry)

XX MD-alpha-E7 malathion resistant mutant.

XX Malathion carboxylesterase; organophosphate; insecticide;

XX pesticide; remediation; biofumigation; decontamination.

XX Musca domestica Rutgers strain.

XX Key Location/Qualifiers

XX Misc-difference 251 /note= "Ser-251 is tryptophan in the susceptible

XX FT allele expression product"

XX PN W09719176-A1.

XX 29-MAY-1997.
 PD 22-NOV-1996; 96MO-AU00746.
 PF 23-NOV-1995; 95AU-0006751.
 PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA Boyce T, Brownlie JC, Campbell PM, Claudianos C;
 PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
 PS WPI: 1997-298113/27.
 DR N-PSDB: AAT68597.

XX DNA encoding enzyme that degrades organophosphate pesticides -
 PT useful for decontamination of soil, water, food etc
 XX Disclosure: Fig 3; 52pp; English.

XX A polypeptide (AAM17767) is the expression product of a malathion
 CC resistant allele of the Musca domestica Md-alpha-E7 gene, and
 CC contains a Ser for Trp substn. at amino acid position 251. The
 CC enzyme is capable of hydrolysing carboxylester and/or
 CC dimethylloxon organophosphates and can be formulated for use
 CC in biofumigation strategies for treatment of soil or water.

XX Sequence 570 AA:

Query Match 76.3%; Score 2345; DB 18; Length 570;
 Best Local Similarity 74.4%; Pred. No. 4.1e-231;
 Matches 424; Conservative 71; Mismatches 75; Indels 0; Gaps 0;

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OY 1 MNFNVSLMEKLEKWKIKICJENKFLNLTNETVVAETEGYKGVKRLTYDDSYSEEG 60
DB 1 MNFNVSLMEKLEKWKIKICJENKFLNLTNETVVAETEGYKGVKRLTYDDSYSEEG 60
OY 61 IRYAOPVGELEFRKAPQRPPTPMDGVDCCNHDKSVQVDFITGKVCSEDCLYLSVTNN 120
DB 61 IRYAOPVGELEFRKAPQRPPTPMDGVDCCNHDKSVQVDFITGKVCSEDCLYLSVTNN 120
OY 121 LNPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLINIOYRLGALGFLSINSEDL 180
DB 121 LNPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLINIOYRLGALGFLSINSEDL 180
OY 181 NYPGNAGLDQYVALRMKIKNNCANFGNPDNITVGEASASTHYMMLTEOTRGLFHRG 240
DB 181 NYPGNAGLDQYVALRMKIKNNCANFGNPDNITVGEASASTHYMMLTEOTRGLFHRG 240
OY 241 ILMSCNAICPMANTOCQAHAFILAKIAGKGEDNDKDVLEFLMKAKPDLIKLEEKVLT 300
DB 241 ILMSCNAICPMANTOCQAHAFILAKIAGKGEDNDKDVLEFLMKAKPDLIKLEEKVLT 300
OY 301 EERTNKVMEFPFGTVPYOTADCVLPKHREWKITAMGNSIPTMGNTSYEGLEFSTSLK 360
DB 301 EERTNKVMEFPFGTVPYOTADCVLPKHREWKITAMGNSIPTMGNTSYEGLEFSTSLK 360
OY 361 QMPLVKELETQVNFVPSSELADETAPELLEMGAKIKAAHYGETPTADNEMDLCSHY 420
DB 361 QMPLVKELETQVNFVPSSELADETAPELLEMGAKIKAAHYGETPTADNEMDLCSHY 420
OY 421 FWEPMHRLQLRNHTSGRPVLYLRFPDSEDLINRYRIMRSRGYKGVSHADELYTFEW 480
DB 421 FWEPMHRLQLRNHTSGRPVLYLRFPDSEDLINRYRIMRSRGYKGVSHADELYTFEW 480
OY 481 NOLAKRMPKESREYKTIERTMTGIMIOFATGNDPYSNEIEGEMENVSDPIKSDVYKCLN 540
DB 481 NOLAKRMPKESREYKTIERTMTGIMIOFATGNDPYSNEIEGEMENVSDPIKSDVYKCLN 540
OY 541 ISDELKMIIDVPEMDKIKQWESMEKRDLP 570
DB 541 ISDELKMIIDVPEMDKIKQWESMEKRDLP 570

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RESULT 6

ABB57850 standard; Protein: 572 AA.

ID ABB57850

AC ABB57850;

DE 26-MAR-2002 (first entry)

KW Drosophila melanogaster polypeptide SEQ ID NO 342.

KM Drosophila; developmental biology; cell signalling; insecticide;

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL01953.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

XX Disclosure; SEQ ID NO 342; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (AB16176-AB130511), expressed DNA

XX sequences (AB101840-AB16175) and the encoded proteins

XX (ABB5737-ABB72072).

XX The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 572 AA;

XX

XX

XX

XX

XX

DB 241 ILQSGSAICPMAYNGDITHNPIRIAKLVGYGENDKVLLEFLQVNAKKDLIREENVLT 300

DB 300 LEERTNKVMPFPGTVEPYQADCVLPKHPREMYKTANGNSIPTMGNTSYGLFTSIL 359

DB 301 LEERNMKNIMFAGPSLEFSTPECYISKPKEMKMTAMNSNIPMGIGTSTYGLIMVPEV 360

DB 360 KQMLVKELETQVNFVSELDADAETAPETLEMGAKIKKAAHVGETPTADNFDLCSHI 419

DB 361 KLMPQVLOQLDAGTPEFTKELLATEPESKEKLSMSAQIRDVHRCGSESTPNYDLCSY 420

DB 420 YFMPFMRLLOLRNHTSGTPVLYLRFPDSEEDLINPYRMRSGRGVSHADELYTF 479

DB 421 YFVFPALRVNHSRRAVAGAVYFRYFDSBELFPIRIRLRGAVGVSHADLSTQF 480

DB 480 WNLAKRMPKESREYKTIERTGIMWIDPATGPNPISNEIEGMENVSPDIKSDVEYKCL 539

DB 481 SSLARLRPKESREYRNIERTVIGWTFPAAGNPSEKINQMDTLTIDPVKRSDEVICL 540

DB 540 NISDELKMDYPEMDKIKQWESMEFKHRL 569

DB 541 NISDLKFTIDLPWPKLKWESLYDDNKDL 570

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Page 5

SQ Sequence 567 AA:

Query Match 46.0%; Score 1412.5; DB 22; Length 567;
Best Local Similarity 48.6%; Pred. No. 2,1e-135;
Matches 267; Conservative 105; Mismatches 164; Indels 13; Gaps 6;

OY 26 RLTNNEVVAETEGKVKYKRLTYDSDYSEEGIPYAOYPVGELEFKAPQRETPMDGV 85
D 19 RLRSNDVIADTYGKVKYKQSIYGNNTYSEGIAPFAPKAPVGELEFKAPVREHMSDV 78
OY 86 RDCNHRDKSVQVDFITGKCGSEDCLYLSTYNNLNLPETKRPVLYIHGGELIGENHR 145
D 79 KRCHVNAKCCQVNTYKQVQSGEDCLYLVNRYELHPRLPVLWYIGGGQMGESAR 138
OY 146 DMGPDYFKKRDVYLNIQYRLGALGFLINSEDLNPNAGLKDOVMALRWIKNCANF 205
D 139 DLYSPDITVMEHVLYVYSRLALGFLSLADELDVPGNAGLKDOVMALRWKRCQFT 198
OY 206 GGNPDITVGESAGASTHYMMLTEQTRGLFHRGLIMSGNAICPMANTQCO-HRAFTLA 264
D 199 GGDPDITVGESAGASTHYMMLTDQAKGLFHKTIIMSSALAPMAQPTTHINWPYRLA 258
OY 265 KLAGYGEDNDKDVLEFLMKAKPQDLIKLEKYLLEERTNKY-MRPFQTVPTQYQAD 323
D 259 QATGYTGADANDRIEFAHLKCKKASSMLKVAEDITIMEERHQRLLTFSPGTEIPYLPHC 318
OY 324 VLPKHPREYKWTANGSIPTMGNTSYEGLEFSTILKQPMVLKELTCVNEPSELADA 383
D 319 VIKPSLEMMRDGMSIPVIGNSFEGILMPREVKNKPELLCOGDCDENLAPQ--DA 375
OY 384 ERTAPTELEMGAKIKKAHTGEP--TADNFDLCSHIYFPPMRLQLKRNHTSGTP 440
D 376 HDEQORAKAFKKVRLYEGDRTPGRRKTLLEYSDLFSTYKFWMGHIRTLLSRHNAHPLAP 435
OY 441 VLYLRDPFSEDLINPYRIMRSGRGVYSHADELTFPFMNOLAKRMPRESREYKTIEM 500
D 436 TFLYRDPFSKH-FNIMRIITGRKVRGCHADDSLYLFYMAAKKLKRTAEFKTIKRL 494
OY 501 TGTWIOFATTGNP---YSNEIEGMENVSMDPIKSKDEVYKCLINISDELKMTIDVPEMDK 556
D 495 VSVVHFAISGDPNIPWQCDEKPEORGMPLPSKDKVFOCLINTSHDVHIDLPEAKEL 554
OY 557 KOMESMEK 565
D 555 RLMDCLTYDR 563

RESULT 8
ABB57866
ID ABB57866 standard; Protein; 554 AA.

AC ABB57866;
DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide seq ID NO 390.
KW Drosophila: developmental biology; cell signalling; insecticide;
pharmaceutical.
OS Drosophila melanogaster.
PN WO200171042-A2.
PD 27-SEP-2001.
PE 23-MAR-2001; 2001WO-US09231.
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
PA (PEKE) PE CORP NY.
XX

PI Venter JC, Adams M, Li PWD, Myers EM;
XX WPI: 2001-656860/75.
DR N-PSDB; ABL01969.
XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -

PS Disclosure: SEQ ID NO 390; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL01840-ABL01969), expressed DNA
CC sequences (ABL01840-ABL01969) and the encoded proteins
CC (ABB57737-ABB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 554 AA:

Query Match 45.8%; Score 1408.5; DB 22; Length 554;
Best Local Similarity 48.5%; Pred. No. 5,1e-135;
Matches 269; Conservative 95; Mismatches 178; Indels 13; Gaps 6;

OY 18 INKFLNRYRLTNETVVAETEGKVKYKRLTYDSDYSEEGIPYAOYPVGELEFKAPQ 77
D 2 VDFKVOQRRTSEKTVSTYTGPIKGVKRSIYQSFSEFRIAPFAPVGELEFKAPQ 61
OY 78 RPTPMDGVADCCNHDKSQVDFITGKCGSEDCLYLSTYNNLNLPETKRPVLYIHGG 137
D 62 PEEVTEVASTCSQGPRLQKHFEVEMTDGSEDCLYLVNRYKLPYPMYVWYIGG 121
OY 138 FTIGENHRDMPDPIKIKKADVYLNIQYRLGALGFLINSEDLNPNAGLKDOVMALRW 197
D 122 POFGEASRECYSPDYLREDDVYISINRYLGLCLDDPELDVPGNAGLKDOVMALRW 181
OY 198 IKNNCANFGNPDNITVGESAGASTHYMMLTEQTRGLFHRGLIMSGNAICPMANTQCO 257
D 182 VKANCSREGCDSANITIGDSAGSASVHYMMITEQTHGLFHKALCMSGNTSLPMAVTPQR 241
OY 258 HRAFTLAKAGKGEDNDKDVLEFLMKAKPQDLIKLEKYLLEERTNKYMRPFQTVPTQY 317
D 242 NMPYRLAVQAGTAGENNTRDYWEFLKNAKGSBITKANGELCIDEEKKRIEFSFGPIEP 301
OY 318 YOTADCVLPKHPREYKWTANGSIPTMGNTSYEGLEFSTILKQPMVLKELTCVNEP 377
D 302 YVTSCHVPPKKPIEMRPTAWSNNIPLLIGVSNBGLLYSETKNPKCLNLDRCRFVPR 361
OY 378 SELADERTAPTELEMGAKIKKAHTGEP--TADNFDLCSHIYFPPMRLQLKRNHTSGTP 440
D 362 TEL-NMDRESALCREYGOQLRCQYGGDTPLDLHEVLQWVSHYEFPIYRTVLSLQ 420
OY 435 HTSGPVLVLRPFSEDLINPYRIMRSGRGVYSHADELTFPFMNOLAKRMPRESREY 494
D 421 YARSAPFLYLRFPDPSKH-FNHLRLTSGKVRGTCCHDDLSLYFYSLARKLNHTREY 479
OY 495 KTIEMTGIWIOFATTGNP-YSNEIEGMENVSMDPIKSKDEVYKCLINISDELKMTIDV 550
D 480 KCIERLVGLMTHTFAACGPNPDPEQEDL---WQVPDPAVEKHLQCLNISDELKMTIDV 535
OY 551 PEMDKIKOMESMEK 565
D 536 PDLKKLWMESEFRR 550

RESULT 9
ABB57867
ID ABB57867 standard; Protein; 572 AA.

[illegible]

Dd		302 DEEKEERIEFGSGPVATPEVYTSHCVPKPKPIEMKRANSNINPILIGVGSENEGILLTSET	361
Oy		360 KQMPVLVEKETCVNFPSELADAEPTAETLEMGARIKKAHVTGETPAD---NFMDLC	416
Dd		362 KNPKACLNELDDCRFVVPIEL-NMDESALCREYGQRLRCGYGDKTPSLDITLHEYLOWM	420
Oy		417 SHITYWEPMAHLLQLRFNNHTSGTIPVLYLRPFDSEDLINPRIMRSGRGKYSHADELT	476
Dd		421 SHEHYWFPPYRYVLSLQAARSAPFLYLRFDFDSKH-FNLRLISCGKKYGTCHGDLS	479
Oy		477 YEFNMOLAKRMKESREYKTIERMGIWIOFATTGNP-VSNELEGMEVSM---DPILKS	532
Dd		480 YLFYSLARKLKNHRTREYCTIERVLGMTHFAACGNPNEDPEDDL---WQPYDPAVE	535
Oy		533 DEVYKCLNISDELKMIDVPEMDKIKOMESMFER	565
Dd		536 KHQKLCLNISDELKVIDVDPLKKIMYWESFFRR	568
		RESULT 10	
ID	ABBS9161	ABBS9161 standard; Protein; 554 AA.	
xx	AC	ABBS9161;	
xx	Df	26-MAR-2002 (first entry)	
xx	DE	Drosophila melanogaster polypeptide SEQ ID NO 4275.	
xx	KM	Drosophila: developmental biology; cell signalling; insecticide;	
xx	KW	Pharmaceutical.	
xx	OS	Drosophila melanogaster.	
Pn	xx	WO200171042-A2.	
xx	PD	27-SEP-2001.	
xx	Pf	23-MAR-2001; 2001WO-US09231.	
xx	Pr	23-MAR-2000; 2000US-191637P.	
xx	PR	11-JUL-2000; 2000US-0614150.	
xx	PA	(PEKE) PE CORP NY.	
xx	PI	Venter JC, Adams M, Li PMD, Myers EM;	
xx	DR	WPI: 2001-656860/75.	
xx	N	N-PsDB; ABL03264.	
Pt		New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -	
Px		Disclosure: SEQ ID NO 4275; 21bp + Sequence Listing; English.	
CC		The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).	
CC		The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
CC			
xx	Sequence	554 AA:	
Query Match	43.1%;	Score 1324.5;	DB 22; Length 554;
Best Local Similarity	45.6%;	Pred No. 2.1e-126;	


```

Db      8  ETCELTPVGQIKGVKRLSYDDPFSEFKIPFAKREPLGELRFKAPVPADPMSGVLCTH 67
QY      91  HKDKSVQVDFITGKVCSEDLCLYSVTYNNLNPEFKRPVLVYIHGGFTIGENHRDMYGP 150
      68  YAEKPTQKGLLRREIEGGEDCLYLVYSQKLSEKRLPVVMVYIYGAVTGEATRELXGP 127
QY      151  DYFIKRDVVLINIOYRLGALGFLSLNSEDLVNPGNAGLKDOVMALRWIKNCANCGNPD 210
      128  DYFEMTKDVLVTLNRYDCLGFLSLKDPSLKVPGNAGLKDQVLAALKWKQYLSNNGDS 187
QY      211  NITVGEESGAASHTYHMLTEQTRGLFHRGILMSGNALICPMANTQCOHRAFTLAKAGYK 270
      188  NITVEESAGCSTHRMCTEGRGLFHAIPMSGTVHYMYANNRAEDAFRLAQDNGET 247
QY      271  GEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTKNVMPREPRVEPYQTADCVLPKHPR 330
      248  GENDAKKVLLEYLGQVAPADLV--NHNLTPREHRRNGLLFAFEPVTEAVYGECCVVPKRPV 305
QY      331  EMVKITAMGNSIPTMGNTSYEGELF---TSILKOMPLVKELETGVNVPSELADAE-R 385
      306  EMARDAMSNFPVMLGTSFEGLEMTPAVSANKALDLSQD-----PRLVAVDVR 357
QY      386  TA---PETLEMGAKIKKAAHYGETPTAD--NEMDLCSHIYFWPMHRLQLRFNHTSGT 439
      358  TVSEKENLEYSQRLMKAVFGYSPSEELLNMLDFYSYKIFWHGFNRTFNALTYAK-A 416
QY      440  PVLVYRPDESDCLINPYRKMSRGVYK-GVSHADELYTFEYVNLAKRMKRESREKKTIE 498
      417  PTYYRRDFDESPN-FNEYRAKFCGDKIKTGVAHADLSYLEFNAGSMKLDKTSAEYRTIE 475
QY      499  RMGVIWQFPTGNGPYNSIEGEMENSWDPIKKSDEYVKCLNTSDELMKIDVEMDKIKO 558
      476  RMGIVTAFAATSNPCRELGHE---WKSTKNDP-KRYINISDVTIIDPEYEKLOI 531
QY      559  WESMEFKHR 567
      532  WDNLXKPNQ 540
Db

```

RESULT 14
 ABB57868 standard; Protein; 530 AA.
 XX
 AC ABB57868;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 396.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 MO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PE 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR N-PSDB: ABL01971.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

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XX
PS Disclosure; SEQ ID NO 396.; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SO Sequence 530 AA;

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Query Match 40.0%; Score 1228.5; DB 22; Length 530;
 Best Local Similarity 44.3%; Pred. No. 1.4e-116;
 Matches 236; Conservative 105; Mismatches 179; Indels 13; Gaps 8;

```

QY      40  GKVGKRLTYVDSYSYFEGIPYAPVGEIRKAPQRPPTMDGVDRDCCNKKDKSVQVD 99
      5  GPVGVKNTIMGSGYSEFEKIPFAKRPVGDLRKFAPEAVRPMQELDCTSPADKPIQTH 64
QY      100  FITGVCSESDCLYSVTYNNLNPEFKRPVLVYIHGGFTIGENHRDMYGGDYFIKKQDV 159
      65  MFFRRYAGSEDCLYLVYVVKLDQPKLRPVWVWYIGGAYQVEASRDYSPDFMSKDV 124
QY      160  LNIQYRLGALGFLSLNSEDLVNPGNAGLKDOVMALRWIKNCANFGGPNITVFGESA 219
      125  IYVAIRLGLALFSLDQPLNPGNAGLKDOIIMLRVQQNIKFAFGSDNNITLFGESA 184
QY      220  GAASHYMLTEQTRGLFHRGILMSGNALICPMANTQCOHRAFTLAKLAGYGEDNDKVL 279
      185  GASTHFALSPQTEGLIKALVMSGVYLCPTQPRNNMVAIRLQKLGYYDGNKDKAIF 244
QY      280  EFLMKAKPQDLIKLEKVLTLEERTKNVMPREPRVEPYQTADCVLPKHPREMYTAGN 339
      245  EFLRMSGGEIYKATATVLSNDEKHHRLIFAGPVVEYRTTHYVAAQPHELQMSNSH 304
QY      340  SIPTMGNTSYEGFTSILKOMPLVKELETGVNVPSELADAEPTLE-MGAKIK 398
      305  RIPMFGGTSFEBLLFYPVSRPATLDEVGNCKNLPSDL--GLNDPKLENYGLQDK 362
QY      399  KAHVGETPTADN--FMDLCSHIYFWPMHRLQLRFNHTSGTVYLYRPDESDCLIN 455
      363  KAYFGDEPCNOANMKFLELCSYREFMHIYRAALNVRQSS-APYILRFPHDSK-LCN 420
QY      456  PYRIMSGRGVKGSHADELYTFEYVNLAKRMKRESREKKTIERMTGIWQFATGPNYS 515
      421  ATRIVLCGHOMRGVCHGDDCLYFHSMLSHQSPDSPEHKVITGMVDVTSFAHGDPP-- 478
QY      516  NETEGMENSWDPIKKSDEYVKCLNTSDELMKIDVEMDKIKO-WESMEFKHR 567
      479  -NCESIKSLKFAPIENVTN-FKCLINIGDQFEVWALPELOKIEPVNMSFYAPMK 529
Db

```

RESULT 15
 AAM47598 standard; Protein; 602 AA.
 XX
 AC AAM47598;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Drosophila cell cycle progression protein #27.
 XX
 KW Antiproliferative; cytosstatic; cardiant; immunosuppressive; meiosis;
 KW antiinflammatory; antiposrotatic; dermatological; antifungal; mitosis;
 KW antiparasitic; antimetarial; antirneumatic; antiarthritic; cell division;
 KW cell cycle progression protein; tumour; proliferative disorder;
 KW cardiovascular; autoimmune; dermatological disorder.

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:33 ; Search time 19.0734 Seconds
(without alignments)
2872.940 Million cell updates/sec

Title: US-09-776-910-8

Perfect score: 3073
Sequence: 1 MNFNVSIMKELKWKIKCIEN.....PEMDKIKQWSEMEKRDLE 570

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1038	33.8	540	2	A35986
2	1035	33.7	540	2	S53370
3	1025	33.4	540	2	S53371
4	929	30.2	503	2	S53372
5	691	22.5	564	2	A34325
6	593	19.3	578	2	F89068
7	593	19.3	658	2	T32053
8	585.5	19.1	547	2	S53233
9	578.5	18.8	489	2	B69680
10	571.5	18.6	583	2	T25690
11	568.5	18.5	564	1	S36787
12	568.5	18.5	602	1	ACHU
13	567	18.5	552	2	S36786
14	565.5	18.4	596	1	ACRYE
15	564.5	18.4	614	2	JH0314
16	558.5	18.2	599	1	A38868
17	557	18.1	746	2	A25363
18	556.5	18.1	614	2	JH0811
19	549.5	17.9	583	1	S10712
20	548.5	17.8	561	2	S47655
21	547.5	17.8	614	2	A39256
22	545	17.7	581	2	C39768
23	538	17.5	562	2	S27782
24	537	17.5	584	2	S48724
25	536	17.5	511	2	D70944
26	536	17.4	548	2	T32907
27	536	17.4	557	2	A47162
28	535	17.4	544	2	A34089
29	535	17.4	544	2	A41426

30	535	17.4	544	2	B40122	carboxylesterase (
31	535	17.4	548	2	A28022	carboxylesterase (
32	534	17.4	544	2	C41426	carboxylesterase (
33	534	17.4	544	2	A40122	carboxylesterase (
34	533.5	17.4	541	2	H41426	carboxylesterase (
35	533.5	17.4	691	2	JE0150	acetylcholinestera
36	533	17.3	544	2	F41426	carboxylesterase (
37	530	17.2	544	2	B41426	carboxylesterase (
38	530	17.2	544	2	D41426	carboxylesterase (
39	528.5	17.2	545	2	S58982	carboxylesterase (
40	528.5	17.2	545	2	S58968	carboxylesterase (
41	528.5	17.2	545	2	S58977	carboxylesterase (
42	528	17.2	544	2	E41426	carboxylesterase (
43	527.5	17.2	544	2	E41426	carboxylesterase (
44	527.5	17.2	545	2	S58972	carboxylesterase (
45	526.5	17.1	545	2	S58980	carboxylesterase (

ALIGNMENTS

RESULT 1

esterase B1 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C:Date: 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change 21-Jul-2000

C:Accession: A35986

R:Mouches, C.; Pauplin, Y.; Agarwal, M.; Lemieux, L.; Herzog, M.; Abadon, M.; Baysat

Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990

A:Title: Characterization of amplification core and esterase B1 gene responsible for

A:Reference number: A35986; MUID:90207238; PMID:2320576

A:Accession: A35986

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-540 <MOD>

A:References: GB:M32328; NID:q156687; PIDN:AAA28289.1; PID:q156688

A>Note: the authors translated the codon CGT for residue 213 as Ala, and CGT for resi

C:Superfamily: cholinesterase; cholinesterase homology

Query Match	33.8%	Score 1038	DB 2	Length 540
Best Local Similarity	37.9%	Pred. No. 1.4e-72		
Matches 206; Conservative 114; Mismatches 201; Indels 22; Gaps 8;				
QY	31	ETVAETFEYGVKVKRLTYDDSYSEFGIPYQPPVGEIRFARAPQPTWMDVRC--	88	
DB	4	ESLVVQTRKGVKRVNLSLGOEYVFOGIPYARABEGELFRAPVPQKTELTDCQ 63		
QY	89	----CNHKDKSVQVDFITGKVGSEDCLYSVYNNLNIPETKRPVLVYIHGGFTIGENH 144		
DB	64	QCEPCYHFDRLQ-----KIVGCEDSLKINVFKEINPSTPLVYMLTYIGGFTTEGTSG 117		
QY	145	RDWGPVYFIKKDVLINIOYRIGALGFLSUNSEDLNVNAGAKDOYALRWIRKNCAN 204		
DB	118	TELVGPFLVQKDLVLVSFNRIGALGFLCCQSDQGVNAGAKDOYALRWVLENTIAA 177		
QY	205	FGGPNMTIVTGESAGASTHYMLTQETRLPHRGILMSGNALCPNANTQOORAFPLA 264		
DB	178	FGGPKRVTLTLAGHSGAASVQYHLISDASKDLFRRLVMSGSSTYSWSLTQRWVEXLA 237		
QY	265	KLAIVKEDNDKDVLEFLMKAKPODLIKLEEKVLTLEERTKVMFPPTPEPYQTADCV 324		
DB	238	KALGWDOGGSSGLRLFRRAKRPEDIYAHQKLLTDQMODDITTPPGPTPEPYLTQCI 297		
QY	325	LPKHREMVKATWAGNSIPTWKGNTSYGLFTSTLKOMPMLVKELETCVNPSELDAE 384		
DB	298	IPKAPFEMARPAWMDKIDIMIGTSEBGLDLQIKILHPELLSHPHFLVGNPNL--K 354		
QY	385	RTAETLEMGAKIKKAVTGETPADN--FMDCSHYTFPFRNRLDLRFNNTSGTPV 441		
DB	355	ISMKEIEFAKLQRYRPPSIPSMENNLGVNHNMSRVFNHGLRTILAAAR--SRAT 413		
QY	442	YLRFDEDSEDLIPRYIRMSRGVSGVSHADELTTFYFMNOLAKRMKESREYTIEMT 501		

Db 414 FVYRICLDSF-FYNNHYRIMIDPKLGTGTAHADELSTYLF-SNFTQOVPEKTEFEYRGLQTL 472
 Oy 502 GIMIOFATGPNYSNEIEGEMENVSMDPIKSDVEYKCLNT-SDELKIDVPEMDKIQWE 560
 Db 473 DVEFSAFVINGDPNCG-MTAKSGVVEEPNAGTKPTFKCLNTANDGVAVDYDPADRLDMMD 531
 Oy 561 SMF 563
 Db 532 AMY 534

RESULT 2

carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
 C:Date: 15-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000
 C:Accession: S53370, S44211
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
 Biochem. J. 305, 651-658, 1995
 A:Title: The independent gene amplification of electrophoretically indistinguishable B
 A:Reference number: S53370; MUID:95134253; PMID:7530448
 A:Accession: S53370
 A:Molecule type: mRNA
 A:Residues: 1-540 <VNU>
 A:Cross-references: EMBL:Z32694; NID:9475067; PIDN:CAA83643.1; PID:9475068
 A:Experimental source: strain PeIR
 A:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase

Query Match

Best local similarity 37.78; Score 1035; DB 2; Length 540;
 Matches 205; Conservative 114; Mismatches 202; Indels 22; Gaps 8;

Oy 31 ETVVAETEVKGVKRVLTVDYSYSEGIPTAOPVGLRFAKAPORPTPMGCVRC-- 88
 Db 4 ESLTVQTKGVPVGRKSVSLQGEVYFQGIPTAPARPEGLRFAKAPVPPOMWETLDCSQ 63
 Oy 89 ----CNHKDKSVQVDFTTGKVCSEDCLYSTNNLNPETKRPVLYIHGGFIIENH 144
 Db 64 QCEPCYHFDRLQ-----KIVGCEDSLKINFAKEINSPKPLVMLYIGGFTGTS 117
 Oy 145 RDMGPRYFIKRDVLTINIOYRGLGFLSLNSEDLVNPGNAGLDQVMALRWIKNCGAN 204
 Db 118 TELGPRFLVQKDLVLSFNVRIGALGFLCCSEODGVGNAGLDQVMALRWIKNCGAN 177
 Oy 145 RDMGPRYFIKRDVLTINIOYRGLGFLSLNSEDLVNPGNAGLDQVMALRWIKNCGAN 204
 Db 178 FGDPKRVTLVGHSAAGASVOYHILSDASKDLFQRAIVSGSYNSLSLRRNMVEKLA 237
 Oy 205 FGPNPNTIVFGESAGASTHYMLTEQTRGLFHRGILSGNAGICPMANTOCORAFILA 264
 Db 178 FGDPKRVTLVGHSAAGASVOYHILSDASKDLFQRAIVSGSYNSLSLRRNMVEKLA 237
 Oy 265 KLAGYKGEDNDKVDLEFLMAKAPODLILKEKYLTLEERTNKVMPFGTVERPYOTADCV 324
 Db 238 KAIGWDGGGEGSGLRFLRAKAPEDIVANOEKLLTDODMODLFTFGPTVEEYLTBOCM 297
 Oy 325 LPHKPREVWKTANGSIFPMGNSTYEGLEFSTILKQMPVLYELETGVNFEVSELADE 384
 Db 298 IKKEPEAKRTVMGKIDIMIGTSEBGLLLQKIKLOPRLSHPHFLGNVPPNL--K 354
 Oy 385 RTAPETLEMGAKIKRAHYTGETPTADN---FMDLCSHYTFEPMHRLQLRFNHTSGT 441
 Db 355 ISMEKRIEFAKIKORYYDSSPSMENNIGYHMSDREVFHGHGRLTLARAAR-SKART 413
 Oy 442 YLYRFDSEDLINPYRIRMSRGVGVSHADELYTFPMNOLAKRMPKESREYKTIERTM 501
 Db 414 FVYRICLDSF-FYNNHYRIMIDPKLGTGTAHADELSTYLF-SNFTQOVPEKTEFEYRGLQTL 472
 Oy 502 GIMIOFATGPNYSNEIEGEMENVSMDPIKSDVEYKCLNT-SDELKIDVPEMDKIQWE 560
 Db 473 DVEFSAFVINGDPNCG-MTAKSGVVEEPNAGTKPTFKCLNTANDGVAVDYDPADRLDMMD 531
 Oy 561 SMF 563
 Db 532 AMY 534

RESULT 3

carboxylesterase (EC 3.1.1.1) B1 - southern house mosquito
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
 C:Accession: S53371
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
 Biochem. J. 305, 651-658, 1995
 A:Title: The independent gene amplification of electrophoretically indistinguishable
 A:Reference number: S53370; MUID:95134253; PMID:7530448
 A:Accession: S53371
 A:Molecule type: mRNA
 A:Residues: 1-540 <VNU>
 A:Cross-references: EMBL:Z32695; NID:9475069; PIDN:CAA83644.1; PID:9780238
 A:Experimental source: strain MRES
 A:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase

Query Match

Best local similarity 33.4%; Score 1025; DB 2; Length 540;
 Matches 203; Conservative 120; Mismatches 197; Indels 24; Gaps 10;

Oy 31 ETVVAETEVKGVKRVLTVDYSYSEGIPTAOPVGLRFAKAPORPTPMGCVRC-- 88
 Db 4 ESLTVQTKGVPVGRKSVSLQGEVYFQGIPTAPARPEGLRFAKAPVPPOMWETLDCSQ 63
 Oy 89 ----CNHKDKSVQVDFTTGKVCSEDCLYSTNNLNPETKRPVLYIHGGFIIENH 144
 Db 64 QCEPCYHFDRLQ-----KIVGCEDSLKINFAKEINSPKPLVMLYIGGFTGTS 117
 Oy 145 RDMGPRYFIKRDVLTINIOYRGLGFLSLNSEDLVNPGNAGLDQVMALRWIKNCGAN 204
 Db 118 TELGPRFLVQKDLVLSFNVRIGALGFLCCSEODGVGNAGLDQVMALRWIKNCGAN 177
 Oy 145 RDMGPRYFIKRDVLTINIOYRGLGFLSLNSEDLVNPGNAGLDQVMALRWIKNCGAN 204
 Db 178 FGDPKRVTLVGHSAAGASVOYHILSDASKDLFQRAIVSGSYNSLSLRRNMVEKLA 237
 Oy 205 FGPNPNTIVFGESAGASTHYMLTEQTRGLFHRGILSGNAGICPMANTOCORAFILA 264
 Db 178 FGDPKRVTLVGHSAAGASVOYHILSDASKDLFQRAIVSGSYNSLSLRRNMVEKLA 237
 Oy 265 KLAGYKGEDNDKVDLEFLMAKAPODLILKEKYLTLEERTNKVMPFGTVERPYOTADCV 324
 Db 238 KAIGWDGGGEGSGLRFLRAKAPEDIVANOEKLLTDODMODLFTFGPTVEEYLTBOCM 297
 Oy 325 LPHKPREVWKTANGSIFPMGNSTYEGLEFSTILKQMPVLYELETGVNFEVSELADE 384
 Db 298 IKKEPEAKRTVMGKIDIMIGTSEBGLLLQKIKLOPRLSHPHFLGNVPPNL--K 354
 Oy 385 RTAPETLEMGAKIKRAHYTGETPTADN---FMDLCSHYTFEPMHRLQLRFNHTSGT 441
 Db 355 ISMEKRIEFAKIKORYYDSSPSMENNIGYHMSDREVFHGHGRLTLARAAR-SKART 413
 Oy 442 YLYRFDSEDLINPYRIRMSRGVGVSHADELYTFPMNOLAKRMPKESREYKTIERTM 500
 Db 414 FVYRICLDSF-FYNNHYRIMIDPKLGTGTAHADELSTYLF-SNFTQOVPEKTEFEYRGLQTL 471
 Oy 501 TGIMIOFATGPNYSNEIEGEMENVSMDPIKSDVEYKCLNT-SDELKIDVPEMDKIQWE 559
 Db 472 DVFTFAVINGDP-NCSMTAKSGVVEEPNSQTKPTFKCLNTANDGVAVDYDPADRLDMMD 530
 Oy 560 SMF 563
 Db 531 AMY 534

RESULT 4

carboxylesterase (EC 3.1.1.1) B - southern house mosquito (fragment)
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
 C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
 C:Accession: S53372; S44212
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
 Biochem. J. 305, 651-658, 1995
 A:Title: The independent gene amplification of electrophoretically indistinguishable

[illegible]

A:Cross-references: GB:J04955; NID:g159222; PID:g159223
C:Superfamily: juvenile-hormone esterase
C:Keywords: carboxylic ester hydrolase

Query Match 22.5%; Score 691; DB 2; Length 564;
Best Local Similarity 33.3%; Pred. No. 1.4e-45;
Matches: 173; Conservative 102; Mismatches 208; Indels 36; Gaps 19;

OY 23 LNYRLTNETVAETEKVKVGRKRLTYDDSYVSFEIGIPAPCPGELRKAQORPTPW 82
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 18 LAMQSTNSRSVAHDSOIINGVRP-SADGIKPSFSLGVPAKQPGELRKLEPLEPW 76
OY 83 DGVRCCHKKDKSVQVDFTSKVCG---SEDCLYLSVT--NNLNPETK----RPVLV 131
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 77 DNILNATNEGPICFOTDVLVGRMLMAEMSEACIANTIHVMOSTL-PRVRGTPLRPILV 135
OY 132 YTHGGFIIEGHHRMVPDPDFIKKDVLLINIOYRLALGLFLSINSDLANVGAGHKDQ 191
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 136 FHHGGGFARGSGHEHLHGPELVTKNVITVFNRNLNVGLSMNT--TKIPNAGLRDQ 193
OY 192 VVALMKIRNMCANGNDNITVEGESGAASATHYMTEDETRGLFHNGILMSGNALCPW 251
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 194 VTLLMWQRNAKNFGCDPSDTITTAGQSAGAANHLTLTSKTBEGFKAILMSTGMSYF 253
OY 252 ANTCQHRAFTLAIAKYG--EDNKDVLFFLKAKPDOLIKLEKYLLEERTKVMF 309
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 254 FTTSPLFAAYISKOLLQILLGNORDGESEIHQLDLPAE--KINEAVALIEQIG--LT 308
OY 310 PGQPIVE-PYQIADCVLKHPREWKTKMGSIPTMGNTSYEGLFSTILKONPMIVKE 368
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 309 TFLPIVESPLRGVTTIIDDPRIILAEGRGKNVPLLIGFTSSKECTFRNRLNPDVLAKI 368
OY 369 LETCVNFVPSIELADERTAPETL-EMGAKIKKANHTGETPADNPMDLSIHYPMPMR 427
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 369 QDNPIIIIPKL-LFMTPRELIMLAKTIERRKYNG-TISIDNFVSCSGFIEYPAIK 425
OY 428 LIQLRFNHTSGTVYLYRFDSEDLINPYRIMSGRGVKVSNADELTYFF-WNOLAKR 486
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 426 LAQKR-AETGCARPLYEFRAFEGQNSLIK-KVM--GLNHESGVIEDLTYFVKYSMSSEA 481
OY 487 M---PKESREYKTIERMTGMTOFATTGNPNPSNEEGME 522
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 482 LHASPSEN-DVAKMKMLMTGYFLNFIKCSOPCEDNNLSLE 519

RESULT 6
F89068
protein T28Cl2.4b [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: F89068
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: F89068
A>Status: preliminary
A:Molecule type: DNA
A:Feature: 1-578 <STO>
A:Cross-references: GB:chr_V; PID:NAB66160.1; PID:g23j5734; GSPDB:GN00023; CESP:T28CL
C:Genetics:
A:Gene: T28Cl2.4b
A:Map position: 5
C:Superfamily: cholinesterase; cholinesterase homology

Query Match 19.3%; Score 593; DB 2; Length 578;
Best Local Similarity 29.1%; Pred. No. 5.8e-38;
Matches 172; Conservative 98; Mismatches 220; Indels 102; Gaps 26;

OY 22 FLNRYLTNETVAETEVKGKVRKRLTYDDSYVSFEIGIPYADPPNGELRFAKAPQRP 81
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Query Match	18.5%	Score 568.5	DB 1	Length 602
Best Local Similarity	29.0%	Pred. NO. 5e-36		
Matches 176; Conservative	96	Mismatches 228	Indels 107	Gaps 25

A: Accession number: S36786; MUID:93384534; PMID:8373371
A: Accession: S36786
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-552 <FIE>
C: Cross-references: EMBL:X74554; NID:9397510; PIDD:CAAS2648.1; PID:9397511
C: Superfamily: cholinesterase; cholinesterase homology
C: Keywords: carboxylic ester hydrolase
F: 52-552/Domain: cholinesterase homology <CHE>

Query Match 18.5%; Score 567; DB 2; Length 552;
Best Local Similarity 29.3%; Pred. No. 5,7e-36;
Matches 167; Conservative 88; Mismatches 226; Indels 88; Gaps 22;

OY 28 TTNETVAETEGKVKYKRLTVYYDDSYSEFGIPYAPPVGELRFAKAPRPMDGYRD 87
 ::: : :::: | | | | | | | | | | | | | | | | | |
DB 22 SASNTPKVQVHSGEITAGCFEFTYNGRKLYSPGLPYASPQNRFKEPQPVPWLGAWN 81
 ::: : :::: | | | | | | | | | | | | | | | | | |
OY 88 CCMHKDKRVQDFDTIG-VYCSEEDCLYSVTNNLNPETK----RPVVYIHGGFIIGE 142
 ::: : :::: | | | | | | | | | | | | | | | | | |
DB 82 ATPGSAQLGLEFGSGSKTIGQEDCLFNVTYPKLPQNSAGDLMNVTLHIHGSGYFGE 141
 ::: : :::: | | | | | | | | | | | | | | | | | |
OY 143 NHRDYGDPDYFT-KKDVLINIOYRLGALGFSLNSEDLANPNAGALKDQVMALRIKN 201
 | | | | | | | | | | | | | | | | | | | | | | | |
DB 142 G-IILGHYLLDNNDPFYVSINRYRLSVLGFS--TGSGVLTGNNGLKDOVALAKMIDQN 197
 | | | | | | | | | | | | | | | | | | | | | | | |
OY 202 CANPGANDNITVGESGAASTHYMLTEOTRGLEPHRGLMSGNALCPMANTQ-COHRA 260
 | | | | | | | | | | | | | | | | | | | | | | | |
DB 198 IVAFGDPSNVTITGMSAGASSVNHLISPMKSGLFNRATIOSGSAPFCMSTAEVNAQKT 257
 | | | | | | | | | | | | | | | | | | | | | | | |
OY 261 FLAKLAVYKGBDNDKVDLEFLMKAKPDQLKLEEKVLTLEERTKKVAFPRGPVE--PY 318
 | | | | | | | | | | | | | | | | | | | | | | | |
DB 258 KYIALMLMCP-TNNSVELVECL-RSRPAKA1-AASYLNEMPKRMFPPTPGPIVEAGY 313
 | | | | | | | | | | | | | | | | | | | | | | | |
OY 319 QTADVLCVHPREWKTAAMGNSIPTMGNTSVEGIFETSII-----KOMPM 364
 | | | | | | | | | | | | | | | | | | | | | | | |
DB 314 EK---FLRPDIKELVP-----HDIVPLISADDEGLFEFTPLGLENGFELNNNEHLPH 366
 | | | | | | | | | | | | | | | | | | | | | | | |
OY 365 LVKELETGVNFPSSELADERTAPETLEMGAIKKAHVGTGP---TADNFMDCSHIY 420
 | | | | | | | | | | | | | | | | | | | | | | | |
DB 367 ILD-----YNVTISNENLRFTAADI-----KEFYGDKPISKETKSMLSKMISDRS 413
 | | | | | | | | | | | | | | | | | | | | | | | |
OY 421 FWFPMHRLLOLRFNHTSG---TPVYLFRPDDSEDLINPYKIMSGKVKGVSHADELIY 477
 | | | | | | | | | | | | | | | | | | | | | | | |
DB 414 FGCGTSKAAQ---HIAKANRTAPVYEFEGYSGNSYVAFPPDKPSXSGSSPTGHDSTY 469
 | | | | | | | | | | | | | | | | | | | | | | | |
OY 478 -----FFMNOLAKMPRESREYKTIERMTOIGWIQFATGPNYSEIIGMENVSMDPTKK 531
 | | | | | | | | | | | | | | | | | | | | | | | |
DB 470 VLKMDGF-----VYNEEDRRKMTKMVMIMATFIKSGVDPDENSE-----TWLPYSK 517
 | | | | | | | | | | | | | | | | | | | | | | | |
OY 532 SDEVYKCINISDELKMIIDVPEMDKIKWE 560
 | | | | | | | | | | | | | | | | | | | | | | | |
DB 518 -----NLADPFRFKITQQOFPEAR 538
 | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
ACRYE
acetylcholinesterase (EC 3.1.1.7) precursor, 11s form [validated] - Pacific electric
N: Alternate names: acetylcholinesterase, asymmetric form
C: Species: Torpedo californica (Pacific electric ray)
C: Date: 17-Mar-1987 #sequence_revision 08-Nov-1996 #text_change 15-Sep-2000
C: Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677
R: Schumacher, M.; Camp, S.; Maullet, Y.; Newton, M.; Macphie-Ouigley, K.; Taylor, S.S.
Nature 319, 407-409, 1986
A: Title: Primary structure of Torpedo californica acetylcholinesterase deduced from i
A: Reference number: A00773; MUID:86118676; PMID:3753747
-A: Accession: A00773
A: Molecule type: mRNA
A: Residues: 'NS', 11-596 <SCH>
A: Cross-references: GB:X03439; NID:g64389
A: Experimental source: electric organ
A: Note: parts of this sequence, including the amino and carboxyl ends of the mature p
R: Schumacher, M.; Camp, S.; Maullet, Y.; Newton, M.; Macphie-Ouigley, K.; Taylor, S.S.

[illegible]

F:234/Active site: Ser #status predicted
F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.4%; Score 564.5; DB 2; Length 614;
Best Local Similarity 29.6%; Pred. No. 1e-35;
Matches 171; Conservative 93; Mismatches 230; Indels 83; Gaps 21;

```

QY 40 GKVKGRRLTYVDSDSYSEFIPYQAPVPELRFKAPQRPMPDGVRCDCNKKDSYQ-V 98
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 46 GQKRGI-RLKAPGPRVSAFLGIPFAEPVSGSRFPMPPEPKRPMGSLDATTQNYCYOY 104
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
QY 99 DFTGKVCG-----SEDCLYL SVYTNLNPETKR PVLVYIIGSGFIIGENHRDMY 148
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 105 DTLVGFEGTEMMNPNREISEDCLYLNVWTPYRPASPTPVLIMYGGGFYSGAASLDYV 164
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
QY 149 GPDYFIK-KDYVLINIQRLGALGFLSINSEDLNPGNAGLKDYMALWIKNNCANFG 207
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 165 DGRFLAQVEGAVLVSMNRYGVTFEGLAPG-SREAPGNVGLDRLALQWQENIAAFGG 223
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
QY 208 NPDNTVFGESAGASTHYMULTEOTRGLFHRGILMSGNAICPMANT--OCQHRATILA 264
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 224 DPMSTVTLFGESAGASVGMHILSLPSRSLFHRAYLQSGTPNGPMATVSGAARRATILLA 283
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
QY 265 KLAGYK--GEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMFPFPTVEPYQTA 321
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 284 RLVGCPGCGAGNDTELACLRTPAQDLVDHEMHLPOE--SIFRSFVYVDGDFLS 340
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
QY 322 DCVLPHKPREWYKTRMGNSIFPMGNTSYEGLEFSTILKQMPILVKELETVCNFPSELA 381
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 341 DT-----PEALINTGDFODLOLVGVKDEGSYF--LVYGVGFSKDNESLISRA-QFLA 392
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
QY 382 DAERTAPETLEMGAKIKKAHYTG---EPTADNFMDCSHIYFWFPMHRL--OLRF 433
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 393 GVRIGVPOASDLAAEAVVLTHTDMLHPEDPT--HLRDAMSAV--VGDNVVCYVAQLAG 447
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
QY 434 N-HTSGTEVLYLRFDDESEDLINPYRIMRSGRGVGVSHADELTYFFWNQLAKRMPKESR 492
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 448 RLAAAGARVAVYIFEHRASTLTWPLM-----GVPHGYEIEIFGLPLDPSLNTYTE 499
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
QY 493 EYKTERMTGIWIOFATGPNPYSNIEGMEVNSWDPPIKSDDEVYKCLNISDELKMDV-- 550
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 500 ERIFAQRLMKYWTNFAFGDP--NDPRDSKSPQMPPTTAQOYVSLN---LKPLEVYR 553
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
QY 551 -----PEM-----DKIKOWESMEK 565
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|
Db 554 GURAQTCAFWNRFLPKLLSATDTLDEAERQMAEFHR 590
   |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::| | |:::|

```

Search completed: April 4, 2003, 09:17:16
Job time : 21.0734 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 4, 2003 09:09:07 ; Search time 10.6371 Seconds

(without alignments)
2222.559 Million cell updates/sec

Title: US-09-776-910-8
Perfect score: 3073
Sequence: 1 MNFVSLMKLKIKICIN.....PMDKIKWESMEKRDLE 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1038	33.8	540	1 EST1_CULPI	P16884 culicx pipie
2	690	22.5	564	1 EST1_HELVI	P12992 heliothis v
3	606	19.7	633	1 ACES_ELEBL	O42275 electrophor
4	583.5	19.0	489	1 PNBA_BACSU	P37967 bacillus su
5	575.5	18.7	634	1 ACES_BRARE	O9d6d3 brachydanio
6	568.5	18.5	564	1 ESTE_MYZPE	P35502 myzus persi
7	568.5	18.5	602	1 CHLE_HUMAN	P06276 homo sapien
8	567	18.5	552	1 ESTE_MYZPE	P35501 myzus persi
9	564.5	18.4	614	1 ACES_MOUSE	P21836 mus musculu
10	562	18.3	586	1 ACES_MOUSE	P04058 torpedo cal
11	558.5	18.2	611	1 ACES_TORCA	O62763 felis silve
12	558	18.2	574	1 CHLE_HORSE	P81908 equus cabal
13	557	18.1	649	1 ACES_DROME	P07140 drosophila
14	556.5	18.1	614	1 ACES_RAT	P37136 rattus norv
15	555.5	18.1	613	1 ACES_BOVIN	P23795 bos taurus
16	552.5	18.0	629	1 ACES_LEPDE	O27677 leptinotars
17	552	18.0	590	1 ACES_TORMA	P07692 torpedo mar
18	551	17.9	581	1 ACES_BUNFA	O92035 bungarus fa
19	548.5	17.8	561	1 EST1_MESAU	O64419 mesocricetu
20	547.5	17.8	584	1 ACES_RABIT	O29499 oryctolagus
21	547.5	17.8	614	1 ACES_HUMAN	P22303 homo sapien
22	545	17.7	581	1 CHLE_RABIT	P19192 oryctolagus
23	545	17.5	562	1 EST1_CARBR	O04456 caenorhabdi
24	536	17.4	557	1 SASB_AKAPL	O04791 anas platyr
25	535	17.4	544	1 ESTE_DROME	P08171 drosophila
26	524	17.1	603	1 CHLE_MOUSE	O03311 mus musculu
27	523.5	17.0	545	1 ESTB_DROPS	P25726 drosophila
28	523	17.0	542	1 EST6_DROMA	P17982 drosophila
29	522	16.9	544	1 EST6_DROSI	O08662 drosophila
30	518.5	16.9	544	1 ESTP_DROME	P18167 drosophila
31	517	16.8	532	1 EST2_RABIT	P14943 oryctolagus
32	516.5	16.8	566	1 EST1_PIG	O29550 sus scrofa
33	516	16.8	545	1 ESTC_DROPS	P25725 drosophila

34	514.5	16.7	547	1 ESTA_DROPS	P25727 drosophila
35	511.5	16.6	561	1 EST4_RAT	O64573 rattus norv
36	507.5	16.5	565	1 EST10_RAT	P16303 rattus norv
37	506	16.5	597	1 BAL_BOVIN	P30122 bos taurus
38	505	16.4	549	1 EST1_RAT	P10959 rattus norv
39	501	16.3	554	1 ESTN_MOUSE	P23953 mus musculu
40	500.5	16.3	561	1 EST5_RAT	O63010 rattus norv
41	499	16.2	599	1 BAL_MOUSE	O64285 mus musculu
42	496	16.1	664	1 ACES_ANOST	P56161 anopheles s
43	495.5	16.1	534	1 ESTM_MOUSE	O63880 mus musculu
44	495	16.1	612	1 BAL_RAT	P07882 rattus norv
45	492	16.0	562	1 EST1_CABEL	O04457 caenorhabdi

ALIGNMENTS

RESULT 1	EST1_CULPI	STANDARD:	PRT:	540 AA.
AC	P16884:			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DE	Esterase B1 precursor (EC 3.1.1.1).			
GN	Bl.			
OS	Culex pipiens (House mosquito).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;			
OC	Culicoidae; Culex.			
OX	NCBI_Taxid=7175;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-TM-R.			
RX	MEDLINE=90207238; PubMed=2320576;			
RA	Mouches C., Pauplin Y., Agarwal M., Lemieux L., Herzog M.,			
RA	Abadon M., Beyssat-Arnaouty V., Hyrien O., de Saint Vincent B.R.,			
RA	Geophilou G.P., Pasteur N.;			
RT	"Characterization of amplification core and esterase B1 gene			
RT	responsible for insecticide resistance in Culex."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2574-2578(1990).			
CC	-1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON			
CC	MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.			
CC	-1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a			
CC	carboxylic anion.			
CC	-1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF			
CC	BOTH A AND B ARE KNOWN.			
CC	-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: M32328; AAA28289.1; -			
CC	PIR: A35986; A35986.			
DR	HSSP: P21836; IMA.			
DR	InterPro: IPR002018; Carboxylesterase.			
DR	InterPro: IPR000379; Ser estersite.			
DR	Pfam: PF00135; Coesterase; 1			
DR	PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.			
DR	PROSITE: PS00941; CARBOXYLESTERASE_B.2; FALSE.NEG.			
KW	Hydrolyase; Serine esterase; Glycoprotein; Multigene family; Signal.			
FT	SIGNAL	1	?	
FT	CHAIN	?	540	ESTERASE B1.
FT	ACT_SITE	191	191	BY SIMILARITY.
FT	ACT_SITE	442	442	BY SIMILARITY.
FT	DISULFID	68	81	BY SIMILARITY.
FT	CARBOHYD	452	452	N-LINKED (GLCNAC...) (POTENTIAL).
SQ	SEQUENCE	540 AA;	60806 MW;	F73B25B3A7157C95 CRC64;

[illegible]

CC JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL
CC ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.
CC -1- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-
CC trimethyltrideca-2,6-dienoate + H₂O = (2E,6E)-(10R,11S)-10,11-
CC epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
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CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: J04955; AAB8629.1; -
CC DR PIR: A34325; A34325.
CC DR HSSP: P37967; 1OE3.
CC DR InterPro: IPR002018; Carbesterase.
CC DR InterPro: IPR000379; Ser_ester_site.
CC DR Pfam: PF00135; Coesterase; 1.
CC DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; FALSE NEG.
CC KM Hydrolyase; Serine esterase; Glycopolym. signal.
CC FT SIGMIL 1 19
CC FT CHAIN 20 564 JUVENILE HORMONE ESTERASE.
FT ACT_SITE 220 220 BY SIMILARITY.
FT ACT_SITE 351 351 BY SIMILARITY.
FT ACT_SITE 465 465 BY SIMILARITY.
FT ACT_SITE 89 109 BY SIMILARITY.
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 29 29 V -> L.
FT VARIANT 52 52 F -> P.
SQ SEQUENCE 564 AA; 62614 MW; D140E5DD91914E8D CRC64;

Query Match 22.5%; Score 690; DB 1; Length 564;
Best Local Similarity 33.4%; Pred. No. 9.6e-46;
Matches 173; Conservative 102; Mismatches 209; Indels 34; Gaps 19.

OY 23 LNVRLTNEVYAEYEGKVKGVKRLVYDDSYSPFGIGFYAOPPGELRFKAPORTPW 82
DB 18 LAMQTSRSRYVAHLDSSIIIRGVR-SADGIKIFASFLGVPAKQPVGELRFEKLEPLEPW 76
OY 83 DGVPRCCNHKKSVQVDFITGKVG-----SDCLILSYVT--NNLNPETK-----RPVLV 131
DB 77 DNLVATNEGPRICFQTDVLYGLRLMASSEACVYANLHPWQSL-PRVKGTPPLRLIV 135
OY 132 YHGGGFLIENGHRMGYPDYFIKKDVLINIOYRLGALGLSLNSBSDLNYPGNAGLKQD 191
DB 136 FTHGGFAFGSGHEDHGPVLYTKNVYITFNFRVLANVFGELSMNT--TKIPGNAGLRDQ 193
OY 192 VALMIRKNNCANFGNPDNITVFESGAGASTHYMLITEQTRGLFNGHGLMSGNALCPW 251
DB 194 VLLRMVQKNNKNGFGDPDITFAGOSAGASAHLLTTSKATGEGLEFKAILMSTGSKSYF 253
OY 252 ANTCQCHRAFTLAKLAGYVG-EDNKDVEYEFMKAKPDDLKLEKVLVLTERTNKWEP 310
DB 254 FTTSPLFAVYISKOLLITIGINETPEELIRDLDPAE--KLNDANVLLIEOLG--LTT 309
OY 311 FGPTVE-PLYOTADCVLPKPHREKWTAMGNSIPTMGKNTSYGLFETTSILKQMPVLVEL 369
DB 310 FLPIVESPLPGVYTTIIDDPBELLIAIGRGKRNPLLLGFTSSSECTFRNNLFLDLVKIQ 369
OY 370 ETCVNVPSLDAERTAPETL-EMQAKIKKAVTGETPTANFMDLCSHIYFWPMHRL 428
DB 370 DNPTIILIPRL--LFMPPELLMELAKTIKRYKNG--TISIDNPFVSCSDGEYEPALK 426
OY 429 LQLEFNTSTGPVYLIFRFDSEDLINPYKIMSGKGVKGVSHADLTFF--WNLQAKM 487
DB 427 AQKR-AETGAPRLVLYFAVEAGQNSIIR-KVM--GJNHGCVGHIEDLTYVFKVNSMAL 482

Qy 488 ---PRESREYKTIEMTGIMIOFATTPGNPYSNIEEGME 522
 Db 483 HASPSEN-DYKMKMLMTGYFLNFKCSQPTCEDNNSLE 519

RESULT 3
 ACES_ELEEL STANDARD; PRT; 633 AA.
 ID ACES_ELEEL
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (Ache).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
 OX NCBI_Taxid=8005;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=98070504; PubMed=9407087;
 RA Simon S., Massoulié J.;
 RT "Cloning and expression of acetylcholinesterase from Electrophorus."
 RT Splicing pattern of the 3' exons in vivo and in transfected mammalian
 RT cells.";
 RL J. Biol. Chem. 272:33045-33055(1997).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O -> choline + acetate.
 CC -1- SUBUNIT: DIMERS AND COLLAGEN-TAILED FORMS, IN WHICH CATALYTIC
 CC TETRAMERS ARE ASSOCIATED WITH ANCHORING PROTEINS THAT ATTACH THEM
 CC TO THE BASAL LAMINA OR TO CELL MEMBRANES. IN THE COLLAGEN-TAILED
 CC FORMS, SUBUNITS ARE ASSOCIATED WITH A SPECIFIC COLLAGEN, COLO.
 CC WHICH TRIGGERS THE FORMATION OF ISOFORM T TETRAMERS FROM DIMERS.
 CC -1- MISCELLANEOUS: NO OTHER ISOFORMS EXIST. THIS PROTEIN CORRESPONDS
 CC TO THE T ISOFORM IN OTHER SPECIES.
 CC -1- SIMILARITY: BELONGS TO THE CARBOXYLESTERASE TYPE-B FAMILY.
 CC
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 CC
 CC -----
 CC EMBL: AF030422; AAB86606.1; -
 CC HSP: P04058; ISOM.
 CC InterPro: IPR002018; CarbesteraseB.
 CC InterPro: IPR000997; Cholinesterase.
 CC InterPro: IPR000379; Ser esters-site.
 CC Pfam: PF00135; Coesterase_1.
 CC PRINTS: PR00878; CHOLNSTRASE.
 CC PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 CC PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 CC Hydroxylase; Serine esterase; Synapse; Membrane; Nerve; Muscle; signal;
 CC Neurotransmitter degradation; Glycoprotein.
 CC SIGNAL 1 23
 CC CHAIN 1 24
 CC ACT_SITE 225 633
 CC ACT_SITE 352 225
 CC ACT_SITE 494 494
 CC DISULFID 91 118
 CC DISULFID 279 290
 CC DISULFID 427 579
 CC DISULFID 630 630
 CC CARBOHYD 133 133
 CC CARBOHYD 184 184
 CC CARBOHYD 283 283
 CC CARBOHYD 368 368
 CC CARBOHYD 511 511
 CC CARBOHYD 591 591
 CC SEQUENCE 633 AA; 71814 MW; FC92FE7E4ADB84C3 CRC64;

Query Match 19.7%; Score 606; DB 1; Length 633;
 Best Local Similarity 29.9%; Pred. No. 3.5e-39;
 Matches 184; Conservative 94; Mismatches 228; Indels 110; Gaps 24;
 Qy 29 TNEFVAETEXGKGVKRLTVYDSDY-YSPGPIYAPDPVGLKFAKQRPPTWDGVD 87
 Db 25 TDPELTITRLGQVOGT-RLPVPDRSHVIAFLGIPFAEPRLGKRFKREKKRPANDVFD 83
 Qy 88 CCHKDKSVQ-VDPITGKVG-----SEDCLYISVTNNINPETKRP---VLIV 132
 Db 84 ARDPASCYQYVDYSYSGFSSTGMNPNRMSSECLYLVWV---PATPRPHNTLVWV 139
 Qy 133 IHGGFIIIGENHRMVGDFYIKKD-VLIINIOYRGLGSLGISELNDLVNPNAGLKDQ 191
 Db 140 IYGGFYSGLSDLVYDGRYLAHSEKVVVSMNRKVSFGFLALNG-SAEPRGNGLDQ 198
 Qy 192 VMAURWIKNCANFGNDNITFGESAGASTHYMMLEOTRGIFHRGILMSNAICPW 251
 Db 199 RLALQWQDNHIFPGGNKQYITFGESAGASVGMHLLSPDSRPKFTAILQSGVPRNPW 258
 Qy 252 ANT---OCQRAFTLAKIAGTKGEDNDKQVLEFLMKAKPQDLIKLEKVTLEERTKVM 308
 Db 259 RTVSFDEARRRAIKRLVGCPR-DGNDPDLIDCLRSKQPODLIQEWLVLPF---SGLPR 314
 Qy 309 FPGPTVEPYQTADCVLPKHPREWKTMGNSIPTMGNTSYEGLEFSLIKQMPMLYKE 368
 Db 315 FSEVPVID---GVFPDTEAMLNSGNFKDQTLILVNONESYF--LYIGAGESKD 367
 Qy 369 LETCV---NVPSELADEARTAPETLENGAK-----IKRAVYGETPYAD 410
 Db 368 NESLITRDF---LQGVKMSVPANIEGLFAVILQYTDWMDENPKINREAMDQIVGDH 423
 Qy 411 NFMDLCSHTYWFPMHRLQ-----LRNHT-----SGTVYLYRPDSED 452
 Db 424 NVQCPLOHFAKMYAQSILQGTQTAQSGNGLGWSGSASNSGNSQSVLYLMEPHRASN 483
 Qy 453 LIPYRIMRSGRGVSHADELTFYFNOLAKRMPKRSREKTIERTGTIMIOFATTPGN 512
 Db 484 LVPEBWM-----GVHGYEIEFVGLPLEKRLNTYLEEKLSRRMKMTWANFARIGN 535
 Qy 513 PYSNIEEGM-ENVSMDPIKSDVEYKCLNISDELK-----MIDVP 551
 Db 536 PNIN-VDSQISRRMPVFTSTQKHVGLN-TDSLKVKHGLKQSCALMNFPLRLNVT 593
 Qy 552 EM--DKIKQESMEPK 565
 Db 594 ENIDDAERQMAEPFR 609
 RESULT 4
 ID PNBA_BACSU STANDARD; PRT; 489 AA.
 AC P37967;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Para-nitrobenzyl esterase (EC 3.1.1.-) (PNB carboxy-esterase) (PNBCE).
 GN PNBA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=1423;
 RN [1]
 RP SEQUENCE FROM N. A., AND SEQUENCE OF 1-22 AND 211-223.
 RC STRAIN=NRRL B8079;
 RX MEDLINE=95129891; PubMed=7828905;
 RA Zock J., Cantwell C., Swartling J., Hodges R., Pohl T., Sutton K.,
 RA Rostock P. Jr., McGilvray D., Queener S.,
 RT "The Bacillus subtilis pnbA gene encoding p-nitrobenzyl esterase:
 RT Cloning, sequence and high-level expression in Escherichia coli.";
 RL Gene 151:37-43(1994).
 RN [2]
 RP SEQUENCE OF 1-22 AND 211-223, AND CHARACTERIZATION.


```
QY 365 LKLELETCVNFVSELSADAEERTPETLEMGARKKKAHNTGMP-----TADNENDICHIY 420
   :::::|||||
Db 367 ILD-----YNTTTSNENLRFKTAODI-----KEFFGDGPIKSKETNSJMSKIDRS 413
```

QY 421 FWFPMRLQLFRNHTSG---TPVYLRFEDFSDLIPIRIMSGRGVSHADELT 477
 Db 414 FGCGTCKAAQ-----HIAAKNTAPVYEFEGSGNVTAFDPKSYSGRSPHGDFTNN 469
 QY 478 -----FFWQOLAKRMKRESREKTERMTGIMIOFATTGNPYSNEIGEMVNSMDPI 529
 Db 470 VLKVDGFTVYDNE-----EDKKMKITWNWATFIKSGVDPDENSE-----TWLPV 515
 QY 530 KKSD-EVYKCLNISDE 544
 Db 516 SKNPADLFRFTKITQ 531

RESULT 7
 CHLE_HUMAN STANDARD; PRT: 602 AA.
 ID CHLE_HUMAN
 AC P06276;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
 DE (Choline esterase II) (Butyrylcholine esterase)
 DE (Pseudochoolinesterase).
 GN BCHE OR CHEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90212557; PubMed-2322535;
 RA Arpagaus M., Kolt M., Vatsis K.P., Bartels C.F., La Du B.N.,
 RA Lockridge O.,
 RT "Structure of the gene for human butyrylcholinesterase. Evidence for
 RT a single copy."
 RT Biochemistry 29:124-131(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Betal;
 RA MEDLINE-8721856; PubMed-3035536;
 RA Prody C.A., Zeylan-Sonkin D., Ghatt A., Goldberg O., Soreg H.,
 RA "Isolation and characterization of full-length cDNA clones coding for
 RA cholinesterase from fetal human tissues."
 RT Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Brain;
 RA MEDLINE-88016155; PubMed-2477799;
 RA McIveran C., Adkins S., Chaconet A., Vaughan T.A., Bartels C.F.,
 RA Kolt M., Rosenberry T.L., La Du B.N., Lockridge O.,
 RA "Brain cDNA clone for human cholinesterase."
 RT Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Skin;
 RA Strausberg R.,
 RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 29-602.
 RC TISSUE-Plasma;
 RX MEDLINE-87109144; PubMed-3542989;
 RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
 RA Johnson L.L.,
 RA "Complete amino acid sequence of human serum cholinesterase."
 RT J. Biol. Chem. 262:549-557(1987).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE-88007487; PubMed-3115973;
 RA Lockridge O., Adkins S., La Du B.N.,
 RA "Location of disulfide bonds within the sequence of human serum
 RT cholinesterase."
 RT J. Biol. Chem. 262:12945-12952(1987).

RN [7]
 RP REVIEW.
 RX MEDLINE-89149758; PubMed-3067729;
 RA Lockridge O.,
 RT "Structure of human serum cholinesterase."
 RL Bioessays 9:125-128(1988).
 RN [8]
 RP VARIANT ATYPICAL GLY-98.
 RX MEDLINE-8912896; PubMed-2915989;
 RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
 RA van der Spek A.F.L., Lockridge O., La Du B.N.,
 RT "Identification of the structural mutation responsible for the
 RT dibucaine-resistant (atypical) variant form of human serum
 RT cholinesterase."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
 RN [9]
 RP VARIANT IDE-358.
 RX MEDLINE-96287386; PubMed-8680411;
 RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
 RA Moriwa K.,
 RT "Mutations of human butyrylcholinesterase gene in a family with
 RT hypocholesterolemia."
 RL Hum. Mutat. 6:349-351(1995).
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H₂O = choline + a
 CC carboxylic acid anion.
 CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED
 CC OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A
 CC DISULFIDE BOND.
 CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
 CC -1- DISEASE: MUTANT ALLELES OF CHEL ARE RESPONSIBLE FOR
 CC HYPOCHOLESTEROLEMIA RESULTING IN SUXAMETHONIUM SENSITIVITY.
 CC HOMOZYGOUS PERSONS SUSTAIN PROLONGED APNEA AFTER ADMINISTRATION
 CC OF THE MUSCLE RELAXANT SUXAMETHONIUM IN CONNECTION WITH SURGICAL
 CC ANESTHESIA.
 CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
 CC ORGANOPHOSPHATE ESTERS.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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 CC -----
 DR EMBL: M32391; AAA99296.1; JOINED.
 DR EMBL: M32389; AAA99296.1; JOINED.
 DR EMBL: M32390; AAA99296.1; JOINED.
 DR EMBL: M16541; AAA98113.1; -.
 DR EMBL: M16474; AAA52015.1; -.
 DR EMBL: BC018141; AAH18141.1; -.
 DR PIR: A00772; ACBU.
 DR PIR: A26613; A26613.
 DR PIR: A33769; A33769.
 DR PIR: A33887; A33887.
 DR HSSP: P21836; IMAA.
 DR Genew: HGNC:983; BCHE.
 DR MIM: 177400; -.
 DR InterPro: IPR002018; Carpesteraseb.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estrs-site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR HydroLase: Serine esterase; Glycoprotein; signal; Disease mutation;
 KW Polymorphism.
 FT SIGNAL 1 28
 FT CHAIN 29 602 CHOLINESTERASE.
 FT ACT_SITE 226 226 BY SIMILARITY.
 FT ACT_SITE 353 353 BY SIMILARITY.
 FT ACT_SITE 466 466 BY SIMILARITY.


```

DB 46 GOLRGI-RLAAGPGVSAFLGIPFAEPVGSRRPMPPEPRMPSGVLDATFQNVQYV 104
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
OY 99 DFTTKAYCG-----SECDLYSYTNNNLMPETKRVLYIYHGGGTTIGENHMDY 148
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 105 DTLVPGEGTEMMNPRLSEDCLYLWMTVPYRPASPTVLLIWIYGGGSGAASLDYV 164
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 149 GPVYFK-KQVVLINIDYRLGALGFLTNSDNLVPSNAGLKQVMAIRIKNNCANFEGG 207
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 165 DGRFLAOVEAVLYSMYRGVTFGLALPG-SREAPGNVCLDQRLALQWQENIAFVG 223
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 208 NPDNITVFGSAGASTHYMMLTQETRGFLFRGLMSGNAICPMANT---OCQHRAPFLA 264
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 224 DPMVTLFGSAGASGMHILSPRSRLFRAVLQSGTFNGRWATYSAGAEARRATLLA 283
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 265 KLAGYK---GEDNDKDYLEFLMAKAPODLIKLEKVLTLERTNNKVPFGPIVEPYQTA 321
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 284 RLVGCGPFGAGGNDTELIACLRTPAPADLVDEHWHVLPQ---SIFRFSPVVDGDFLS 340
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 322 DCVLPKPRRMVKTAMGNSIPTMGNTSYEGLEFETSLKMPMLYKLELCVNFVSELA 381
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 341 DT-----PEALINTGPDQIDVLGVVKKDGSYF--LVYGVPGFSKNESLISRA-OFLA 392
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 382 DARTAPETLEMGAKIKKAHVTG---ETPTADNFMDCSHIYFWPMHRL---OLRF 433
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 393 GVRIGVPQASDLAAEAVVLYHTDMLHPEDPT--HLRDAMSAV---VEDHNVCPVQAQLAG 447
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 434 N-HTSGTPVLYLRPDEPSEDLINPYRIMSGRGYKVSADDELTYFWNOLAKRMPRESR 492
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 448 RLAAOGARVAYJFEHNASLTWPLWM-----GVPHGYEIEFGLPLDPSLANTTE 499
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 493 EYKTERMTGIWIOFATGTPGPNYSNEIGMENVSMDPIKSDDEVKCNINDELKMDIV-- 550
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 500 ERIFAQNLMTWYNFAATGTP--NDPRDSKSPQMPPTTAAQYVSLN---LKPLEYRR 553
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 551 -----PEN-----DKIKOMESMFEK 565
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 554 GLRAQTCAPFNRRFLPKLLSATDTLDEAEARQWKAFFHR 590
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 10
ACCS_TORCA
ID ACES_TORCA STANDARD; PRT; 586 AA.
AC P04058;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACNE).
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristiogaster; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxID=7787;
RN [1]
RP SEQUENCE OF 10-586 FROM N.A.
RX MEDLINE=86118676; PubMed=3753747;
RA Schumacher M., Camp S., Maulet Y., Newton M., McPhee-Quigley K.,
RA Taylor S.S., Friedmann T., Taylor P.,
RA "Primary structure of Torpedo californica acetylcholinesterase
deduced from its cDNA sequence."
RL Nature 319:407-409(1986).
RN [2]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=89066695; PubMed=3198606;
RA Schumacher M.;
RA "Multiple messenger RNA species give rise to the structural diversity
in acetylcholinesterase."
RL J. Biol. Chem. 263:18979-18987(1988).
RN [3]
RP SEQUENCE OF 552-558.
RX MEDLINE=8087239; PubMed=3335534;
RA Gibney G., MacPhee-Quigley K., Thompson B., Vedvick T., Low M.G.,
RA Taylor S.S., Taylor P.;

```

RT "Divergence in primary structure between the molecular forms of
 RT acetylcholinesterase.";
 RL J. Biol. Chem. 263:1140-1145(1988).

RN [4]
 RP ALTERNATIVE SPLICING.

RX MEDLINE=90166618; PubMed=2306366;

RA Maulet Y., Camp S., Gibney G., Ráchnitsky T.L., Ekstroem T.J.,

RA Taylor P.;

RT "Single gene encodes glycopospholipid-anchored and asymmetric
 RT acetylcholinesterase forms: alternative coding exons contain inverted

RT repeat sequences.";
 RL Neuron 4:289-301(1990).

RN [5]
 RP DISULFIDE BONDS.

RX MEDLINE=87008586; PubMed=3759980;

RA McPhee-Quigley K., Vedvick T.S., Taylor P., Taylor S.S.;

RT "Profile of the disulfide bonds in acetylcholinesterase.";
 RL J. Biol. Chem. 261:13565-13570(1986).

RN [6]
 RP STRUCTURE OF THE GPI-ANCHOR.

RX MEDLINE=94079692; PubMed=8257440;

RA Wehlert A., Varon L., Silman I., Homans S.W., Ferguson M.A.;

RT "Structure of the glycosyl-phosphatidylinositol membrane anchor of
 RT acetylcholinesterase from the electric organ of the electric-fish,

RT Torpedo californica.";
 RL Biochem. J. 296:473-479(1993).

RN [7]
 RP GPI-ANCHOR.

RX MEDLINE=96176849; PubMed=8597567;

RA Bucht G., Hjalmarsson K.;

RT "Residues in Torpedo californica acetylcholinesterase necessary for
 RT processing to a glycosyl phosphatidylinositol-anchored form.";
 RL Biochim. Biophys. Acta 1292:223-232(1996).

RN [8]
 RP NOTAGENESIS.

RX MEDLINE=91017542; PubMed=2217185;

RA Gibney G., Camp S., Dionne M., McPhee-Quigley K., Taylor P.;

RT "Mutagenesis of essential functional residues in
 RT acetylcholinesterase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).

RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

RX MEDLINE=91343928; PubMed=1678899;

RA Sussman J.L., Harel M., Frolow F., Oefner C., Goldman A., Toket L.,

RA Silman I.;

RT "Atomic structure of acetylcholinesterase from Torpedo californica: a
 RT prototypic acetylcholine-binding protein.";
 RL Science 253:872-879(1991).

RN [10]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH FASCICULIN.

RX MEDLINE=96363673; PubMed=8747462;

RA Harel M., Klewegt G.J., Ravelli R.B., Silman I., Sussman J.L.;

RT "Crystal structure of an acetylcholinesterase-fasciculin complex:
 RT interaction of a three-fingered toxin from snake venom with its

RT target.";
 RL Structure 3:1355-1366(1995).

RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RX MEDLINE=97143314; PubMed=8989325;

RA Raves M.L., Harel M., Pang Y.P., Silman I., Kozlikowski A.P.,

RA Sussman J.L.;

RT "Structure of acetylcholinesterase complexed with the nootropic
 RT alkaloid, (-)-huperzine A.";
 RL Nat. Struct. Biol. 4:57-63(1997).

RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).

RX MEDLINE=99249780; PubMed=10231521;

RA Bartolucci C., Perola E., Cellai L., Brufani M., Lamba D.;

RT "Back door' opening implied by the crystal structure of a
 RT carbamoylated acetylcholinesterase.";
 RL Biochemistry 38:5714-5719(1999).

RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RX MEDLINE-99282167; PubMed-10353814;
 RA Milled C.B., Kryger G., Orendlich A., Greenblatt H.M., Harel M.,
 RA Raves M.L., Segall Y., Barak D., Shafterman A., Silman I.,
 RA Susman J.L.;
 RT "Crystal structures of aged phosphorylated acetylcholinesterase:
 RT nerve agent reaction products at the atomic level.";
 RT Biochemistry 38:7032-7039(1999).
 RN [14]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RP MEDLINE-20074924; PubMed-10606746; T., Silman I., Susman J.L.;
 RA Greenblatt H.M., Kryger G., Lewis T.,
 RA "Structure of acetylcholinesterase complexed with (-)-galanthamine at
 RT 2.3-A resolution.";
 RT FEBS Lett. 463:321-326(1999).
 RN [15]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RP MEDLINE-99197295; PubMed-10368299;
 RA Kryger G., Silman I., Susman J.L.;
 RT "Structure of acetylcholinesterase complexed with E2020 (Aticept(R)):
 RT implications for the design of new anti-Alzheimer drugs.";
 RT Structure 7:297-307(1999).
 RL Structure 7:297-307(1999).
 CC -1- FUNCTION: RAPIDLY HYDROLYSES CHOLINE RELEASED INTO THE SYNAPSE.
 CC MAY BE INVOLVED IN CELL-CELL INTERACTIONS.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: THE H FORM IS AN HOMODIMER; THE ASYMMETRIC FORM IS A
 CC DISULFIDE-BONDED OLIGOMER COMPOSED OF A COLLAGENIC SUBUNIT (Q) AND
 CC A VARIABLE NUMBER OF T CATALYTIC SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: THE H FORM IS ATTACHED TO THE MEMBRANE BY A
 CC GPI-ANCHOR.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: H/GLOBULAR (SHOWN HERE)
 CC AND T; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: AChE IS FOUND IN THE SYNAPSES AND TO A LOWER
 CC EXTENT IN EXTRAJUNCTIONAL AREAS OF MUSCLE AND NERVE, AND ON
 CC ERYTHROCYTE MEMBRANES.
 CC -1- PTM: AN INTERCHAIN DISULFIDE BOND IS PRESENT IN WHAT BECOMES
 CC POSITION 593 OF THE T ISOFORM.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
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 CC entities requires a license (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X03439; CAA27169.1; -
 DR EMBL: X56516; -; NOT_ANNOTATED_CDS.
 DR EMBL: X56517; -; NOT_ANNOTATED_CDS.
 DR PIR: A00773; ACHE.
 DR PIR: A34026; A34026.
 DR PIR: A31962; A31962.
 DR PDB: 2ACE: 08-NOV-96.
 DR PDB: 3ACE: 16-DEC-98.
 DR PDB: 4ACE: 16-DEC-98.
 DR PDB: 1ACJ: 31-AUG-94.
 DR PDB: 2ACK: 11-FEB-98.
 DR PDB: 1ACL: 31-AUG-94.
 DR PDB: 1AMN: 03-APR-96.
 DR PDB: 1ESS: 03-SEP-97.
 DR PDB: 1VOT: 16-JUN-97.
 DR PDB: 1AX9: 11-FEB-98.
 DR PDB: 1EVE: 22-MAR-99.
 DR PDB: 1CEJ: 01-APR-99.
 DR PDB: 1OCE: 18-MAY-99.
 DR PDB: 2DEP: 28-JUN-99.
 DR PDB: 1SQM: 25-JUN-99.
 DR PDB: 1DX6: 02-JAN-00.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser-estr-5ite.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTRASE.

DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; 1.
 KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 KW Neurotransmitter degradation; Glycoprotein; GPI-anchor; 3D-structure;
 KW Alternative splicing.
 KM SIGMALT 1 22 564
 FT CHAIN 565 586
 FT PROPEP 221 221
 FT ACT_SITE 221 348
 FT ACT_SITE 348 461
 FT ACT_SITE 461 115
 FT DISULFID 88 115
 FT DISULFID 275 286
 FT DISULFID 423 542
 FT DISULFID 558 558
 FT DISULFID 80 80
 FT CARBOHYD 437 437
 FT CARBOHYD 478 478
 FT CARBOHYD 554 554
 FT LIPID 564 564
 FT VARSPLIC 557 586
 FT INTERCHAIN.
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT GPI-ANCHOR.
 FT ACCELSSTSSSTSGIIFVFLSLYLIF -> ETIDEAL
 FT ROMTEFHRMSSTIMMKWQFPHYSHESCAEL (IN
 FT ISOFORM T).
 Query Match 18.3%; Score 562; DB 1; Length 586;
 Best Local Similarity 28.4%; Pred. No. 8e-36;
 Matches 166; Conservative 28; Mismatches 211; Indels 112; Gaps 22;
 Db 27 LKNTKSGKVMGT-RVPLVSHISAFLGIPFAEPVGMRRRREPPKPSGWNASTYP 85
 QY 33 VVAETEGKVKGYKRLTYVDSYSFEGIPYAOPVGLRKAPOPTPMGVDCCNH 92
 QY 93 DKSYVDFTGKVC-----SEDLVSVYTNINLPETKRPVLYIHGGFI 139
 Db 86 NNCQ--YVDEQPPGSGSEMNPNNREMSDCLYINWPSRPS--TVVWVLYGGFY 142
 QY 140 IGENHRDMGPDYF-IRKDVYLINIOYRGALGFLINSSEDLVNGAGLKDQVALRWI 198
 Db 143 SGGSTLDVYNKYLYATEEVLVLSYRGAFGLHSGQ-EAGGVNGLDQVALRWI 201
 QY 199 KNCANFGNPDITVFGESGAASHTHYMLTEOTRGLFHRLGSLGNACIPMAN--TQ 255
 Db 202 HNIQFEGGDKRYTYITIGESAGASVGMHILSPGSHDLFRALOSGNCMAVSVAE 261
 QY 256 COHRAFTLAKGYKGEDNDKVLEFLMKAKPDILKLEKYLTLLEERTKNVPPGPTV 315
 Db 262 GRRRAVELGRNLNC-NLNSDELHCLREKKPDELIDVENNVLPD--SIRFSEVPVI 317
 QY 316 EPIQFADVLPRKPREVKYTAGNSIPTMGNTSYEGFLFTSLIKQMPILYKELCVNF 375
 Db 318 DGE-----FFPISLMSLNSGNFKKTOILLGVNNDGSEFF-LLYGAGFSKDSSES 366
 QY 376 VPSELDAERTAPETLEMGAKIKKRN-----VTGETPADNFMD----- 414
 Db 367 -----KISHREDPMGSKLVSPHANDGLDVAITLQYTMDDNGGIKNRGLDLDIV 417
 QY 415 -----LCSHIYFWPMRLRLDLRFNHTSGTPVLYLFDFDSEDLNPRKNSGKGVGS 470
 Db 418 DHNVICPLMF---VKNYTKF-----GNGTYLFEFNHRAASLWPEWM-----GVI 460
 QY 471 HADELYTFEWNQIAKRMKPSREYKTIERTMTGWIQFATGPNYSLIEGEMVSWDPIK 530
 Db 461 HGEIEFEVFGIPLVKELNTYAEEDALSRLIMHYATFATGNP--NEPHSOS-KWP--- 514
 QY 531 KSDEYKCLNSDELKMDV-PEMDKIKO-----WESFEK 565
 Db 515 -----LFTTKDOKFIDLNTERPKVHQRLVOMCVFNQPLPK 551
 RESULT 11
 ACES_FELCA STANDARD; PRT; 611 AA.
 ID ACES_FELCA
 AC 062763; 062762;

CC ORGANOPHOSPHATE ESTERS.
-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

DR HSSE; P21836; JANA. Carbesterase.
DR InterPro; IPR002018; Carbesterase.
DR InterPro; IPR000397; Cholinesterase.
DR InterPro; IPR000379; Ser-esterase.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTERASE.
DR PROSITE; PS00121; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW PROSITE; Serine esterase; Glycoprotein.
FT ACT_SITE 198 198 BY SIMILARITY.
FT ACT_SITE 325 325 BY SIMILARITY.
FT ACT_SITE 438 438 BY SIMILARITY.
FT DISULFID 252 252 BY SIMILARITY.
FT DISULFID 400 400 BY SIMILARITY.
FT DISULFID 571 571 INTERCHAIN (BY SIMILARITY).
FT DISULFID 571 571 N-LINKED (GLCNAc. . .).
FT CARBOHYD 106 106 N-LINKED (GLCNAc. . .).
FT CARBOHYD 241 241 N-LINKED (GLCNAc. . .).
FT CARBOHYD 256 256 N-LINKED (GLCNAc. . .).
FT CARBOHYD 341 341 N-LINKED (GLCNAc. . .).
FT CARBOHYD 455 455 N-LINKED (GLCNAc. . .).
FT CARBOHYD 481 481 N-LINKED (GLCNAc. . .).
FT CARBOHYD 486 486 N-LINKED (GLCNAc. . .).
SQ SEQUENCE 574 AA; 65641 MW; 07755EE9FB9CB33E CRC64;

Query Match 18.28; Score 558; DB 1; Length 574;
Best Local Similarity 29.24; Pred. No. 1,6e-35;
Matches 167; Conservative 100; Mismatches 232; Indels 72; Gaps 21;

OY 31 ETVAAETGYGVKKRLTVYDSDYSFEGIPYADPVGELRFKAPQRTPTMDGV----- 85
DB 2 EDLITTTNGKVRGM-NLPFGVGTAFGLIPYADPGLRFRKFKPOSTLRKSNINNAWK 60
OY 86 --RDCCNKKDKSVQVDFITGKVC-----SEDCLYLSYVNNLNPERRKRVLYIHGGF 138
DB 61 YANSVCQYNTDQSF-PGLGSEMMNPNTLSDCLLWVMPAPPK-NATVMIWYGGF 118
OY 139 IGENNHRDYGDPYFIKDD-VLLINIOYRLGALGFLSNDLVPNGACLKQOVMLRW 197
DB 119 QGTGSLPYDQKFLARVERVYVSMNYRGALGFLAL-SENPRAPGMLGFDQLALOW 177
OY 198 IKNNCANEGNPNTVRESNGASTHYMMLEBOTRGLFHRGLMSNAICPANT--- 254
DB 178 VQKINIAFGNPRSVTLFEGESAGASVSLHLSPSQGLFTRAILQSSSNAPAVTSLX 237
OY 255 QOCHRAFTLAKLAGYKGEENDKDVLEFLMKANPQDLKLEEKVLTLEERTKKNVFEQPT 314
DB 238 EARNRLTLAKRMGC-SRDNETEMIKLRDKPOEILNEVAVPYD---TLISVNEGPT 293
OY 315 VEPYQADCVLPKHPREMYKTANGSIPTPMGNTSEGLEFTSILKOMPVLKELETQVN 374
DB 294 VDGGLFLDM-----PDLTLDLGCFKRTQLVGVNKGDEGAF--LYVGAPGEKDNNSIT- 345
OY 375 FVPSLADART-APETLEWGAIRKRAHYTG--ETPTADNEMD-----LCSHY 420
DB 346 -TRKEFEGKLFPPRNVSEGRSILFHYMDLDDQRAENYRDLDDVVDYNNICPALE 404
OY 421 FWFPMHRLDLRFNHTSGTIVYLYLRDEDEDLINPYRIMRSRGVKGVSHADLTYFFW 480
DB 405 FTRKFSFL-----GNDAFYFFEFHRSTKLPRPBM-----GVNHGGEIEFVG 447
OY 481 NQLAKRMKESREYKTIETRMGIWICPATGPNPYSEIEGMENV--WPIKKSDEYKGC 538
DB 448 LPLERVYVYTAELLSISIKRANFAKGNP-----NOTQNNSTRFWPFKSTQKYLT 502
OY 539 LNISDELKIDVPEMDKIKQESMFKEHRL 569
DB 503 LN-TESPKVYTKLRMOOCRFWTLFFPKVLEL 532

RESULT 13
ACES_DROME STANDARD; PRT: 649 AA.
ID ACES_DROME
AC P07140; Q9VY0;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AcHe).
GN ACE OR CG17907.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN (1)
RX MEDLINE=87080281; PubMed=3024971;
RT Hall L.M.C., Spierer P.;
RL "The Ace locus of Drosophila melanogaster: structural gene for acetylcholinesterase with an unusual 5' leader.";
RL EMBO J. 5:2949-2954(1986).
RN (2)
RX STRAIN=MH9; Canton-S. and Oregon-R; TISSUE=Embryo, and pupae;
RC MEDLINE=90064544; PubMed=2511327;
RA Fournier D., Karch F., Bride J.-W., Hall L.M.C., Berge J.-B., Spierer P.;
RT "Drosophila melanogaster acetylcholinesterase gene. Structure, evolution and mutations.";
RL J. Mol. Biol. 210:15-22(1989).
RN (3)
RX SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D., Abril J.F., Agbayani A., An H.-J., Andrews-Planck C., Balwin D., Ballew R.M., Basu A., Baxendale J., Bock J., Brokstein P., Brotler P., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borovica D., Botchan M.R., Bouch J., Cadieu E., Center A., Chandra I., Burks K.C., Busam D.A., Butler H., Cadenhead L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Fostler K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W., Fosler K.J., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Harits N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jallat M., Kalush F., Karp G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Merkllov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Nusskern D.R., Pacle J.M., Palazolo M., Piltan G.S., Pan S., Pollard J., Puri V., Reese M.G., Nelson K.A., Nixon K., Saunders R.D.C., Skupski M.P., Smith T., Reinert K., Remington K., Simpson M., Skupski M.P., Smith T., Shue B.C., Spradling A.C., Stapleton M., Strong R., Sun E., Svirsky R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weissstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
RL Science 287:2183-2195(2000).
[4]

RP SUBUNITS.
 RX MEDLINE=89005711; PubMed=3139459;
 RA Fournier D., Bide J.-M., Karsch F., Borge J.-B.;
 RT "Acetylcholinesterase from *Drosophila melanogaster*. Identification of
 RT two subunits encoded by the same gene.";
 RL FEBS Lett. 238:333-337(1988).
 RN [5]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=92112889; PubMed=1730712;
 RA Mulero A., Fournier D.;
 RT "Post-translational modifications of *Drosophila* acetylcholinesterase.
 RT in vitro mutagenesis and expression in *Xenopus* oocytes.";
 RL J. Biol. Chem. 267:1695-1700(1992).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC IT CAN HYDROLYZE BUTYRYLTHIOCHOLINE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H₂O = choline + acetate.
 CC SUBUNIT: THE ACTIVE ENZYME SEEMS TO BE COMPOSED OF THE NON-
 CC COVALENT ASSOCIATION OF A 55 KDA AND A 16 KDA POLYPEPTIDE. TWO
 CC ACTIVE UNITS ARE LINKED TOGETHER BY A DISULFIDE BOND AT THE C-
 CC TERMINUS OF THE 55 KDA PEPTIDE.
 CC -1- SUBCELLULAR LOCATION: LINKED TO THE MEMBRANE OF THE NEURONAL
 CC CHOLINERGIC SYNAPSE BY A GPI-ANCHOR.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.
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 CC -----
 DR EMBL: X05893; CAA29326.1; -;
 DR EMBL: AE003699; AAF54915.1; -;
 DR PIR: A25363; A25363.
 DR PIR: A33469; A33469.
 DR HSSP: P21836; IMAA.
 DR FLYBase: FBgn0000024; Ace.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYL ESTERASE B.1; 1.
 DR PROSITE: PS00941; CARBOXYL ESTERASE B.2; 1.
 KW Hydrolyase; Serine esterase; Synapse; Membrane; Nerve; Signal;
 KW Neurotransmitter degradation; GPI-anchor; Glycoprotein.
 FT SIGNAL 1 38
 FT CHAIN 39 649
 FT CHAIN 39 649
 FT CHAIN 39 649
 FT ACT_SITE 276 649
 FT ACT_SITE 405 649
 FT ACT_SITE 518 649
 FT DISULFID 104 131
 FT DISULFID 330 345
 FT DISULFID 480 598
 FT DISULFID 615 615
 FT CARBOHYD 126 126
 FT CARBOHYD 174 174
 FT CARBOHYD 331 331
 FT CARBOHYD 531 531
 FT CONFLICT 99 99
 SQ SEQUENCE 649 AA; 71785 MW; 5863C73FF99028C0 CRC64;
 Query Match 18.1%; Score 557; DB 1; Length 649;
 Best Local Similarity 27.8%; Pred. No. 2, 2e-35;
 Matches 172; Conservative 93; Mismatches 223; Indels 130; Gaps 25;

QY 91 HKDSVO--VDFTTG-----KVCSEDCLYSYVT----- 118
 DB 100 LSATCVDREYERPGSGEETIWPNTVSEDCLYINWPAKALRLRGANGGEHPNGK 159
 QY 119 -----NNLNPETRK--PVLYYINGGFIIGENHRDYGPDYFK-KDVLINTQYR 166
 DB 160 QADTDLHINGNPQNTNGPLILIMYIGFGFMGSATLDIYNADIMAVGNVYASFOYR 219
 QY 167 LGALGFLSLNSE-----DLVPGNAGLKDOVMALRLTKNCCANGCPNDITVGEESGA 221
 DB 220 VGFAGFLHLAPEMPSEPAEAPGPNVGLMDALATRLMLKNAHAAGCNPEWMTLEGESAGS 279
 QY 222 ASTHYMLLTOTRGLPFRGLIMSGNAICPWNATOCORAFITLAKYKGDNDKDLFEF 281
 DB 280 SYVAQILMSVYTKGLVYKRGMAQSTMAFMSH-MTSEKAVEIGAL-----INDCNCNAS 333
 QY 282 LMKAKPDLT---KLEEKVLTLEE--RTNKVMPFGPVEPYQTADCVLPKHPREMKV 334
 DB 334 MLKTNPAHVMSCMRSYDAKTISVQWMSYSGILSPAPPID-----GAFLPADPMTLMK 388
 QY 335 TAMGNSIPTMMGNSYSGLEF-----TSILQMPMLVKELETGVFVPSSEL 380
 DB 389 TADLKDYDILMGVNRDGTFFLLYDFIDYDKDATALPRD-----KYLE-IMNNIFGA 442
 QY 381 ADAERTAPETLEMGAKIKKAHVIGE-TPRADNFMDLCSHI--YFEPMPHRLQLRFNHT 436
 DB 443 TQAEEREA-----IIFQYTSWEGNPGYONQOIGRAVDHFFCTPTNEYAQLALER- 492
 QY 437 SCGPVLYRFDPSDDLNPYRIMRSGRGV-KGVSHADELYTFFWNOLAKRMPRESREYK 495
 DB 493 -GASVHYHYF-----THRTSTSLMGEMWGLHGDIEYFEGQPL-----NNSIQYR 537
 QY 496 TIE-----RMTGIMIORATGNPNPSNIEGEMNSMPDIKSDVYKCLNISDL-IMID 549
 DB 538 PVRELGRMLSAVIEFAKGNP-----ADGGEWPNFSKEDPVYIIFSTDKITEKLR 591
 QY 550 VPENDRIKOWESMPFEXR 567
 DB 592 GPLAARCSFNDYLPKYR 609
 RESULT 14
 ACES_RAT STANDARD: PRT; 614 AA.
 ID ACES_RAT
 AC P37136;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM T).
 RX MEDLINE=93107932; PubMed=8417155;
 RA Legay C., Bon S., Vernier P., Coussen F., Massoulie J.;
 RT Cloning and expression of a rat acetylcholinesterase subunit:
 RT generation of multiple molecular forms and complementarity with a
 RT Torpedo collagenic subunit.";
 RL J. Neurochem. 60:337-346(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS H AND R).
 RX MEDLINE=93114454; PubMed=8417973;
 RA Legay C., Bon S., Massoulie J.;
 RT "Expression of a cDNA encoding the glycolipid-anchored form of rat
 RT acetylcholinesterase.";
 RL FEBS Lett. 315:163-166(1993).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H₂O = choline + acetate.
 CC SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
 CC CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-

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Db      284  RLVGRRPGAGAGNDELISCLTRRPAADLVDHNMHVLPE---SLFRSFVPVVDGDFLS      340
QY      322  DCVLPHKPREMKATMGNSIPTMGNTSYEGLEFTSILKQMPALMYKELLETCVNPVSELA      381
Db      341  DT-----PRLINTDQFDQDLQVLGVGVKDGSGYF--LVYGVGFGSKDNESSLISHA-QFLA      392
QY      382  DAERTAPPELLENGAKIKKHAHTG---EFTADNFMDLSHLYFMPNHRLL-----QLRF      433
Db      393  GVRIQVQASDILAAAVLVLTDMILHEDDA--HLDAMSAV---VGHNIVCPVQAOLAG      447
QY      434  N-HTSGTPVYLRFDFDESDILINPYRIMRSRGVKGYSNADDELTYFENNQLAKRPKESR      492
Db      448  RLAAQAGARYAVILFEHRASLTLPWLM-----GVPHGYELTEFGLDLPDSINTVE      493
QY      493  EYKTIERMGICINQFATTCGNPNVSNIEGEMENVSNDPIKSKDEYVKKCNLSIDELKNIDV--      550
Db      500  ERIFPAQLMQYMTNFRITDGP--NDPRSKSPRRPPTTAAQOYVSLN---LKPLEYVR      551
QY      551  -----PDM-----DKIKQWESFEX      565
Db      554  GLRAQTCAPWNRFLPKLLSATDTLDEARQWKAEFHR      590

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RESULT 15
AC05 BOVIN STANDARD; PRT; 613 AA.
AC P23795; 097579;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHe).
GN AChE.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI;taxid=9913;
XX (1)
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Kidney;
RC MEDLINE=98359754; PubMed=9693127;
RA Mendelson I., Kronman C., Ariel N., Shaffer A., Velan B.;
RT 'Bovine acetylcholinesterase: cloning, expression and
RT characterization.";
RL Biochem. J. 334:251-259(1998).
RL [2]
RP SEQUENCE OF 31-613 (ISOFORM H).
RC TISSUE=Fetal serum;
RX MEDLINE=90306335; PubMed=2365060;
RX Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M.,
RA Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;
RT "Complete amino acid sequence of fetal bovine serum
RT acetylcholinesterase and its comparison in various regions with other
RT cholinesterases.";
RL FEBS Lett. 266:123-127(1990).
RL -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: ISOFORM H GENERATES MULTIPLE STRUCTURES, RANGING FROM
CC LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM
CC MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED
CC FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING
CC PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
CC MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOFORM T SUBUNITS ARE
CC ASSOCIATED WITH A SPECIFIC COLLAGEN, COL4, WHICH TRIGGERS THE
CC FORMATION OF ISOFORM T TETRAMERS, FROM MONOMERS AND DIMERS.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; H AND T (SHOWN HERE); ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:58 ; Search time 56.8533 Seconds
(without alignments)
2065.788 Million cell updates/sec

Title: US-09-776-910-8
Perfect score: 3073
Sequence: 1 MNPNVSLMKIKKIKICIN.....PEMDKIKOWSMERKRDLE 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21: *
1: sp.archaea: *
2: sp.bacteria: *
3: sp.fungi: *
4: sp.human: *
5: sp.invertebrate: *
6: sp.mammal: *
7: sp.mhc: *
8: sp.organelle: *
9: sp.phage: *
10: sp.plant: *
11: sp.podent: *
12: sp.virus: *
13: sp.vertibrate: *
14: sp.unclassified: *
15: sp.virus: *
16: sp.bacteriap: *
17: sp.archaeap: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3073	100.0	570	5	Q25252 lucilia cup
2	2431	79.1	570	5	Q9XZ70 musca domes
3	2348	76.4	570	5	Q9U409 haemaphys
4	2006.5	65.3	572	5	Q9VIB5 drosophila
5	1966.5	64.0	556	5	Q24201 drosophila
6	1412.5	46.0	567	5	Q9VIB3 drosophila
7	1411.5	45.9	558	5	Q24202 drosophila
8	1408.5	45.8	554	5	Q9VIB0 drosophila
9	1389.5	45.2	572	5	Q9VIB1 drosophila
10	1378.5	44.9	572	5	Q24203 drosophila
11	1353.5	44.0	565	5	Q9N159 drosophila
12	1330.5	43.3	566	5	Q961M0 drosophila
13	1324.5	43.1	554	5	Q9VIC2 drosophila
14	1322.5	43.0	554	5	Q24195 drosophila
15	1306.5	42.5	564	5	Q9N161 drosophila
16	1302.5	42.4	566	5	Q9W243 drosophila

17	1295.5	42.2	565	5	Q9VIC3 drosophila
18	1276.5	41.5	553	5	Q24194 drosophila
19	1248.5	40.6	345	5	Q9N153 drosophila
20	1238	40.3	342	5	Q95030 drosophila
21	1238	40.3	542	5	Q9VIB9 drosophila
22	1233.5	40.1	549	5	Q24204 drosophila
23	1230	40.0	542	5	Q24198 drosophila
24	1228.5	40.0	530	5	Q91715 drosophila
25	1123	36.5	540	5	Q8W089 drosophila
26	1114	36.3	540	5	Q92025 drosophila
27	1112	36.2	540	5	Q8W088 drosophila
28	1109	36.1	540	5	Q23733 drosophila
29	1073	34.9	551	5	Q9VIC1 drosophila
30	1069.5	34.8	543	5	Q8SZW5 drosophila
31	1069.5	34.8	548	5	Q24196 drosophila
32	1053	34.3	446	5	Q9N155 drosophila
33	1045	34.0	540	5	Q9G095 drosophila
34	1036	33.7	540	5	Q91920 drosophila
35	1035	33.7	540	5	Q23734 drosophila
36	1025	33.4	540	5	Q23735 drosophila
37	1022.5	33.3	541	5	Q9VIC0 drosophila
38	1019.5	33.2	541	5	Q24197 drosophila
39	995	32.4	541	5	Q9N158 drosophila
40	955.5	31.1	568	5	Q9VIB6 drosophila
41	940.5	30.6	467	5	P91597 culix pipie
42	938.5	30.5	467	5	P91596 culix pipie
43	937	30.5	401	5	Q9N160 drosophila
44	934.5	30.4	467	5	P91598 culix pipie
45	933	30.4	505	5	Q23736 culix quing

ALIGNMENTS

RESULT 1
ID Q25252 PRELIMINARY; PRT; 570 AA.
AC Q25252: Q25247;
DC 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
LN Alpha esterase (LCAE7) (Carboxylesterase).
GN LCAE7.
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS7;
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RL Insect Mol. Biol. 0:0-0(0).
RN [2]
RP SEQUENCE OF 70-181 FROM N.A.
RC STRAIN=LS2;
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RL Insect Mol. Biol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; U56636; AAB67728.1; -;
DR EMBL; U49421; AAA92012.1; -;
DR HSSP; P37967; IOE3.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000379; Ser-estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
SQ SEQUENCE 570 AA; 65416 MW; 399D72B3A0F338FD CRC64;

Query Match 100.0%; Score 3073; DB 5; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.2e-246;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MNFVSLMEKLMKIKCIENKFLNYRLTTEVVAETFEYKGVKRVRLVYDSDYSYFEG 60
DB 1 MNFVSLMEKLMKIKCIENKFLNYRLTTEVVAETFEYKGVKRVRLVYDSDYSYFEG 60
OY 61 IPYAPRYGELRFKAPQRPMPDGVRCDCNHNKDSVOVDFTGKVGCSDECLYLSYTTN 120
DB 61 IPYAPRYGELRFKAPQRPMPDGVRCDCNHNKDSVOVDFTGKVGCSDECLYLSYTTN 120
OY 121 LNPETKRPVLYIHGGGFIIGENHRDYGPDYFIKKDVLINIOYRLGALGFLSLNSED 180
DB 121 LNPETKRPVLYIHGGGFIIGENHRDYGPDYFIKKDVLINIOYRLGALGFLSLNSED 180
OY 181 NPGNAGLKDOYVALRWKLNKNCANFGNPDITVFGESAGASTHYMMLTEQTRGLFHRG 240
DB 181 NPGNAGLKDOYVALRWKLNKNCANFGNPDITVFGESAGASTHYMMLTEQTRGLFHRG 240
OY 241 ILMGNAICPMANTOCQHRAPFLAKLAGYKGEDNDKDYLEFLMKAKPODDLKLEKVLTL 300
DB 241 ILMGNAICPMANTOCQHRAPFLAKLAGYKGEDNDKDYLEFLMKAKPODDLKLEKVLTL 300
OY 301 EERTNKVMEFPFGTVPBYOTACVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFSTILK 360
DB 301 EERTNKVMEFPFGTVPBYOTACVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFSTILK 360
OY 361 OMPMLVKELETCVNFVPSSELADERTAPETLEMGAKIKKAHYTGEPADNFMDCSHIY 420
DB 361 OMPMLVKELETCVNFVPSSELADERTAPETLEMGAKIKKAHYTGEPADNFMDCSHIY 420
OY 421 FWFPMHRLDLRFNHTSGTPVLYLRPFDESEDLINPYRIMRSGRGVKGVSADDELTYFPW 480
DB 421 FWFPMHRLDLRFNHTSGTPVLYLRPFDESEDLINPYRIMRSGRGVKGVSADDELTYFPW 480
OY 481 NOLAKRMKESREYKTIERTMTGIWIOFATTGNPSNEIEGEMENVSDPIKKSDEYVKCLN 540
DB 481 NOLAKRMKESREYKTIERTMTGIWIOFATTGNPSNEIEGEMENVSDPIKKSDEYVKCLN 540
OY 541 ISDELKMTDVPMDKIKOMESMEKHRDLF 570
DB 541 ISDELKMTDVPMDKIKOMESMEKHRDLF 570

RESULT 2
OYXZ70 PRELIMINARY: PRT: 570 AA.
ID 09XZ70
AC 09XZ70:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Carboxylesterase MdaE7 (EC 3.1.1.1).
GN MDAE7.
OS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscidae; Muscidae; Musca.
OX NCBI_TaxID=7370;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=RUTGERS DIAZINON-R.
RC MEDLINE=99381228; PubMed=10451921;
RX Claudanos C., Russell R.J., Oakesholt J.G.;
RT "The same amino acid substitution in orthologous esterases confers
RT organophosphate resistance on the house fly and a blowfly.";
RL Insect Biochem. Mol. Biol. 29:675-686(1999).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DB EMBL: AF133341; AAD29685.1;
DR HSSP: P37967; 1OE3
DR InterPro: IPR002018; Carbesterase.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
KW Hydrolase.
SQ SEQUENCE 570 AA: 65421 MW: 08AFBEF284003BB CRC64:

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Query Match 79.1%; Score 2431; DB 5; Length 570;
Best Local Similarity 76.3%; Pred. No. 4,2e-193;
Matches 435; Conservative 70; Mismatches 65; Indels 0; Gaps 0;

OY 1 MNFVSLMEKLMKIKCIENKFLNYRLTTEVVAETFEYKGVKRVRLVYDSDYSYFEG 60
DB 1 MNFVSLMEKLMKIKCIENKFLNYRLTTEVVAETFEYKGVKRVRLVYDSDYSYFEG 60
OY 61 IPYAPRYGELRFKAPQRPMPDGVRCDCNHNKDSVOVDFTGKVGCSDECLYLSYTTN 120
DB 61 IPYAPRYGELRFKAPQRPMPDGVRCDCNHNKDSVOVDFTGKVGCSDECLYLSYTTN 120
OY 121 LNPETKRPVLYIHGGGFIIGENHRDYGPDYFIKKDVLINIOYRLGALGFLSLNSED 180
DB 121 LNPETKRPVLYIHGGGFIIGENHRDYGPDYFIKKDVLINIOYRLGALGFLSLNSED 180
OY 181 NPGNAGLKDOYVALRWKLNKNCANFGNPDITVFGESAGASTHYMMLTEQTRGLFHRG 240
DB 181 NPGNAGLKDOYVALRWKLNKNCANFGNPDITVFGESAGASTHYMMLTEQTRGLFHRG 240
OY 241 ILMGNAICPMANTOCQHRAPFLAKLAGYKGEDNDKDYLEFLMKAKPODDLKLEKVLTL 300
DB 241 ILMGNAICPMANTOCQHRAPFLAKLAGYKGEDNDKDYLEFLMKAKPODDLKLEKVLTL 300
OY 301 EERTNKVMEFPFGTVPBYOTACVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFSTILK 360
DB 301 EERTNKVMEFPFGTVPBYOTACVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFSTILK 360
OY 361 OMPMLVKELETCVNFVPSSELADERTAPETLEMGAKIKKAHYTGEPADNFMDCSHIY 420
DB 361 OMPMLVKELETCVNFVPSSELADERTAPETLEMGAKIKKAHYTGEPADNFMDCSHIY 420
OY 421 FWFPMHRLDLRFNHTSGTPVLYLRPFDESEDLINPYRIMRSGRGVKGVSADDELTYFPW 480
DB 421 FWFPMHRLDLRFNHTSGTPVLYLRPFDESEDLINPYRIMRSGRGVKGVSADDELTYFPW 480
OY 481 NOLAKRMKESREYKTIERTMTGIWIOFATTGNPSNEIEGEMENVSDPIKKSDEYVKCLN 540
DB 481 NOLAKRMKESREYKTIERTMTGIWIOFATTGNPSNEIEGEMENVSDPIKKSDEYVKCLN 540
OY 541 ISDELKMTDVPMDKIKOMESMEKHRDLF 570
DB 541 ISDELKMTDVPMDKIKOMASIFDKKELF 570

RESULT 3
OYXZ70 PRELIMINARY: PRT: 570 AA.
ID 09XZ70
AC 09XZ70:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha E7 esterase.
GN AE7.
OS Hemetobia irritans irritans.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscidae; Muscidae; Haematobia.
OX NCBI_TaxID=75445;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CAMP COOLEY 4/97;
RC MEDLINE=20445807; PubMed=10989298;
RX Guerrero F.D.;
RT "Cloning of a horn fly cDNA, HialphaE7, encoding an esterase whose
RT transcript concentration is elevated in diazinon-resistant flies.";
RL Insect Biochem. Mol. Biol. 30:1107-1115(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DB EMBL: AF139082; AAF14517.1;
DR HSSP: P37967; 1OE3
DR InterPro: IPR002018; Carbesterase.
DR Pfam: PF00135; Coesterase; 1.

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DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 KM Hydrolyase.
 SQ SEQUENCE 570 AA; 65613 MW; 18DA0A9A4AB970D CRC64;
 Query Match 76.4%; Score 2348; DB 5; Length 570;
 Best Local Similarity 73.9%; Pred. No. 3,3e-186;
 Matches 421; Conservative 66; Mismatches 83; Indels 0; Gaps 0;

OY 1 MNFVSLMEKRLKRIKICLENKFLNRLTNTETVAETEGYGVKKRLTYVDDSYSEEG 60
 DB 1 MNFVSLMEKRLKRIKICLENKFLNRLTNTETVAETEGYGVKKRLTYVDDSYSEEG 60
 OY 61 IPYAPPGVGLRFRKAPQRPPTMDGVRDCCNKKDKSVQVDFITGKCGSEDCLYLVYNN 120
 DB 61 IPYAPPGVGLRFRKAPQRPPTMDGVRDCCNKKDKSVQVDFITGKCGSEDCLYLVYNN 120
 OY 121 LNPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNSEDL 180
 DB 121 LNPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNSEDL 180
 OY 181 NVPGNAGLKDVMLRWIKNNCANFGNPDNITVFGESAGASTHYMMLTQTRGLFHRG 240
 DB 181 NVPGNAGLKDVMLRWIKNNCANFGNPDNITVFGESAGASTHYMMLTQTRGLFHRG 240
 OY 241 ILMGNAICPMANTQCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPDLILKEKVLTL 300
 DB 241 ILMGNAICPMANTQCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPDLILKEKVLTL 300
 OY 301 EERTNKVWFRPGVPEYQADCVLPKHPREKVTAMGNSIPTMKGNTSYEGLEFETSILK 360
 DB 301 EELDKVAFAGPTPEYEDCVLPKPNREMLKTAMGNSIPTLIGNTSYEGLEFETSIVGK 360
 OY 361 QMPMLVKLELCVNPVPELADAEPTALEMGAIKKIKKAVTGPDAFMDNCSTLY 420
 DB 361 QMPMLVKLELCVNPVPELADAEPTALEMGAIKKIKKAVTGPDAFMDNCSTLY 420
 OY 421 FMFPMHRLQLRFNHTSGTPYLYLRFDFSEDLINPYRIMSGRGVSHADELTTFYM 480
 DB 421 FMFPMHRLQLRFNHTSGTPYLYLRFDFSEDLINPYRIMSGRGVSHADELTTFYM 480
 OY 481 NOLAKRMKESREKTIETRMGIWQPTTGNPNYSNEIEGEMVSWDPDIKSDEYVKCLN 540
 DB 481 NOLAKRMKESREKTIETRMGIWQPTTGNPNYSNEIEGEMVSWDPDIKSDEYVKCLN 540
 OY 541 ISDELKMLDVPMDKIKQWESMEKHRDLF 570
 DB 541 ISDELKMLDVPMDKIKQWESMEKHRDLF 570

RESULT 4
 ID 09VIB5 PRELIMINARY: PRT: 572 AA.
 AC 09VIB5;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Alpha-EST7 protein (GHI3950P).
 GN ALPHA-EST7 OR CG1112.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abriil J.F., Agbayan A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotilier P.,
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle K., Davenport L.B., Davies P.,
 RA de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Hochia S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbagman C.,
 RA Jajall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Slden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zheng G., Zhou Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Fise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celiker S.,
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/PLIPASE FAMILY.
 DR EMBL: AE003671; AAF54010.1; -
 DR EMBL: AY051473; AAK92897.1; -
 DR HSSP: P21836; IMAA
 DR FlyBase: FBgn0015575; alpha-Est7.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 KW Hydrolyase.
 SO SEQUENCE 572 AA; 65435 MW; 693D9360DA18AE27 CRC64;

Query Match 65.3%; Score 2006.5; DB 5; Length 572;
 Best Local Similarity 64.0%; Pred. No. 7.3e-158;
 Matches 365; Conservative 91; Mismatches 113; Indels 1; Gaps 1;

OY 1 MNFVSLMEKRLKRIKICLENKFLNRLTNTETVAETEGYGVKKRLTYVDDSYSEEG 60
 DB 1 MNFVSLMEKRLKRIKICLENKFLNRLTNTETVAETEGYGVKKRLTYVDDSYSEEG 60
 OY 61 IPYAPPGVGLRFRKAPQRPPTMDGVRDCCNKKDKSVQVDFITGKCGSEDCLYLVYNN 120
 DB 61 IPYAPPGVGLRFRKAPQRPPTMDGVRDCCNKKDKSVQVDFITGKCGSEDCLYLVYNN 120
 OY 121 LNPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNSEDL 180
 DB 121 LNPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLLINIOYRLGALGFLSNSEDL 180
 OY 181 NVPGNAGLKDVMLRWIKNNCANFGNPDNITVFGESAGASTHYMMLTQTRGLFHRG 240
 DB 181 NVPGNAGLKDVMLRWIKNNCANFGNPDNITVFGESAGASTHYMMLTQTRGLFHRG 240

RA Rheinhart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamon I., Simpson M., Skupski M.P., Smith T.,
RA Splier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Vector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woadate T., Worley K.C., Wu D., Yang S., Yao Q.,
RA Ye J., Yeh R.-F., Zavadil J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*." ,
RL Science 287:1185-2195(2000).
CC -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY
DR EMBL: AE003671.1; AAF54012.1; -.
DR HSSP: P37967.1OE3.
DR FLYBASE: FBgn0015576; alpha-Est8.
DR InterPro: IPR002018; CarbestereaseB.
DR InterPro: IPR000379; Ser_est8s_site.
DR Pfam: PF001135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydroxylase.
SO SEQUENCE 567 AA: 64831 MW: 07D6ACC72786F1A4 CRC64;

Query Match	46.0%;	Score 1412.5;	DB 5;	Length 567;
Best Local Similarity	48.6%;	Pred. NO. 1.4e-108;		
Matches 267;	Conservative 105;	Mismatches 164;	Indels 13;	Gaps 6

[illegible]

RESULT 7	
024202	
ID 024202	PRELIMINARY;
AC 024202;	PRT; 558 AA
DT 01-NOV-1996 (T=EMBLrel. 01, Created)	

DT 01-NOV-1996 (Tremblrel 01, last sequence update)
 DT 01-JUN-2002 (Tremblrel) 21, last annotation update)
 DE Alpha esterase (Fragment).
 GN ALPHA-EST8 OR CG112.
 OS Drosophila melanogaster (Fruit fly).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha.
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;

RA SEQUENCE FROM N.A.
RP Robin C., Medvecky K.M., Russell R.J., Oakeshott J.G.;
RL J. Mol. Evol. 0:0-0(0).
- - - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY
CC EMBL: U51052; AAB0151.1; - -
DR HSSP: P37967; I0E3.
DR FLYBASE: FBGN015576; alpha-Est8.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; 1.
KW Hydrolase.
FT NON_TER 1 1
SQ SEQUENCE 558 AA; 63916 MW; B6F6FC68FF212720 CRC64;

Query Match	45.98;	Score 1411.5;	DB 5;	Length 558;
Best Local Similarity	48.58;	Pred. No. 1.7e-108;		
Matches 266;	Conservative 106;	Mismatches 164;	Indels 13;	Gaps 6

QY	26	RTTMEETVAEEXKCVKGVKRYLTUDDYSUSPFCITPAORPVEJLRFKAPORPTPMQV	85
Db	10	RLRSDMKVIADIVYKVGKVMQOSTYGNNTYSFBCIPAKPPVGBELFKAVPEBHSDV	69
QY	86	RDCSNHKKSVQVDFITKCVKGSBDCLTLSYTNLNLNETKRPVLYVTHGGGFTIGENHR	145
Db	70	KCHTVRAKPCQVNLVLKQVQGSBDCLTLYNTRFLRPHRPLVLYWLYGGGFQMGASR	122
QY	146	DMYGFDFYFKKDVULINTQYRLGALGFLSLNSEDILNPGNAGLKDQVALLWKNNCANF	205
Db	130	DLYSDYDIMEHEIVLYVLYSTRGALGFLSLADEELDVPGNAGLKDQVALLWKVRKNCQF	189
QY	206	GGNPNTVYFGSAGASTHYMLTEOPRGLPHNGILMSGNAIPMANTQOQ--HRAFLA	266
Db	190	GGDPNTVYFGSAGASTHYMLTDOQKGLFHKTIVLMSGALAWAOTPTNHMPYKLA	245
QY	265	KLAGYKGEDNDQVLEFPLMAKAPODLILKEKVLTLBERTKV--MFRPGPYVEYQYADC	322
Db	250	QATGYTGANDPDIPIHLKKKCLASSMLKVAEDITIMEERHORLTMYFSGPTIEPYLRHC	307
QY	324	VLPKPREKVKWTAMGNSIPTMMGNTSYBGLFTTSLKOMPIUYELETGVNFPVSELA	383
Db	310	VLPKSPLEMKRMCWNSIPRYIGVSGFGLLMFPEVNKWPBELLQDGCENMLAQ--DA	366
QY	384	ETPAETLEMAKKIKAHVGETP--TADNPMDCSHITYFMPFMRHLLDLRFNHTSPT	444
Db	367	HVDEOORAKFAFGKRYVELYFGDTPRKCTILEXSDLFYSKYFMHGJHRTLSRAHNAPLAP	420
QY	441	VLYRFPDQFSEDLIPRYLRMSGRGVKVSNADELTYYFMMQOLAKRMYKESREKXTERM	500
Db	427	TLYLYFDDDSKH--FIMIKITICGRKVRKGTCHADOLSYLYPAAAKKLRKRAEKTIKRL	487
QY	501	TGIMQIQAFTTGNP---YSNLEIEGMEVNSMPPIKKSDEYVYKCLNSIDELMKIDVPEMDKI	556
Db	486	VSMYVHFAISGDPNIPMYCQDEKEQRPQAMLPISDKDQVFCPLNISHDVIVDLPEAEKL	544
QY	557	KQWESMEK 565	
Db	546	RLMDCIYDR 554	

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Db      546  RLMDCIYDR 554
      . 1 . . . . .
RESULT 8
Q9VIB0

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18 ENKFLNRLTNTNVTAAETKGVKRVRLVYDVSFEFGIYPADPVGELRFAQD 77

Db	2	VDFAVQRRVRYRTESEKTVNSTYTPGIKVGKRSITYGQSYFSERTPEAKPPVGLRYAKAPQ	61
Oy	78	RPTWMDVRRCCNHNKSKVQVPEITGKVGSGEDCLYLSVYTNINLPETKRPVLYTHGGG	137
Db	62	PRVWTEHTRCSTSGQRPRLQKHVFEMFTDGSBDCLYLVVYTNKLYPTRKPMVWMIYGGI	121
Oy	138	FLIGENHRMDXGPDYFIKQDVILINQYLGALGFLNSLEDLVNVPAGLAKDQVVALRW	197
Db	122	FOFGASFECSPPDYLLREDVVVISTNRYLRGLPGLCELDDELDVPGNAGLKDQVVALRW	181
Oy	198	IKNNQANGAGNDPIYVFGESAGAASTHYMMLEOTRGLFHRGLMSNAICPMANQOQ	257
Db	182	VNANSRFGSGSANITTFGDSAGSASVHYMMITFQHGHLFKALCMSGNTLSPMANVTPQR	241
Oy	258	HRAFTLAKIAGYKGBDNDKVDLEFLMKAKQODLKLKEVLLLEFRTKKVWFPGPVPYR	317
Db	242	NMPYRLAIVQAGAGENNTRDWMELMLNAKSGSELIKANGELCLDEKKRBRIGSFQVPEP	301
Oy	318	YQTACVLPKPHREKVTWANGSIPTMGNTSYEGLEFTSLIKOMPILYKLETCVNPV	377
Db	302	YVTSHCVPKPKTLEMKRTANSNPIPLIIGVSNBGLLTLSEFTNKRCINLELDDCREVP	361
Oy	378	SELADAETAPETLEMGAKIKKANVTGETPAD---NFMDLCSHYFMPMRRLDQLEFN	434
Db	362	IEL-NMDRESALCREGDQRLRCYGYGDTPELDLHEYLDMVSHKFWPPIYRVYLSRQ	420
Oy	435	HTSGTGVYLYRPDESEDLINPRTIRMSGRGVSHADELTYTFPMNLAKKPKRESREY	494
Db	421	YANSAPLYLRPEPDSKH-FNHLRILSCGKKYRGTCHGDDLSYLFVNSLARKKKNHREY	479
Oy	495	KTERMTGWIOTFATGNP-YSNLEEGMENVSW---PIPKSDSEVYKCLNISDELKMDV	550
Db	480	KCIERLGLMTHTFAAGCNFDEPBDL-----WQVDPANAKERQQLCLNISDELKMDV	535
Oy	551	PEMDIKRQMSMEFK 565	
Db	536	PDLKKLWMSFEFRR 550	
RESULT 9			
OYVIB1 PRELIMINARY; PRT: 572 AA.			
AC	09VIB1:		
DT	01-MAY-2000 (TReMBLrel. 13, Created)		
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)		
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)		
DE	Alpha-EST9 protein.		
GN	ALPHA-EST9 OR CG1128.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tycheta; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephyridae; Drosophilidae; Drosophila.		
ON	NCBI_Taxid=7227;		
OX	(1)		
RA	SEQUENCE FROM N.A.		
RC	STRAIN=BERKELEY;		
RX	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Goebye J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	Georje R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miles G.L.G.,		
RA	Ballif R.M., Besu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Busan D.A., Butler J., Brokstein P., Brothier P.,		
RA	Cheriy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.		
RA	Foster C., Gabrielian A.E., Gay N.S., Gelbart W.M., Glasser K.,		

RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Holstin D., Houston K.A., Howland T.J., Wei M.-H., Ibbagwam C.,
RA Jattali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacleb J.M.,
RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svaykhas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "the genome sequence of Drosophila melanogaster",
RL Science 287:2185-2195(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AE003671; AAF54015.1; -.
DR HSSP; P37967; 10E3.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 2.
KW Hydrolase.
SQ SEQUENCE 572 AA; 65767 MW; 9138FB95713DF350 CRC64;

Query Match 45.2%; Score 1389.5; DB 5; Length 572;
Best Local Similarity 46.9%; Pred. No. 1.2e-106;
Matches 269; Conservative 95; Mismatches 178; Indels 31; Gaps 7;

QY 18 IENKFLNRLTNETVVAETEGYKGVKRLTVYDDSYSEFGIPYAOFPVGLERFKAQ 77
DB 2 VDFKVOQRRTSEKTVSTYTGPIKGVKRSIYGOSYSEFRIIPFAKPPVDVRKAQ 61
QY 78 RPTPMDGVRCDCNHRKDSVOYDFITGKVGSGSDCLYLSYTNLNLPEKRPVLYIHGG 137
DB 62 PREVTVEVRSCTSGCPKPLQKHFEMTDGSDCLYLVNLYTKLPTKPMVWVIYGG 121
QY 138 FLIGENHRDMGPDYFIKRDVLLINQYRLGAL-----GFLSNSBD 179
DB 122 FQFGASRECSYDYLREDVVISINRYLGLGINDTGWKKHFNISLPGFLCLDPE 181
QY 180 LNVPGNAGLKDQVALRWIKNNCANFGNPNITVFGESAGAASHYMLTBTOTRGLFHR 239
DB 182 LDVPGNAGLKDQVALRWIKNNCANFGNPNITVFGESAGAASHYMLTBTOTRGLFHR 241
QY 240 GLMSGNAICPMANTQOCHRAFTLAKLAGYKGEDNDKVDLEFLMAKPODLIKLEKVL 299
DB 242 AICMSGNTLSMAVTPQKRWMPYRLAVQAGYAGENNTRDWEFLMAKPODLIKLEKVL 301
QY 300 LEERTNKVMPFGPTVEPYQTADCVLPKHPREMYVTAMGNSIPTMMGNTSYEGLEFSTIL 359
DB 302 DEEKERIGSFSGVPIEYVSHCVVPPKPIEMRTAMSNINPLITIGVSNGLLYSET 361
QY 360 KQMPALVLETCVNFVSELADEARTAPETLEMAKAKIKKAVHGETPTAD---NFMOLC 416
DB 362 KTNPKCLNELDRCRVVPIEL--NMDRESALCREYGDOLROCYGDKTPTDLTHLEYLQW 420
QY 417 SHIYFWPMHRLDOLRFNHTSGTPYLYLRFDPDSEDLINPRYIMSGKGVGSHADELT 476
DB 421 SHEYFWPIYKTVLSRLQYARSAPTYLYLRFDPDSKH--FNHLRILISCGKVKVCTGDDLS 479
QY 477 YEFWNLAKRMPKESREKVTIERMTGIWQATGPN--YSNEIEGMENVSW---DPIKKS 532

DB 480 YLFYNSLARKLKNTREYKCIERLGLWTHFAACGNPNDEPQEDL---MOPVDAVE 535
QY 533 DEVYKCLINSDCLKMIDVPENDKIKOWESMFEK 565
DB 536 KQHLKCLINSDCLKMIDVPENDKIKLWESFEFR 568

RESULT 10

ID 024203 PRELIMINARY; PRT; 572 AA.

AC 024203;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Alpha esterase.

GN ALPHA-EST9 OR AE9 OR CG1128.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;

RL J. Mol. Evol. 0:0-0(0).

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; U51053; AAB01152.1; -.
DR HSSP; P37967; 10E3.
DR InterPro; IPR001557; alpha-Est9.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
SQ SEQUENCE 572 AA; 65680 MW; 37F1440F8AD2BD8 CRC64;

Query Match 44.9%; Score 1378.5; DB 5; Length 572;
Best Local Similarity 46.6%; Pred. No. 9.7e-106;
Matches 267; Conservative 96; Mismatches 179; Indels 31; Gaps 7;

QY 18 IENKFLNRLTNETVVAETEGYKGVKRLTVYDDSYSEFGIPYAOFPVGLERFKAQ 77
DB 2 VDFKVOQRRTSEKTVSTYTGPIKGVKRSIYGOSYSEFRIIPFAKPPVDVRKAQ 61
QY 78 RPTPMDGVRCDCNHRKDSVOYDFITGKVGSGSDCLYLSYTNLNLPEKRPVLYIHGG 137
DB 62 PREVTVEVRSCTSGCPKPLQKHFEMTDGSDCLYLVNLYTKLPTKPMVWVIYGG 121
QY 138 FLIGENHRDMGPDYFIKRDVLLINQYRLGAL-----GFLSNSBD 179
DB 122 FQFGASRECSYDYLREDVVISINRYLGLGINDTGWKKHFNISLPGFLCLDPE 181
QY 180 LNVPGNAGLKDQVALRWIKNNCANFGNPNITVFGESAGAASHYMLTBTOTRGLFHR 239
DB 182 LDVPGNAGLKDQVALRWIKNNCANFGNPNITVFGESAGAASHYMLTBTOTRGLFHR 241
QY 240 GLMSGNAICPMANTQOCHRAFTLAKLAGYKGEDNDKVDLEFLMAKPODLIKLEKVL 299
DB 242 AICMSGNTLSMAVTPQKRWMPYRLAVQAGYAGENNTRDWEFLMAKPODLIKLEKVL 301
QY 300 LEERTNKVMPFGPTVEPYQTADCVLPKHPREMYVTAMGNSIPTMMGNTSYEGLEFSTIL 359
DB 302 DEEKERIGSFSGVPIEYVSHCVVPPKPIEMRTAMSNINPLITIGVSNGLLYSET 361
QY 360 KQMPALVLETCVNFVSELADEARTAPETLEMAKAKIKKAVHGETPTAD---NFMOLC 416
DB 362 KTNPKCLNELDRCRVVPIEL--NMDRESALCREYGDOLROCYGDKTPTDLTHLEYLQW 420
QY 417 SHIYFWPMHRLDOLRFNHTSGTPYLYLRFDPDSEDLINPRYIMSGKGVGSHADELT 476
DB 421 SHEYFWPIYKTVLSRLQYARSAPTYLYLRFDPDSKH--FNHLRILISCGKVKVCTGDDLS 479
QY 477 YEFWNLAKRMPKESREKVTIERMTGIWQATGPN--YSNEIEGMENVSW---DPIKKS 532

Db 361 RKDPAWLNKFNH---NILPREVRETSLEGGDL-LVRLRLKQLYFNNEQMSMEMFEALNIF 416

Qy 417 SHITFPMRHLQLRNHNHSGTPLYLRDPDSEDILNIPYRIRSGRGVSHADELT 476

Db 417 SHROIMDTHRFILAROSYAKFTPTLYLRFDSPH-FNQRRLVCGDRINGVAHADEL5 475

Qy 477 YEFNOLAKRPMKREKTERMTGIMQFATGNPNPSNIEGMENSWDPIK-KSEYV 535

Db 476 YLFNTIILASKDKSSMEKTERNVGMWTSFASGNPCPE---LGSAKWEAVOLKENAV 532

Qy 536 YKCLNISDELKMDVPEMDKIKOWSMFEK 565

Db 533 EKCENISHDLEMRDLPESSDCLAVMDTFEPR 562

RESULT 13

ID QYVIC2 PRELIMINARY; PRT; 554 AA.

AC QYVIC2

DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Alpha-EST2 protein.

GN ALPHA-EST2 OR CG2505.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Phrygotea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,

RA Men K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abell J.F., Agbayan A., An H.-J., Andrews-Piannoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,

RA Buttle K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher S., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,

RA Jaitell M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mocherson D.,

RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzzy D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacib J.M.,

RA Palazono M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Styrtas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2193(2000).

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.

DR EMBL: AE003671; AAF54003.1; -

DR HSSP: P37967. 10E3.

DR FlyBase; FBgn0015570; alpha-Est2.

DR InterPro; IPR002018; CarbinesteraseB.

DR InterPro; IPR000997; Cholinesterase.

DR InterPro; IPR000379; Ser_estr_site.

DR Pfam; PF00135; Coesterase; 1.

DR PRINTS; PR00878; CHOLINESTRASE.

KW Hydrolase.

SO SEQUENCE 554 AA; 63254 MW; 6E4AC221A445B02D CRC64;

Query Match 43.1%; Score 1324.5; DB 5; Length 554;

Best Local Similarity 45.6%; Pred. No. 2.8e-101;

Matches 252; Conservative 112; Mismatches 176; Indels 13; Gaps 7;

Qy 18 IENKFLNRYLTNETVVAETEGYKVKVRLTYVD-DSYSEFGIIPVADPPYGLRFRAP 76

Db 6 VGHKVOQYRLSTGHTVIIDTKYGVGRQIRKTYVDKEFYAFEGIPYAKPPVGDRLFRAP 65

Qy 77 QRPFMGCVPRCCNKKDSYQVDFITGKVGSEDCLYSYTNLNPETKRPVLYYING 136

Db 66 QPPEWGVLCCTNRSKPMQRMMLGIVESEDC.LHNVYKALKSEKPLVYIWIYGG 125

Qy 137 GFIIGENHRDYGDPDYFTKKDVLINIOYRLGALGFLSLNSEDNLVPGNAGLKDVMLR 196

Db 126 GFQGEASRDYSPDYFMKKPVFAIVYRLAALGFLSLKDKRLDVPAGAGLKDVMLR 185

Qy 197 WIKNNCANFGNPDNIYVFGESAGASTHYWMLTEOTRGLFRGLMSGNAICPMANTOC 256

Db 186 WISONIAHFNDPNNITLMGASGASVHVMTTETOTRGLFRKAIKMOGSCALSEWVESPD 245

Qy 257 QHRAFTLAKLKGEDNDKVDLEFLMKAKPODILKLEKYLTEERNKVMFPPGPRYE 316

Db 246 NNMAFRLQNTGKGEDEADADYLSKVCARQAIADODVYNLDEVNSFLFAFGVYIE 305

Qy 317 PYQTADCVLPKPRRMVYTAGNSIPTMGNTSYEGLEFTSLKOMPMLVKELETCVNFV 376

Db 306 PYETDHCVPVRHKKLLEBANGNDIPYVGVSGFGLTSYQVLRDPAWLNKFNH---NIL 362

Qy 377 PSELADARLAPETLEMKAKIKKAVHGTETPPADNF---MDLCSITTFPMRHLQLR 433

Db 363 PREVETSSLEGGDL-LVRLRLKQLYFNNEQMSMEMFEALNIFSHROIMDTHRFILARQ 421

Qy 434 NHTSGPYLYLRFPDSEDILNIPYRIRSGRGVSHADELTTFYFNOLAKRMPKRESRE 493

Db 422 SYAKFTPTLYLRFPDSDH-FNQRRLVCGDRIRGVAAHADELSTLYFNITASKLKSSNE 480

Qy 494 YKTERMTGIMQFATGNPNPSNIEGMENSWDPIK-KSEYVYKCLNISDELKMDVPE 552

Db 481 YKTERMTGIMQFATGNPNPSNIEGMENSWDPIK-KSEYVYKCLNISDELKMDVPE 537

Qy 553 MDKIKOWSMFEK 565

Db 538 SDCIAVMDTFEPR 550

RESULT 14

ID Q24195 PRELIMINARY; PRT; 554 AA.

AC Q24195

DT 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Alpha esterase.

GN ALPHA-EST2 OR AE2 OR CG2505.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Phrygotea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.,

RL J. Mol. Evol. 0:0-0(0).

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: U51044; AAB01143.1; -.
DR HSSB: P37967; IOE3.
DR FlyBase: FBgn0015570; alpha-Est2.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_ester_s-site.
DR Pfam: PF00133; Coesterase; 1.
DR HydroLase.
SQ SEQUENCE 554 AA; 63242 MW; 17B4CCD344E2PDBE CRC64.
Query Match 43.0%; Score 1322.5; DB 5; Length 554;
Best Local Similarity 45.6%; Pred. No. 4,1e-101;
Matches 252; Conservative 109; Mismatches 179; Indels 13; Gaps 7;
QY 18 IENKFLNRLTTNEVVAETETGKKGKVKRLTYVD-DSTYSREGIPADRPAGLEKFKAP 76
DB 6 VHKHQVQYRLSTGHVILDTTKYGVNGLDKRKTYVDDEPFAFEGELTAPRPVGLDFKRP 65
QY 77 QRPPTDGVDRDCNNHKDKSVQVDFITGKCGSEDCLYLTSVYNNLNPETKRPVLYIHGG 136
DB 66 QREPRQVGLACTTNKSKRMQRMLLGITYEGSDCHLWVYKALSEKRPVIVYIYGG 125
QY 137 GELIENHDMYGRDYFIKKDVLLINQYRLGALGFLSLNSELNPNAGAKLDQYMAIR 196
DB 126 GFQCKGASRDYIPDYFMKKPVYFVAINYRLALGFLSLKDPKLDVPGNGLDQYMAIR 185
QY 197 WIKNNCANFGNPDNTITGESAGASTHYMLTEQTRGLEFHRIIMSGNAICPMANTOC 256
DB 186 WISQNTIAQFQGDNDNTITLGMESAGSVHYMMTTEQTRGLEFHRIIMSGNAICPMANTOC 245
QY 257 QHSAPTLAKLAGYKGEDNDKDVLEFLMKAKPDILKLEKVLTLEERTKVMPEFGTVE 316
DB 246 NNMAFRLAQNLGVMGDEKDVLEFLSKVSARQIAIDQDVINLDEVRSLFLAFEGVIE 305
QY 317 PYQTADCVLPKHNREMKWTAMGNSIPRMGNTSEGLEFTSILKOMPLKKELETVCYVF 376
DB 306 PYELDHCVWPKRPDILSEMGNDIPYIVGNSFEGELFSYQLVAKDWALKNFH--NIL 362
QY 377 PSELDAERTAPETLEMGAKIKKAVTGETPTADNF--MDLCSHIYFWPPIRLDLRF 433
DB 363 PREVERETSLSEGOOL-LVRLRLKQLYFNMDESMEMFEALINFSHROIMWDTHTREILARQ 421
QY 434 NHSTGTVEYLYRPFQSEDLINPYRIRKSGGVKGVSHADELYTFENQOLAKRPKESRE 493
DB 422 SYARKTPIYLYRPFQSDPH-FNQXRLVCGDRIGVAHADSLTSLFYNIISKIDKSME 480
QY 494 YKTERMTGWIQDPATGTNPYSNEIEGMEVSWDPK-KSDEYKCKLINSDELKMDIYPE 552
DB 481 YKTERMTGWMTSFSSSCNPNCPF---LGSAKWEAVQLKENAVKCFNISHDLEWRDLE 537
QY 553 MDKIKOWESMEFK 565
DB 538 SDCLAWDTFFYR 550
RESULT 15
Q9N161 PRELIMINARY; PRT; 564 AA.
AC Q9N161:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DR 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Alpha-esterase 1a.
GN AE1A.
CU Drosophila buzzatii (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyraoidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7264;
RN [1]
RP SEQUENCE FROM N.A.
RP Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;
RT "The alpha-esterase cluster of Drosophila buzzatii.";

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RL - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTERASE/LIPASE FAMILY.
 CC EMBL: AF216208; AAF26721.1; -.
 DR HSSP: P37967; I0E3.
 DR PLYBASE: FBgn0029453; Dbuz\AE1A.
 DR InterPro: IPR002018; Carbesters.
 DR InterPro: IPR000379; Ser-esters_sile.
 DR Pfam: PF00135; Coesterase; 1.
 DR HydroLase.
 SQ SEQUENCE 564 AA: 64540 MW: DBA42E91038B9D12 CRC64;

Query Match	42.5%	Score 1306.5	DB 5	Length 564
Best Local Similarity	46.0%	Pred. No. 9e-100		
Matches 262	Conservative 101	Mismatches 192	Indels 15	Gaps
QY	1	MNFNVSLMEKLEKWKIKCJLENKFLNRLTNTNTVAETEGYKVKQKRLIVYDD-STYSEE	59	
Db	1	MNIQMSVGDLLKMGAKLLGHRTEQYLNATFKITTYVAVDITDOLGVRGLORKTLYDHFHLYFEE	60	
QY	60	GIYPAQPPYVGEJREFAPQRPPTMPCVDRCCCHNRKKSVOVDITGKVGCSBDCCLYSLYRN	119	
Db	61	GIYFAPRPGLGEJREFRPOSPEDEGIRCTHPRAKRPVQKHLMYHVLGSSDCLLYNATYK	120	
QY	120	NLNEPKRPPVLYYIHGGFETIGENHDMYGDYFIKDVLYLINIQRLGALGFLSNSED	179	
Db	121	TKSESPLRPVWVIFPGGFGOTGEARNVDVSPDYFKOXIDVLYLTNRYLGALGFUSLSDR	180	
QY	180	LNPVGNAGLKDDOMALRWIKNNKANGFNPDITVFGECSAGASTHYMMLTEOTRGLFHR	239	
Db	181	LDPVGNAGLKDDOMALRWYDNIANFNNGRPEITLTMGLSAGASTQIMMTTEQTRGLFK	240	
QY	240	GLIMSGNAICPMANTOCQHRAFTLAKLAGYKCEDNDKRYLEFLMKAKRODITKLEEVLT	299	
Db	241	AIIMSGSGLDMMANENHNDMPYRLACHILGAYSDNEKEFRFLORASAKKDILG-SALPS	299	
QY	300	LEERTKNVMPFPGPVEPYOTADCVLPKRPBRMYATWANGSIPITMGNTSYEGLP-FTSI	358	
Db	300	LVERKVDILFEPGPVLEPYTASCVISQPPVELTSLAEMGNKRLPLMIGASSEGLEGFYOFV	359	
QY	359	LKQPMPLVKELEFCVNFVPSGLADARTPTPELLMGAKIKRKHVGVGPTADNF---MDL	415	
Db	360	MRDATHVLSQFEA---ITPREVEVS-TPELKEHRIIRLAKVFFDDATRGSMEEFECJOL	415	
QY	416	CSHITVEFPMHRLQLEFNHTSGTPYLYTRFDESDLLINPRIMRSRGVYGSVHADEL	475	
Db	416	LSLKHFMHAIHRTVLLARRAAYPTMPYLYRFEDDS-VTFNHRIMLCGHEHGVCHADDF	474	
QY	476	TYFPMNDLAKMPKESREKYRTIERMGIWIOFATTCNPYSNIEGEMVNSWDPIKSDSEV	535	
Db	475	FYLENCIPAMKLKNSSESEYRTIERMIGOMWTAFLENSPOCPRE---LEPIOWEPL-DSNAT	530	
QY	536	YKCLINISDELKMDIVPEMDKIKOMESMEEK	565	
Db	531	AKCLINISQQLFKLPERKOLKAVNDSTYER	560	

Search completed: April 4, 2003, 09:16:18
Job time : 59.8533 secs

OS *Drosophila buzzatii* (Fruit fly).
 OC *Eukaryota*: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta;
 OC *Eukaryota*: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha;
 OC Ephydroidea: Drosophilidae, Drosophila.
 OX NCBI_TaxID=7264;
 RN [1]
 RN SEQUENCE FROM N.A.
 RN Robin C., Claudianos C., Russell R.J., Oakshott J.G.,
 RA "The alpha-esterase cluster of *Drosophila buzzatii*."
 RT

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:57 ; Search time 15.7722 Seconds
(without alignments)
1063.331 Million cell updates/sec

Title: US-09-776-910-8

Perfect score: 3073
Sequence: 1 MNFVSLMEKIKKIKICIN.....PEMDKIKOWSEKRDLE 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3073	100.0	570	4	US-09-068-960-8
2	3067	99.8	570	2	US-08-669-524-3
3	3060	99.6	570	4	US-09-068-960-2
4	3060	99.6	570	4	US-09-068-960-6
5	3060	99.6	570	4	US-09-068-960-10
6	3060	99.6	570	4	US-08-669-524-4
7	3040	98.9	570	2	US-08-669-524-4
8	2348	76.4	570	4	US-09-068-960-13
9	1994.5	64.9	572	2	US-08-669-524-8
10	1089	35.4	207	4	US-09-068-960-43
11	856	27.9	528	3	US-08-747-221B-37
12	856	27.9	528	4	US-09-005-051-37
13	825	26.8	207	4	US-09-068-960-15
14	785.5	25.6	530	3	US-08-747-221B-53
15	785.5	25.6	530	4	US-09-005-051-53
16	785.5	25.6	550	3	US-08-747-221B-19
17	785.5	25.6	550	4	US-09-005-051-19
18	779.5	25.4	550	3	US-08-747-221B-58
19	779.5	25.4	550	4	US-09-005-051-58
20	771.5	25.1	505	3	US-08-747-221B-14
21	771.5	25.1	505	4	US-09-005-051-14
22	623	20.3	570	3	US-08-747-221B-55
23	623	20.3	570	4	US-09-005-051-55
24	623	20.3	595	3	US-08-747-221B-31
25	623	20.3	595	4	US-09-005-051-31
26	612	19.9	570	3	US-08-747-221B-54
27	612	19.9	570	4	US-09-005-051-54

28	612	19.9	596	3	US-08-747-221B-25	Sequence 25, Appl
29	612	19.9	596	4	US-09-005-051-25	Sequence 25, Appl
30	586.5	19.1	489	1	US-08-589-893-18	Sequence 18, Appl
31	586.5	19.1	489	2	US-09-020-991-18	Sequence 18, Appl
32	586.5	19.1	489	2	US-09-062-890-18	Sequence 18, Appl
33	583.5	19.0	489	1	US-08-124-674-2	Sequence 2, Appl
34	583.5	19.0	489	1	US-08-589-893-4	Sequence 4, Appl
35	583.5	19.0	489	1	US-08-589-893-6	Sequence 6, Appl
36	583.5	19.0	489	1	US-08-589-893-16	Sequence 16, Appl
37	583.5	19.0	489	2	US-09-020-991-4	Sequence 4, Appl
38	583.5	19.0	489	2	US-09-020-991-6	Sequence 6, Appl
39	583.5	19.0	489	2	US-09-062-890-16	Sequence 16, Appl
40	583.5	19.0	489	2	US-09-062-890-4	Sequence 4, Appl
41	583.5	19.0	489	2	US-09-062-890-6	Sequence 6, Appl
42	583.5	19.0	489	2	US-09-062-890-16	Sequence 16, Appl
43	583.5	19.0	489	2	US-09-062-890-28	Sequence 28, Appl
44	583.5	19.0	489	2	US-09-062-890-34	Sequence 34, Appl
45	583.5	19.0	489	2	US-09-062-890-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-068-960-8
; Sequence 8, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 501/9-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Lucilia cuprina
; US-09-068-960-8

Query Match	100.0%	Score 3073;	DB 4;	Length 570;
Best Local Similarity	100.0%	Pred. No. 2.6e-313;		
Matches 570;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNFVSLMEKIKKIKICINENKELNYRLTNETVAEFYGVKVKRTLYDDSYSEF	60	
DB	1	MNFVSLMEKIKKIKICINENKELNYRLTNETVAEFYGVKVKRTLYDDSYSEF	60	
QY	61	IPYAPVGEGLRFPAPRPTPMDGVDCNHRKDSVQVFTTGKVCSEDDLYLSVYNN	120	
DB	61	IPYAPVGEGLRFPAPRPTPMDGVDCNHRKDSVQVFTTGKVCSEDDLYLSVYNN	120	
QY	121	LNPEKRPVLYITGGGFIIEENHRDMYGPDYFIKKDVLINIOYRLGALFSLNSDL	180	
DB	121	LNPEKRPVLYITGGGFIIEENHRDMYGPDYFIKKDVLINIOYRLGALFSLNSDL	180	
QY	181	NVPGNAGIKDDVMLRWTKNNKCANFGNPDITVFGESAGASRHYMLTJOTGLFRG	240	
DB	181	NVPGNAGIKDDVMLRWTKNNKCANFGNPDITVFGESAGASRHYMLTJOTGLFRG	240	
QY	241	ILMSGNAICPAPNOCORAFPTLAKLAGYKGEDNDKDLFEFLMKAKPDDLITKEKYVTL	300	
DB	241	ILMSGNAICPAPNOCORAFPTLAKLAGYKGEDNDKDLFEFLMKAKPDDLITKEKYVTL	300	
QY	301	EERTNNKVFPGPVEPYQTAQCVLPKHPREMYKATAMGNSIPTMMGNTSYEGLEFTSLK	360	
DB	301	EERTNNKVFPGPVEPYQTAQCVLPKHPREMYKATAMGNSIPTMMGNTSYEGLEFTSLK	360	

QY 361 QMPMLVKELETCVNFVPSSELADEKTAPELLEMGAKIKKAHVTEGPTADNFMDCSHY 420
DB 361 QMPMLVKELETCVNFVPSSELADEKTAPELLEMGAKIKKAHVTEGPTADNFMDCSHY 420
QY 421 FWFPMHRLDOLRFNHTSGTPVLYLRFDFDSEDLLNPRIMSGRGVGVSHADELTYFEW 480
DB 421 FWFPMHRLDOLRFNHTSGTPVLYLRFDFDSEDLLNPRIMSGRGVGVSHADELTYFEW 480
QY 481 NOLAKRMPKESREKTIERTMTGIMIOFATGPNYSNEIEGMEVSWDPKKSDEYKCLN 540
DB 481 NOLAKRMPKESREKTIERTMTGIMIOFATGPNYSNEIEGMEVSWDPKKSDEYKCLN 540
QY 541 ISDELKMDVPEMDKIKOWESMEFKEHRDLF 570
DB 541 ISDELKMDVPEMDKIKOWESMEFKEHRDLF 570

RESULT 2
US-08-669-524-3
Sequence 3, Application US/08669524
Patent No. 5843758

GENERAL INFORMATION:
APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKSHOTT, John G.
APPLICANT: SMYTH, Keirle A.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669, 524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-524-3

Query Match 99.8%; Score 3067; DB 2; Length 570;
Best Local Similarity 99.6%; Pred. No. 1,le-312;
Matches 568; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFVSLMEKLMKWKIKCIENKFLNRLTNTNVAETEGYGVKVRKRLTYVDDSYSEEG 60
DB 1 MNFVSLMEKLMKWKIKCIENKFLNRLTNTNVAETEGYGVKVRKRLTYVDDSYSEEG 60
QY 61 IPYADPPVGELEFRKAPQRPPTMDGVRDCCNHNKDKSVQVDFITGKVGCSDEDCLYLSVTNN 120

DB 61 IPYADPPVGELEFRKAPQRPPTMDGVRDCCNHNKDKSVQVDFITGKVGCSDEDCLYLSVTNN 120
QY 121 LNPETKRPVLYIYHGGGFIIGENHRDMYGPDYFIKKQVVLINIOYRIGALGFLSLNSED 180
DB 121 LNPETKRPVLYIYHGGGFIIGENHRDMYGPDYFIKKQVVLINIOYRIGALGFLSLNSED 180
QY 181 NYPGNAGLKDOVMALRWIKNNCANFGNPDNITVFGESAGASTHYMMLTEQRTGLFHRG 240
DB 181 NYPGNAGLKDOVMALRWIKNNCANFGNPDNITVFGESAGASTHYMMLTEQRTGLFHRG 240
QY 241 IIMSGNAICPMANTOCORAFPTLAKLAGYKGEDNDKDLFELMAKAKPODLIKLEKVLTL 300
DB 241 IIMSGNAICPMANTOCORAFPTLAKLAGYKGEDNDKDLFELMAKAKPODLIKLEKVLTL 300
QY 301 EERTKVMPPGPTVPRYOTADCVLPKHREWKATWANGSIPTMGNSTYEGLEFSTSLK 360
DB 301 EERTKVMPPGPTVPRYOTADCVLPKHREWKATWANGSIPTMGNSTYEGLEFSTSLK 360
QY 361 QMPMLVKELETCVNFVPSSELADEKTAPELLEMGAKIKKAHVTEGPTADNFMDCSHY 420
DB 361 QMPMLVKELETCVNFVPSSELADEKTAPELLEMGAKIKKAHVTEGPTADNFMDCSHY 420
QY 421 FWFPMHRLDOLRFNHTSGTPVLYLRFDFDSEDLLNPRIMSGRGVGVSHADELTYFEW 480
DB 421 FWFPMHRLDOLRFNHTSGTPVLYLRFDFDSEDLLNPRIMSGRGVGVSHADELTYFEW 480
QY 481 NOLAKRMPKESREKTIERTMTGIMIOFATGPNYSNEIEGMEVSWDPKKSDEYKCLN 540
DB 481 NOLAKRMPKESREKTIERTMTGIMIOFATGPNYSNEIEGMEVSWDPKKSDEYKCLN 540
QY 541 ISDELKMDVPEMDKIKOWESMEFKEHRDLF 570
DB 541 ISDELKMDVPEMDKIKOWESMEFKEHRDLF 570

RESULT 3
US-09-068-960-2
Sequence 2, Application US/09068960A
Patent No. 6235515

GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068, 960A
CURRENT FILING DATE: 1998-05-20
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-2

Query Match 99.6%; Score 3060; DB 4; Length 570;
Best Local Similarity 99.8%; Pred. No. 5,9e-312;
Matches 569; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNFVSLMEKLMKWKIKCIENKFLNRLTNTNVAETEGYGVKVRKRLTYVDDSYSEEG 60
DB 1 MNFVSLMEKLMKWKIKCIENKFLNRLTNTNVAETEGYGVKVRKRLTYVDDSYSEEG 60
QY 61 IPYADPPVGELEFRKAPQRPPTMDGVRDCCNHNKDKSVQVDFITGKVGCSDEDCLYLSVTNN 120
DB 61 IPYADPPVGELEFRKAPQRPPTMDGVRDCCNHNKDKSVQVDFITGKVGCSDEDCLYLSVTNN 120
QY 121 LNPETKRPVLYIYHGGGFIIGENHRDMYGPDYFIKKQVVLINIOYRIGALGFLSLNSED 180
DB 121 LNPETKRPVLYIYHGGGFIIGENHRDMYGPDYFIKKQVVLINIOYRIGALGFLSLNSED 180

Qy	181	NVPCNAGIKDOVYALRYMINKNCAFGGNPNITVFGESACAASHYMYLLEOTRGJLFPHNG	240
Db	181	IVPGNAGIKDOVYALRYMINKNCAFGGNPNITVFGESACAASHYMYLLEOTRGJLFPHNR	240
Qy	241	ILMSGNACIPRANPOCQOHRATFLAKLGYGKEDNDKOVLEFLMKAKPODLIKLEEKYLTJ	300
Db	241	ILMSGNACIPRANPOCQOHRATFLAKLGYGKEDNDKOVLEFLMKAKPODLIKLEEKYLTJ	300
Qy	301	EERTNKVAFPRGPTEVERPYQTADCVLPKHPREMYKTAWGNSIPTMGCNTSYEGJLFSTSILK	360
Db	301	EERTNKVAFPRGPTEVERPYQTADCVLPKHPREMYKTAWGNSIPTMGCNTSYEGJLFSTSILK	360
Qy	361	QMPRLUYELELCVAFVSESLADARTKAPETLEBMCAKIKKKAHVYGETPTADNFMDCCSHYJ	420
Db	361	QMPRLUYELELCVAFVSESLADARTKAPETLEBMCAKIKKKAHVYGETPTADNFMDCCSHYJ	420
Qy	421	FMPRHRLLDLPFHNHSTGPYUYLERFGPDESDLLNPRIKRSGRGVGSVSHADELYFFW	480
Db	421	FMPRHRLLDLPFHNHSTGPYUYLERFGPDESDLLNPRIKRSGRGVGSVSHADELYFFW	480
Qy	481	NOLAKRMPKESREYKTIERTMTGIWQATGPNPYSNIEBGMENVSMDPIKSSDEVYKCLN	540
Db	481	NOLAKRMPKESREYKTIERTMTGIWQATGPNPYSNIEBGMENVSMDPIKSSDEVYKCLN	540
Qy	541	ISDELKATDVBEMDKIKOWESMEFKHNDLF	570
Db	541	ISDELKATDVBEMDKIKOWESMEFKHNDLF	570

RESULT 4
 US-09-068-960-4
 : Sequence 4, Application US/09068960A
 : Patent No. 6235515
 : GENERAL INFORMATION:
 : APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
 : TITLE OF INVENTION: MALATION CARBOXYL ESTERASE
 : FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 : CURRENT APPLICATION NUMBER: US/09/068,960A
 : CURRENT FILING DATE: 1998-05-20
 : EARLIER APPLICATION NUMBER: PCT/AU96/00746
 : EARLIER FILING DATE: 1996-11-22
 : EARLIER APPLICATION NUMBER: AU 6751
 : EARLIER FILING DATE: 1995-11-23
 : NUMBER OF SEQ ID NOS: 43
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 4
 : LENGTH: 570
 : TYPE: PRT
 : ORGANISM: *Lucilia cuprina*
 : US-09-068-960-4

Query Match	99.6%	Score 3060	DB 4	Length 570
Best Local Similarity	99.8%	Pred. No. 5.9e312		
Matches 569	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

Qy	1	MNFVSLMEKJLKKMKIKCLENENFLVRLTJMETVVAEFEEYKSVGVRKLRYDDSDYSFEQ	60
Db	1	MNFVSLMEKJLKKMKIKCLENENFLVRLTJNETVVAEFEEYKSVGVRKLRYDDSDYSFEQ	60
Qy	61	IPYAPQPVGELRFRKAPQRPFRPMDGVRCCHNHKDKSVQVDFITGKVCSESDCLVSYTNN	120
Db	61	IPYAPQPVGELRFRKAPQRPFRPMDGVRCCHNHKDKSVQVDFITGKVCSESDCLVSYTNN	120
Qy	121	LNPERKRPVLYYIHGGGFIIGENHRDMVGPDYFKKKVVLINIQYRIGALGFSLNSED	180
Db	121	LNPERKRPVLYYIHGGGFIIGENHRDMVGPDYFKKKVVLINIQYRIGALGFSLNSED	180
Qy	181	NVPAGAGLKDDVYMLRWTKNNCANGFNPDIIYFEGESAGASTHYMLLEOTRGLEPHRG	240
Db	181	NVPAGAGLKDDVYMLRWTKNNCANGFNPDIIYFEGESAGASTHYMLLEOTRGLEPHRG	240
Qy	241	ILMSGNATCIPWANTQCOHRAFTLAKLAGYKGEKDNDRKVLVEFLMKARPODILIKIEEKVLT	300

Dd	241	ILMSGNATCPLANNOCQBARFTLAKGLGYKCEDNDKVOLEFLIMKAKPODLIKLEEKVLT	3000
Qy	301	EEPTNKVIFERRGPVPERQTADCVLPKPKRPMVKTANGNSIPTMAGTSTEGLEFITSILK	3600
Dd	301	EEPTNKVIFERRGPVPERQOTADCVLPKPKRPMVKTANGNSIPTMAGTSTEGLEFITSILK	3600
Qy	361	OMPMVLKLEFCVNPVDSBELADARTRAPETLEMAKAKKKAHVGEPTTANPMDLCHIT	4200
Dd	361	OMPMVLKLEFCVNPVDSBELADARTRAPETLEMAKAKKKAHVGETTANPMFDLCHIT	4200
Qy	421	FWEPMHRLQLEFHNHSTSTPYULVLRPFDSDDLNPYRIMSGRGVGVSHADELTFFW	4800
Dd	421	FWEPMHRLQLEFHNHSTSTPYULVLRPFDSDDLNPYRIMSGRGVGVSHADELTFFW	4800
Qy	481	NOLAKRMPKESREYKTERMTGMIQOPATGPNPYSNETEGMENVSMDPIKKSDEYVKCLN	5400
Dd	481	NOLAKRMPKESREYKTERMTGMIQOPATGPNPYSNETEGMENVSMDPIKKSDEYVKCLN	5400
Qy	541	ISDELKMTDVPBMDIKOMESMEFKHRLFF	570
Dd	541	ISDELKMTDVPBMDIKOMESMEFKHRLFF	570

```

: RESULT 5
: US-09-068-960-6
: Sequence 6, Application US/09068960A
: Patent No. 6235515
: GENERAL INFORMATION:
: APPLICANT: Commonwealth Scientific and Industrial Rsch. Org
: TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
: FILE REFERENCE: Attorney Docket No. 6235515 50179-051
: CURRENT APPLICATION NUMBER: US/09/068,960A
: CURRENT FILING DATE: 1998-05-20
: EARLIER APPLICATION NUMBER: PCT/AU96/00746
: EARLIER FILING DATE: 1996-11-22
: EARLIER APPLICATION NUMBER: AU 6751
: EARLIER FILING DATE: 1995-11-23
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 570
: TYPE: PRT
: ORGANISM: Lucilia cuprina
: US-09-068-960-6

```

Query Match	99.6%	Score 3060	DB 4	Length 570
Best Local Similarity	99.8%	Pred. No. 5.9e312		
Matches 569	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

QY	1	MNFNFSLMEKLRKWKJKCIENFELNRLTNTNVAEFTYGVKCVKRLTYVDSYSFEFG	60
Db	1	MNFNFSLMEKLRKWKJKCIENFELNRLTNTNVAEFTYGVKCVKRLTYVDSYSFEFG	60
QY	61	IPYAPPVAGELRFKAPORPTFMDGVDDCCNHKDKSVQVDFTTGKVGSGEDCLVLSYTTNN	120
Db	61	IPYAPPVAGELRFKAPORPTFMDGVDDCCNHKDKSVQVDFTTGKVGSGEDCLVLSYTTNN	120
QY	121	LNPERKRPVLVYIHGGFTIIGENHRDMGPRPYFLFKDDVLNTIORYGALGFSLNSED	180
Db	121	LNPERKRPVLVYIHGGFTIIGENHRDMGPRPYFLFKDDVLNTIORYGALGFSLNSED	180
QY	181	NVPGNAGLKDQYMALRWIKNNCANFGNPDNIITVFGESAGAATHYMLTBTQRTGLFHRG	240
Db	181	NVPGNAGLKDQYMALRWIKNNCANFGNPDNIITVFGESAGAATHYMLTBTQRTGLFHRG	240
QY	241	ILMSGNALCPMANNTCCORAFFLKLKLAGYKSEDDNDKIVLEFLTMAKPODILKLEEKVLT	300
Db	241	ILMSGNALCPMANNTCCORAFFLKLKLAGYKSEDDNDKIVLEFLTMAKPODILKLEEKVLT	300
QY	301	BEETNKVMPFPGPIVETQADCVLPKPIRBMVKTAMGNSIPTVMGNTSEGLEFTSILK	360
Db	301	BEETNKVMPFPGPIVETQADCVLPKPIRBMVKTAMGNSIPTVMGNTSEGLEFTSILK	360

QY 361 QMPMLVKELETCVNFVPSGLADAERTAPETLEMGAKIKKAVHTGPTPADNEMDLCSHIT 420
 DB 361 QMPMLVKELETCVNFVPSGLADAERTAPETLEMGAKIKKAVHTGPTPADNEMDLCSHIT 420
 QY 421 FWFPMRLLOLRNHTSGTPVLYRDFPSEDLINPYRIMSRGKGVKGVSHADELTYFEW 480
 DB 421 FWFPMRLLOLRNHTSGTPVLYRDFPSEDLINPYRIMSRGKGVKGVSHADELTYFEW 480
 QY 481 NOLAKRMPKESREYKTIERTMTGIMIOFATTGNPYSNEIEGMEVNSMDPKKSDEYKCLN 540
 DB 481 NOLAKRMPKESREYKTIERTMTGIMIOFATTGNPYSNEIEGMEVNSMDPKKSDEYKCLN 540
 QY 541 ISDELKMDVPEMDKIKOMESMEKRDLE 570
 DB 541 ISDELKMDVPEMDKIKOMESMEKRDLE 570

RESULT 6

US-09-068-960-10
 : Sequence 10, Application us/09068960A
 : Patent No. 6235515
 : GENERAL INFORMATION:
 : APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
 : TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
 : FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 : CURRENT APPLICATION NUMBER: US/09/068,960A
 : EARLIER FILING DATE: 1998-05-20
 : EARLIER APPLICATION NUMBER: PCT/AU96/00746
 : EARLIER FILING DATE: 1996-11-22
 : EARLIER APPLICATION NUMBER: AU 6751
 : NUMBER OF SEQ ID NOS: 43
 : SOFTWARE: Patent In Ver. 2.0
 : SEQ ID NO 10
 : LENGTH: 570
 : TYPE: PRT
 : ORGANISM: Lucilia cuprina
 : US-09-068-960-10

Query Match 99.6%; Score 3060; DB 4; Length 570;
 Best Local Similarity 99.8%; Pred. No. 5.9e-312;
 Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNFVNSLMKLMKIKICENKFLNRLTNETVVAETEGKVGKVRLLTYDDSYSEFG 60
 DB 1 MNFVNSLMKLMKIKICENKFLNRLTNETVVAETEGKVGKVRLLTYDDSYSEFG 60
 QY 61 IPYAPPVGELRFRKAPQRTPMGVDGCCNHRKDSYQVDFITGKVCSEDCILSYTYNN 120
 DB 61 IPYAPPVGELRFRKAPQRTPMGVDGCCNHRKDSYQVDFITGKVCSEDCILSYTYNN 120
 QY 121 LNPETKRPVLYIHGGFTIGENHRDMYGPDIYFKKDVLYINIOYRLGALGFLSINSEDL 180
 DB 121 LNPETKRPVLYIHGGFTIGENHRDMYGPDIYFKKDVLYINIOYRLGALGFLSINSEDL 180
 QY 121 LNPETKRPVLYIHGGFTIGENHRDMYGPDIYFKKDVLYINIOYRLGALGFLSINSEDL 180
 DB 121 LNPETKRPVLYIHGGFTIGENHRDMYGPDIYFKKDVLYINIOYRLGALGFLSINSEDL 180
 QY 181 NVPGNAGLKQVVALRWIKNNCANFGNPDNITVFGEASGAATHYMLTEOTRGFLPHRG 240
 DB 181 NVPGNAGLKQVVALRWIKNNCANFGNPDNITVFGEASGAATHYMLTEOTRGFLPHRG 240
 QY 241 ILMSGNAICPMWANTOCOHRAFTLAKLAGYGEENDKDVLEFLMKAPRODILKEEVVLL 300
 DB 241 ILMSGNAICPMWANTOCOHRAFTLAKLAGYGEENDKDVLEFLMKAPRODILKEEVVLL 300
 QY 301 EERTNKWMPRTGPTVERPYQTADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFTSILK 360
 DB 301 EERTNKWMPRTGPTVERPYQTADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFTSILK 360
 QY 361 QMPMLVKELETCVNFVPSGLADAERTAPETLEMGAKIKKAVHTGPTPADNEMDLCSHIT 420
 DB 361 QMPMLVKELETCVNFVPSGLADAERTAPETLEMGAKIKKAVHTGPTPADNEMDLCSHIT 420
 QY 421 FWFPMRLLOLRNHTSGTPVLYRDFPSEDLINPYRIMSRGKGVKGVSHADELTYFEW 480

DB 421 FWFPMRLLOLRNHTSGTPVLYRDFPSEDLINPYRIMSRGKGVKGVSHADELTYFEW 480
 QY 481 NOLAKRMPKESREYKTIERTMTGIMIOFATTGNPYSNEIEGMEVNSMDPKKSDEYKCLN 540
 DB 481 NOLAKRMPKESREYKTIERTMTGIMIOFATTGNPYSNEIEGMEVNSMDPKKSDEYKCLN 540
 QY 541 ISDELKMDVPEMDKIKOMESMEKRDLE 570
 DB 541 ISDELKMDVPEMDKIKOMESMEKRDLE 570

RESULT 7

US-08-669-524-4
 : Sequence 4, Application us/08669524
 : Patent No. 5843758
 : GENERAL INFORMATION:
 : APPLICANT: RUSSELL, Robyn J.
 : APPLICANT: NEWCOMB, Richard D.
 : APPLICANT: ROBIN, Geoffrey C.
 : APPLICANT: BOYCE, Thomas M.
 : APPLICANT: CAMPBELL, Peter M.
 : APPLICANT: PARKER, Anthony G.
 : APPLICANT: OAKSHOTT, John G.
 : APPLICANT: SMITH, Kerrie A.
 : TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
 : NUMBER OF SEQUENCES: 22
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lowe Price Leblanc & Becker
 : STREET: 99 Canal Center Plaza, Suite 300
 : CITY: Alexandria
 : STATE: Virginia
 : COUNTRY: USA
 : ZIP: 22314
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/669,524

: FILING DATE: 435
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Price, Robert L.
 : REGISTRATION NUMBER: 22,685
 : REFERENCE/DOCKET NUMBER: 1451-021
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 703-684-1111
 : TELEFAX: 703-684-1124
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 570 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : US-08-669-524-4

Query Match 98.9%; Score 3040; DB 2; Length 570;
 Best Local Similarity 98.8%; Pred. No. 7.4e-310;
 Matches 563; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MNFVNSLMKLMKIKICENKFLNRLTNETVVAETEGKVGKVRLLTYDDSYSEFG 60
 DB 1 MNFVNSLMKLMKIKICENKFLNRLTNETVVAETEGKVGKVRLLTYDDSYSEFG 60
 QY 61 IPYAPPVGELRFRKAPQRTPMGVDGCCNHRKDSYQVDFITGKVCSEDCILSYTYNN 120
 DB 61 IPYAPPVGELRFRKAPQRTPMGVDGCCNHRKDSYQVDFITGKVCSEDCILSYTYNN 120
 QY 121 LNPETKRPVLYIHGGFTIGENHRDMYGPDIYFKKDVLYINIOYRLGALGFLSINSEDL 180

Db 121 LNPEKRPVLYIHGGXFIIGENHRDMYGPDIYFKKDVLLINIOYRLGALGFLSLNSDL 180
QY 181 NVPAGAKDDOVMALRWIKNNCANPGNDITVGSAGASTHYMLTETOTGLFHRG 240
Db 181 NVPAGAKDDOVMALRWIKNNCANPGNDITVGSAGASTHYMLTETOTGLFHRG 240
QY 241 ILMGNAICPMANTOCQHRATFLAKLAGYKGEDNDKDVLEFLMKAKPODLLIKLEEVLT 300
Db 241 ILMGNAICPMANTOCQHRATFLAKLAGYKGEDNDKDVLEFLMKAKPODLLIKLEEVLT 300
QY 301 EERTNKVFPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMNGNTSYEGLEFSTSLK 360
Db 301 EERTNKVFPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMNGNTSYEGLEFSTSLK 360
QY 361 OPMPLVKELETCVNFVSELDARETAPETLEMGAIRKKAHVGTETPADNMDLCSHIX 420
Db 361 OPMPLVKELETCVNFVSELDARETAPETLEMGAIRKKAHVGTETPADNMDLCSHIX 420
QY 421 FWFPMHRLQLRFNHTSGTPVYLYRFEDSEDLINPYRIMSGRGVKGVSADDELTFEWM 480
Db 421 FWFPMHRLQLRFNHTSGTPVYLYRFEDSEDLINPYRIMSGRGVKGVSADDELTFEWM 480
QY 481 NOLAKRMPKESREYKTIERTMTGIWQFATGPNYSNEIEGMENSWDPIKKSDEYKCLN 540
Db 481 NOLAKRMPKESREYKTIERTMTGIWQFATGPNYSNEIEGMENSWDPIKKSDEYKCLN 540
QY 541 ISDELKMDVPEMDKIKOMESMEKHRDLF 570
Db 541 ISDELKMDVPEMDKIKOMESMEKHRDLF 570

RESULT 8

US-09-068-960-13
Sequence 13, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068, 960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 570
TYPE: PRF
ORGANISM: Musca domestica
US-09-068-960-13

Query Match 76.4%; Score 2348; DB 4; Length 570;
Best Local Similarity 74.2%; Pred. No. 2.9e-237;

Matches 423; Conservative 73; Mismatches 74; Indels 0; Gaps 0;

QY 1 MNEVSIAMEKIKKIKCIENKFLNRLTTNETVAETIEYGVKVKRILTYVDSYSFEG 60
Db 1 MTFLEKOFIFRLKLCVKCVNKYTNVRLSTNETQIIDTEYGOIKGVKRTVYDDSYSES 60
QY 61 IPYOPPVGELRFAKAPORPFWDCVROCCNKHDKSVQVDFITGKVGSGEDLTVSYTNN 120
Db 61 IPYAKPPVGELEFRAPQKPPVWEGVDCCGPANSVQVDFITGKVGSGEDLTVSYTND 120
QY 121 LNPEKRPVLYIHGGXFIIGENHRDMYGPDIYFKKDVLLINIOYRLGALGFLSLNSDL 180
Db 121 LNPEKRPVLYIHGGXFIIGENHRDMYGPDIYFKKDVLLINIOYRLGALGFLSLNSDL 180
QY 181 NVPAGAKDDOVMALRWIKNNCANPGNDITVGSAGASTHYMLTETOTGLFHRG 240
Db 181 NVPAGAKDDOVMALRWIKNNCANPGNDITVGSAGASTHYMLTETOTGLFHRG 240

QY 241 ILMGNAICPMANTOCQHRATFLAKLAGYKGEDNDKDVLEFLMKAKPODLLIKLEEVLT 300
Db 241 ILMGNAICPMANTOCQHRATFLAKLAGYKGEDNDKDVLEFLMKAKPODLLIKLEEVLT 300
QY 301 EERTNKVFPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMNGNTSYEGLEFSTSLK 360
Db 301 EERTNKVFPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMNGNTSYEGLEFSTSLK 360
QY 361 OPMPLVKELETCVNFVSELDARETAPETLEMGAIRKKAHVGTETPADNMDLCSHIX 420
Db 361 OPMPLVKELETCVNFVSELDARETAPETLEMGAIRKKAHVGTETPADNMDLCSHIX 420
QY 421 FWFPMHRLQLRFNHTSGTPVYLYRFEDSEDLINPYRIMSGRGVKGVSADDELTFEWM 480
Db 421 FWFPMHRLQLRFNHTSGTPVYLYRFEDSEDLINPYRIMSGRGVKGVSADDELTFEWM 480
QY 481 NOLAKRMPKESREYKTIERTMTGIWQFATGPNYSNEIEGMENSWDPIKKSDEYKCLN 540
Db 481 NOLAKRMPKESREYKTIERTMTGIWQFATGPNYSNEIEGMENSWDPIKKSDEYKCLN 540
QY 541 ISDELKMDVPEMDKIKOMESMEKHRDLF 570
Db 541 ISDELKMDVPEMDKIKOMESMEKHRDLF 570

RESULT 9

US-08-669-524-8
Sequence 8, Application US/08669524
Patent No. 5843758
GENERAL INFORMATION:

APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKSHOTT, John G.
APPLICANT: SMYTH, Kerrie A.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669, 524
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-524-8

Query Match 64.9%; Score 1994.5; DB 2; Length 572;

Db 145 LEIE--GAPGNVGLLDQVAALKWTKENIEKFGDPENITIGGVSAGASVHYLLSHTTT 20

Best Local Similarity	34.38	Prec. No. Zile 1997	
Matches	182	Conservative	87
		Mismatches	204
		Indels	57
		Gaps	15

Query Match	25.08;	Score 705.5;	
Best Local Similarity	34.38;	Pred. No. 2,1e-73;	
Matches 182;	Conservative	87;	Mismatches 204;
			Indels 57;
			Gaps 15

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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:16:33 ; Search time 24.5753 Seconds

(without alignments)
1417.991 Million cell updates/sec

Title: US-09-776-910-8

Perfect score: 3073

Sequence: 1 MNFNVSIMKELKWKIKCIEN.....PEMDKIKQWSEKHKRDLF 570

Scoring table:

BLOSUM62
Gapop 10.0 , gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	718	23.4	574	9 US-10-023-515-4	Sequence 4, Appl1
2	718	23.4	612	9 US-09-875-353-4	Sequence 4, Appl1
3	707.5	23.0	585	10 US-09-934-323-4	Sequence 4, Appl1
4	571.5	18.6	602	10 US-09-748-739A-2	Sequence 2, Appl1
5	565	18.4	574	10 US-09-748-739A-6	Sequence 6, Appl1
6	564	18.4	574	10 US-09-748-739A-17	Sequence 8, Appl1
7	563	18.3	574	10 US-09-748-739A-17	Sequence 17, Appl1
8	563	18.3	574	10 US-09-748-739A-20	Sequence 20, Appl1
9	561	18.3	574	10 US-09-748-739A-4	Sequence 4, Appl1
10	558	18.2	574	10 US-09-748-739A-19	Sequence 19, Appl1
11	558	18.2	574	10 US-09-748-739A-21	Sequence 21, Appl1
12	556	18.1	574	10 US-09-748-739A-18	Sequence 18, Appl1
13	554	18.0	574	10 US-09-748-739A-22	Sequence 22, Appl1
14	548	17.8	537	9 US-09-738-626-4754	Sequence 4754, Ap
15	526	17.1	574	10 US-09-748-739A-23	Sequence 23, Appl1
16	525.5	17.1	581	9 US-10-023-515-2	Sequence 2, Appl1
17	522	17.0	549	9 US-10-102-806-689	Sequence 689, App
18	507.5	16.5	565	10 US-09-895-860-5	Sequence 5, Appl1
19	495.5	16.1	554	10 US-09-895-860-4	Sequence 4, Appl1

20	486.5	15.8	583	10 US-09-925-301-1177	Sequence 1177, Ap
21	485	15.8	816	9 US-09-875-353-2	Sequence 2, Appl1
22	483.5	15.7	568	9 US-09-418-176-4	Sequence 4, Appl1
23	483.5	15.7	722	9 US-09-418-176-3	Sequence 3, Appl1
24	483.5	15.7	745	9 US-09-418-176-2	Sequence 2, Appl1
25	479	15.6	816	9 US-09-978-295A-375	Sequence 375, App
26	479	15.6	816	9 US-09-978-697-375	Sequence 375, App
27	479	15.6	816	9 US-09-978-192A-375	Sequence 375, App
28	479	15.6	816	9 US-09-999-832A-375	Sequence 375, App
29	479	15.6	816	9 US-09-978-189-375	Sequence 375, App
30	479	15.6	816	9 US-09-978-608A-375	Sequence 375, App
31	479	15.6	816	9 US-09-978-191A-375	Sequence 375, App
32	479	15.6	816	9 US-09-978-403A-375	Sequence 375, App
33	479	15.6	816	9 US-09-978-564A-375	Sequence 375, App
34	479	15.6	816	9 US-09-978-585A-375	Sequence 375, App
35	479	15.6	816	9 US-10-017-081A-375	Sequence 375, App
36	479	15.6	816	9 US-09-978-824-375	Sequence 375, App
37	479	15.6	816	9 US-09-981-915A-375	Sequence 375, App
38	479	15.6	816	9 US-09-999-833A-375	Sequence 375, App
39	479	15.6	816	9 US-10-167-749-375	Sequence 375, App
40	479	15.6	816	9 US-09-918-585A-375	Sequence 375, App
41	462	15.0	547	10 US-09-895-860-2	Sequence 2, Appl1
42	462	15.0	571	9 US-10-036-041-23	Sequence 23, Appl1
43	462	15.0	571	9 US-10-028-072-542	Sequence 542, App
44	462	15.0	571	9 US-10-035-855-23	Sequence 23, Appl1
45	462	15.0	571	9 US-10-121-049-542	Sequence 542, App

ALIGNMENTS

RESULT 1
US-10-023-515-4
; Sequence 4, Application US/10023515
; Publication No. US20020182636A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A. J.
; APPLICANT: Sinos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYL ESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023, 515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256, 369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279, 508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
; US-10-023-515-4

Query Match 23.4%; Score 718; DB 9; Length 574;

Best Local Similarity 33.6%; Pred. No. 1.1e-57;
Matches 187; Conservative 83; Mismatches 223; Indels 64; Gaps 18;

QY 40 GKVGKVRKLTYY-DDSYSEFQIYAPQVPELRFKRAQ-RPTPDGVRDCCNKKDKVQ 97
DB 1 GKVGKVRKLTNGSQSYFLGIPAEPPVGNLRFKRAQPYKEPWSVDLTKTKYPPSCLO 60
QY 98 VDFI-----TKRVCG---SEDLTYLSVYT--NNLNPETKRPVLYIHGG 136
DB 61 DDDGFGFSLDKVALKMLSGMNKLTVGLKLSDEDTILNVYTPKTKRPVWMIHGG 120
QY 137 GTTIGENHR---DMYGPDYFIK-DVYLINTQYRIGALGFLSLNSEDLVNCGNGLKDOV 192
DB 121 GFMGSGHSPLSLTYDGSGLARREGNIVIVSYNVRGLGFLSTGDDKJPGSGNGLDOR 180

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QY 193 MALMIKNNCANCGNPDNITVGCESGASTHYMMLTE-----GRCGLFHHGILMSGN 246
Db 181 LALKWVDNITAAFGDGNNSVITFGEESGAASVSLLLTSCGNDPPSGGLFHRAISOGS 240
QY 247 AICPMA---MTCOCHRAFTLAKLGVYKGEENDKDVLEFLKAKRPODILKLEEKVYLTEER 303
Db 241 ALSMWAIOSESNANGRAKKELARLLGC-NETSSSLDCLASKSAEELLEATRSLLFEYV 299
QY 304 TNKVMF-PFGFTVEPYGTADCVLRKHPREMYKTAWMSGIFPMGNTSYEGLEFISIL--- 355
Db 300 PFLPLFLAFGVYGDGDAPEAFIPEDEBELKEKGFADVPYLLIGVTDEGGYFAMALNA 359
QY 360 -----KQMLVKELETGVNFPSPB---LADAPRAPETLE-MGAKIKKAHTYGE 405
Db 360 SSKGEDELAKKTNDVWMLLELKYTLFFASELMNKKMDLADAKYLEKPGDVDDFVSER 419
QY 406 TPTADNEMDLOSHIFYEMFPMHRLQLRNNHTSGTPVYLYRFEDFSEDLINBYRIMSRGC 465
Db 420 KP-----NIQDMLTDLFLKCPRTVAADLNAKH-CGSPVAYAYVDHPASFGICGFLAKRPDPE 475
QY 466 VKGVSHADELTYFFWNLAKRM---PKESREYKTIERTGTWIDPATGNGYNSIEIGME 522
Db 476 FGGAVHGEDEIFVVGNPPLKEDQLYKATBEKESSSKTMMYANFAKTGNNNGTSGNL- 534
QY 523 NVSWDPIKKSDEYVKCL 539
Db 535 -VVMWKYTSSEOKYSL 550

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RESULT 2
 US-09-875-353-4
 Sequence 4, Application US/09875353
 Patent No. US20020168713A1
 GENERAL INFORMATION:
 APPLICANT: CURTIS, RORY A.J.
 TITLE OF INVENTION: 46960, A NOVEL HUMAN NEUROLIGIN FAMILY
 TITLE OF INVENTION: MEMBER AND USES THEREOF
 FILE REFERENCE: 10448-0588001
 CURRENT APPLICATION NUMBER: US/09/875,353
 CURRENT FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/209,949
 PRIOR FILING DATE: 2000-06-06
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 612
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: consensus sequence
 US-09-875-353-4

Query Match	23.48;	Score 718;	DB 9;	Length 612;
Best Local Similarity	33.68;	Pred. NO. 1.3e-57;		
Matches 187;	Conservative 83;	Mismatches 223;	Indels 64;	Gaps 18;

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0y 40 GKVKGYKRLTVY--DDSYVSFEGICVPAACPPVLEAFKKAPQ-RPMPDSDVRCCHNKDKSQY 97
      |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 39 GIVRGVNEKXTDNGEOSVYSFUGIPFAEPVYNLFKFAQPKPEKMSVDLDTATKPSBCLQ 98
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
0y 98 VPEI-----TGKVCG---SEDCLYLSVYT--NNLNBEFKRPLYLVYIHGG 136
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 99 DDDFEGSLDLKVALKMLSLGNNKLVGLKLESDCLYLNVYTPKNTKPKNSKLPVWVYIHGG 158
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
0y 137 GFTIGENHR---DMYGPDPYFIKK--DVYLINIQYRLGALGFLSLSEDLNPNPGNAGKDOY 192
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 159 GFMEFGSGHSLPLSLVDGEIAREGVNIVYSINYLGRGFLSTGDDKLPSSGNTGLDQOR 218
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
0y 193 MLLRMTKNCANFGANPDIVTFEGESAGAASTHYVMLE-----QTRGFLFHRIGLMSGN 246
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 219 LALKWQDIIANFAGGDPNSVYTFEGSAGAAVSULLLSNGGDNPSSSGKGLFHRALISQSGS 278
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
0y 247 AICPMA--NTOCOHRAFTLAKLACYKGEDNDKDVLEFLMAKAKODLLIKLEKVLTLER 303

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Db 279 ALSPWALQSSNARGRAKKEIARLLGC-NFSSSELDCLRSSABEELATRSFLLEFV 337
QY 304 TNKVMF-PFGPTVEPYQFADCVLPKHPREKVTAMGNSIPTMGKNTSYGLEFTSL--- 359
Db 338 PFLPFLFAGPVVDGDPAEPAFPEDEPEELIKGKPADVPYLLGVKKDGGYFAALLNA 397
QY 360 -----KQMLLVKLETELGVNFPSE---LAAERTAPETE-MGAKIKKAHTGE 405
Db 398 SSKGEDELKKEITNDVWLELTKILFYASALNIKMDLADKVLKERYGVDVDFEVSER 457
QY 406 TP7ADNEMDLCSHIYFWMPHMRLLOLRNFHTSGTPVLYKREDFSEDLINPYRIMSGCG 465
Db 458 KP---NIQDMUTDLFLFCPTRVADLPAKH-GSPYAVYAFEDHPASFGIOFLAKRVDBE 513
QY 466 VKGVSHADELTYFPMNOLAKRM---PRESREYKTIERTGTWIOFATGPNYSNIEGME 522
Db 514 FGGAVHGELEIFYGVNPLLEQLYKATTEEBEKSSKTMNMYANFPAKTGNPNNGTENG- 572
QY 523 NVSMDDPIKRSDEVYKCL 539
Db 573 -VVMFKTYSSEQKYSLL 588

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1  RESULT 3
2  US-09-934-323-4
3  : Sequence 4, Application US/09934323
4  : Patent No. US20020150910A1
5  : GENERAL INFORMATION:
6  : APPLICANT: Cutlis, RORY A. J.
7  : TITLE OF INVENTION: 33410. A NOVEL HUMAN CARBOXYESTERASE
8  : TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
9  : FILE REFERENCE: 10448-081001
10 : CURRENT APPLICATION NUMBER: US/09/934,323
11 : CURRENT FILING DATE: 2001-08-21
12 : PRIOR APPLICATION NUMBER: US 60/226,774
13 : PRIOR FILING DATE: 2000-08-21
14 : NUMBER OF SEQ ID NOS: 8
15 : SOFTWARE: FastSeq for Windows Version 4.0
16 : SEQ ID NO 4
17 : LENGTH: 585
18 : TYPE: PRT
19 : ORGANISM: Artificial Sequence
20 : FEATURE:
21 : OTHER INFORMATION: Consensus sequence
22 US-09-934-323-4

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Query Match	23.0%;	Score 707.5;	DB 10;	Length 585;
Best Local Similarity	33.5%;	Pred. No. 1.1e-56;		
Matches 187;	Conservative .83;	Mismatches 223;	Indels 65;	Gaps 19

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Oy      40 GKKKKVKKRTLVY--DSSYYSPFETIYPAQPVPELSEFKPQ--RPFWDSQVRCCHHKRSYQ
Db      11 GAVGVNKEKTNGDSQSVISFLGIPFAEPVGNLNFKAQPKQPKEMSDVLDATKYPSCDQ 70
Oy      98 VDFI-----TGKVCQ---SEDCLYLSVYT--NNLNPETKRPVLVIYHGG 136
Db      71 DDDFGSLSDLKVALKMLSLGWNKRLVGLKLSLSEDCLYLTVYPRKTKPNKSLPVMWHGG 130
Oy      137 GFITGENHR---DMYGPDYFIKK--DYVLINIQYRLGALGELSLNSELPANPGNAG--LKDQ 191
Db      131 GFMFSGSHSLPLSLVDGSLAREGVIVYSINYIRGLGFLSTGDDKLPGSGNYGLLDDQ 190
Oy      192 VMLRLKIKKNCANFGGPNPINTVFGESSGAASTHYMMLTE-----OTRGLFHRIIGMS 245
Db      191 RLALKWQONIAFAFGSDPNSTVITFEESGAGASVLLLSLNSGDNPNPSSKGLFHAISQSG 250
Oy      246 NAICPWA---NTQCOHRAFTLAKIAGYKGEQNDKDVLEFLMKAKPQDILIKIEEVYLTLE 302
Db      251 SALSPPAIISESNAQRARAKELARLLGC--NETSSSELDDCLSRKSAEELLEATRSFLFEY 309
Oy      303 RINKWVF--PFGPVEVYQIADCVLKKHPREMKKTIMAGNSITPMNGNSIYELFTSLT-- 359

```

Db 310 VFPLFLAAGPVVVDGDAEAFIPEDEPEELIKEGKFAVDYLLIGVTIKDEGYFAAMLN 369
QY 360 -----KQMPMLVKELETCVNVPSF---LADAEKTAPELLE-MGAKIKKAHVTG 404
Db 370 ASSGEDELKKTENPDWMLKYLFLYASALNIKMDLADLVAKYPPGVDFDSVES 429
QY 405 ETPADNFMDLCSHIYFMPHRLLOLRFNHTSGTPVYLYRFPDSEDLINPYRIMSGR 464
Db 430 RKP---NLQDMLTDLFLKCPTRVAADLHAH-GSPVYAVFDPHAPASFGIOFLAKRVD 485
QY 465 GVGKVSADLETTYFNMQLAKRM---PKSREYKTIEMTGIWQATGPNPSNEIEGM 521
Db 486 EFGGAVGHDETFEYFGNPLLEKQLYKATEEBSKSSKTMNMYANFAKTCGNPNNGTSNGL 545
QY 522 ENVSMDDPKKSDEYKCL 539
Db 546 --VWPKYTSSEOKYSLL 561

RESULT 4
US-09-748-739A-2
; Sequence 2, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748.739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-2

Query Match 18.6%; Score 571.5; DB 10; Length 602;
Best Local Similarity 29.0%; Pred. No. 4e-44;
Matches 176; Conservative 97; Mismatches 227; Indels 107; Gaps 25;

QY 12 KWKIKCIENKFLNRYLT-----TNETVVAETEGYKVGKRLTYVYDSDYSFEGIP 62
Db 4 KVTIICI-REFLEWFLILCMILIGKSHTEDDIITKNGKVGGM-NLTVFGGTVAFLGIP 60
QY 63 YAOBPVELARFKAPORPTPMDCV-----RDCCNHNKDSV-----QVDFITGK 104
Db 61 YAOBPPLRLRKRKPKQSLTKWSDINNAATKYANSCQNDIDQSPGFGHSEMMNPNTDL--- 116
QY 105 VCGSEDLVLSVTYNNINPETKRPVLVYIHGGFLIGENHHRDYGPDYFIKD--VVLINI 163
Db 117 ---SEDLVILNWIIPAPKPK-NATVILMIWYGSGFOTGSSLSHYVDKGFALAEVERIYVSM 172
QY 164 QYRLGALGFLSL--NSEDLVNPGNAGLKDOYALRWIKNNCANFGNPDNITVFGESAGA 221
Db 173 NYRGALGFLALPGNPE---APGNMGJLFDQDLALQWQKNIAGFGNPKSVTLFGESAGA 229
QY 222 ASTHYMMLTBETRGFLFRHGLMSGNATCPMANT---OCQNHAFPLAKLAGYKGEDNCKDV 278
Db 230 ASVSLHLILSPGSHLFTFRAIILQSGSFNAPMAVTSLYEARNNTLMLAKLTGCSRE-NETEI 288
QY 279 LEFLMKAKPODLIKLEEVLTLEERTNKVMPFGPTVEPYOTADCVLPKPHREWAKTAMG 338
Db 289 IKCIRNNDPOEILNFAFVYV---GTPLSVNFPGPTVDGDLTDM---PDILLELGQF 340
QY 339 NSIPTMGNNTSYEGLEFSTSIKQMPMLVKELETCVNVPSSELADAERT-APETLEMGAKI 397
Db 341 KKTQILVGVNDEGTWF--LVYGAPGFSKDNNSIIT--TRKEFGGLKIFPGVSEFGKES 396

QY 398 KKAHVTG--ETPTADNFMD-----LCSHIYF-----WPMHRLLOLRFNHTSG 438
Db 397 ILFHYTMDWDQRENTREALGDVGYNFIQCPALFETKRESEM-----G 441
QY 439 TPVLYLRFPDSEDLINPYRIMSGRGVKGVSHADELTFFWNOLAKRMPRESREYKTE 498
Db 442 NNAFFYYFEHRSSKLPEWEM-----GVMHGYEIEFVGLPLERDNTYKAEILSR 493
QY 499 RMTGIMQFATGTPNPSIEEGMENVSMDPIKKSDEYKCLANISDELKMDIVPEMDIKQ 558
Db 494 SIVRMANFAKYGNP--NETQN-NSTSWPKSTEQKYTLTN-TESTRIMTKLRAGQCRF 549
QY 559 WESMEFEK 565
Db 550 WTSFEPPK 556

RESULT 5
US-09-748-739A-6
; Sequence 6, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748.739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-6

Query Match 18.4%; Score 565; DB 10; Length 574;
Best Local Similarity 29.0%; Pred. No. 1.5e-43;
Matches 168; Conservative 95; Mismatches 220; Indels 96; Gaps 23;

QY 31 ETVVAETEGYKVGKRLTYVYDSDYSFEGIPYAPQPRYGEIARFAPORPTPMDCV----- 85
Db 2 DDIIITATKNGKVGGM-NLTVFGGTVAFLGIPYAPQPRYGEIARFAPORPTPMDCV----- 85
QY 86 --RDCCNHNKDSV-----QVDFITGKVGSEDLVLSVTYNNINPETKRPVLVY 132
Db 61 YANSCQNDIDQSPGFGHSEMMNPNTDL-----SEDLVILNWIIPAPKPK-NATVILMI 112
QY 133 IHGGFLIGENHHRDYGPDYFIKD--VVLINIQYRLGALGFLSL--NSEDLVNPGNAGLK 189
Db 113 IYGGFGFGTSSLYHYDQKFLAEVERIYVSMNYRNGALGFLALPGNPE---APGNMGJL 169
QY 190 DQWALNRIRKNNCANFGNPDNITVFGESAGAASHYMMLTBQTRGLFRHGLMSGNATC 249
Db 170 DQDLALQWQKNIAGFGNPKSVTLFGESAGAASVSLHLSPGSHLFTFRAIILQSGSFNA 229
QY 250 PMANT---OCQNHAFPLAKLAGYKGEDNCKDVLEFLMKAKPODLIKLEEVLTLEERTNK 306
Db 230 PMATVTSLEARNRNLNLAFLKLTGCSRE-NETELICLRKPDQOELILNFAFVYV---GTQ 285
QY 307 VMPFGPTVEPYOTADCVLPKPHREWAKTAMGSIPTMGNNTSYEGLEFSTSIKQMPMLV 366
Db 286 LSVNFGPTVDGDLTDM---PDILLELGQFKKQTLVGVNKEGTAF--LVYGAPGFS 338
QY 367 KELETCVNVPSSELADAERT-APETLEMGAKIKKAHVTG--ETPTADNFMD----- 414
Db 339 KDNNSIIT--TRKEFGGLKIFPGVSEFGKESILFHYDWDQDQRENTREALGDVGY 396
QY 415 --LCSHIYF-----WPMHRLLOLRFNHTSGTPVYLYRFPDSEDLINPYRIMSGRGV 466

Db 397 NFIGALEFTKKFSEW-----GNNAFYFEHRSSKLPWEMM----- 434
Qy 467 KGVSHADELTYFFWNOQLAKRMPKESREKYTEIRMTGIMIOFATGPNPYNEIEGEMVSW 526
Db 435 -GVMHGEIEFVGLPLERRDNVTKAEILSRISIVKRANFAKGNP--NETON-NSTSW 490
Qy 527 DPKKSEVYKCLNISDELKMDVPEMDKIKOWESMEFK 565
Db 491 PVFKSTEQKYLTLN-TESTRIMTKLRAOCCRFWTSFEPK 528

RESULT 6
US-09-748-739A-8
Sequence 8, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Walkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 574
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-8

Query Match 18.48; Score 564; DB 10; Length 574;
Best Local Similarity 29.08; Pred. No. 1.8e-43;
Matches 168; Conservative 94; Mismatches 221; Indels 96; Gaps 23;
Qy 31 ETVVAETEGYKGVKRLTYVDSYSFEGIPYAOPVGELEKRAQRPMPDGV----- 85
Db 2 DDIITATKNGVYRGV-NLTVFGTVAFLGIPYAOPVGELEKRAQRPMPDGV----- 60
Qy 86 --RDCNHRKDSV-----QVDFITGKVGSEDCLYLSYTNLNPETKRPVLY 132
Db 61 YANSCQWIDQSPFGHSEGMNPNITDL-----SEDCLYLNWIPAPRK-NATVLIW 112
Qy 133 IHGGFTIIGENHRDYGPDYFIKRD-VVLINIOYRLGALGLSL--NSEDLNPGNGLK 189
Db 113 IYGGFQGTSSLHYDCKFLARVERIVYVSMNRVGLGLALPGNE--ARGNGLF 169
Qy 190 DQVALMRITKNNCANFGNPNITVGEESAGASTHYMLTEQTRGLFHRGILMSGNAIC 249
Db 170 DQGLALWQKRIAAFGGPKSVTLFEGSAGASVSLHLSPGSHSLFTRAILDQSGSFNA 229
Qy 250 PMANT---OCQRAFTIAGYKGEDNDKYLEFLMAKPODLIKLEKYLTEERTNK 306
Db 230 PMAVISLYEARRNTLNALATGCSRE-NETETIKLRKNDQOELILNFAFVVPY---GTS 285
Qy 307 VMFPFGTVEPYQTADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLFSTILKOMPMLV 366
Db 286 LSVNFGPTVDGDFLIDM-----PDILLELGQFKKTOILLGVNKKDGTAF--LVYGAPGFS 338
Qy 367 KELETGVNFPSELDAERT-APETLEMGAKIKKAHVTC--ETPADNFM----- 414
Db 339 KDNNSIT--TRKEFQGLKIFPPGVSEFKESILFHYTWDQDPENYREALGVDY 396
Qy 415 --LCSHIYF-----WPMHRLQLRFNHTSGTPVLYLFEDDSDDLNPYIMSGRGV 466
Db 397 NFIGALEFTKKFSEW-----GNNAFYFEHRSSKLPWEMM----- 434
Qy 467 KGVSHADELTYFFWNOQLAKRMPKESREKYTEIRMTGIMIOFATGPNPYNEIEGEMVSW 526
Db 435 -GVMHGEIEFVGLPLERRDNVTKAEILSRISIVKRANFAKGNP--NETON-NSTSW 490

Qy 527 DPKKSEVYKCLNISDELKMDVPEMDKIKOWESMEFK 565
Db 491 PVFKSTEQKYLTLN-TESTRIMTKLRAOCCRFWTSFEPK 528

RESULT 7
US-09-748-739A-17
Sequence 17, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Walkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 574
TYPE: PR
ORGANISM: Homo sapiens
US-09-748-739A-17

Query Match 18.38; Score 563; DB 10; Length 574;
Best Local Similarity 29.08; Pred. No. 2.3e-43;
Matches 168; Conservative 94; Mismatches 221; Indels 96; Gaps 23;
Qy 31 ETVVAETEGYKGVKRLTYVDSYSFEGIPYAOPVGELEKRAQRPMPDGV----- 85
Db 2 DDIITATKNGVYRGV-NLTVFGTVAFLGIPYAOPVGELEKRAQRPMPDGV----- 60
Qy 86 --RDCNHRKDSV-----QVDFITGKVGSEDCLYLSYTNLNPETKRPVLY 132
Db 61 YANSCQWIDQSPFGHSEGMNPNITDL-----SEDCLYLNWIPAPRK-NATVLIW 112
Qy 133 IHGGFTIIGENHRDYGPDYFIKRD-VVLINIOYRLGALGLSL--NSEDLNPGNGLK 189
Db 113 IYGGFQGTSSLHYDCKFLARVERIVYVSMNRVGLGLALPGNE--ARGNGLF 169
Qy 190 DQVALMRITKNNCANFGNPNITVGEESAGASTHYMLTEQTRGLFHRGILMSGNAIC 249
Db 170 DQGLALWQKRIAAFGGPKSVTLFEGSAGASVSLHLSPGSHSLFTRAILDQSGSFNA 229
Qy 250 PMANT---OCQRAFTIAGYKGEDNDKYLEFLMAKPODLIKLEKYLTEERTNK 306
Db 230 PMAVISLYEARRNTLNALATGCSRE-NETETIKLRKNDQOELILNFAFVVPY---GTP 285
Qy 307 VMFPFGTVEPYQTADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLFSTILKOMPMLV 366
Db 286 LSVNFGPTVDGDFLIDM-----PDILLELGQFKKTOILLGVNKKDGTAF--LVYGAPGFS 338
Qy 367 KELETGVNFPSELDAERT-APETLEMGAKIKKAHVTC--ETPADNFM----- 414
Db 339 KDNNSIT--TRKEFQGLKIFPPGVSEFKESILFHYTWDQDPENYREALGVDY 396
Qy 415 --LCSHIYF-----WPMHRLQLRFNHTSGTPVLYLFEDDSDDLNPYIMSGRGV 466
Db 397 NFIGALEFTKKFSEW-----GNNAFYFEHRSSKLPWEMM----- 434
Qy 467 KGVSHADELTYFFWNOQLAKRMPKESREKYTEIRMTGIMIOFATGPNPYNEIEGEMVSW 526
Db 435 -GVMHGEIEFVGLPLERRDNVTKAEILSRISIVKRANFAKGNP--NETON-NSTSW 490
Qy 527 DPKKSEVYKCLNISDELKMDVPEMDKIKOWESMEFK 565
Db 491 PVFKSTEQKYLTLN-TESTRIMTKLRAOCCRFWTSFEPK 528

RESULT 8
US-09-748-739A-20
Sequence 20, Application US/09748739A

```
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-748-739A-20

Query Match          18.3%; Score 563; DB 10; Length 574;
Best Local Similarity 29.0%; Pred. No. 2,3e-43;
Matches 168; Conservative 94; Mismatches 221; Indels 96; Gaps 23;

OY 31 ETVVAETEGYKVKVRLTVYDSDYSFEGIPYAPVGEIRKAPQRPMPDGV----- 85
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 DDIIATKNGKVRGM-NLTVEGTVTAFLGIPYAPGLRFRKKPQSLTKMSDIMNATK 60
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 86 --RCCNHKDSV-----QVDFITGKCGSEDCILSYTNNLNPETRKRVLY 132
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YANSCCONIDSPFGHSEGMNPNPTDL-----SEDCILNWIWIPAPKPK-NATVLIW 112
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 133 IHGGFTIGENHRDMYGPDPYFIKRD-VVLINIOYRLGALGFLSL--NSEDLVNPGNAGLK 189
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 IYGGFGTGTSSLHYDGKFLARVERIVYVSMNTRVAGLGLALPGNE--AAGNMGFLF 169
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 190 DQVALRMKKNKCNFGNPNITVFGESAGASTHYMTEQTRGLFHRGILMSGNAIC 249
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 DQDALQWQVKNIAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILLOGSFNA 229
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 250 VMFPGPTVEYQYADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFSTILKOMPIV 366
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 PMATVSYEARNRKTLNLAKLKLGCSRE-NETELICLRKRDQDEILNFAFVVPY--GTP 285
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 307 VMFPGPTVEYQYADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFSTILKOMPIV 366
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 LSVNFGPTVDGDFLDM-----PDILLELQGFKKQLIVGNKDEGTAFA--LVYGARPGFS 338
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 367 KELETGVNVPVSELADEART-APETLEMGAKIKKAHYTG--ETPADNPMD----- 414
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 339 KDNNISII--TRKEFOEGKIFFPVSEFGKESILFHYTDWDDORPENYREALGDVVG 396
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 415 --LCSHYF-----WPFMRHLQLRFNHTSGTPVLYLRPDESDLLINPRIRMSGGV 466
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 397 NFICPALEFTKKFSEW-----GNNAFYFEEHRSKSLPWPWM----- 434
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 467 KGVSHADELTFYFNNOLAKRMPKESREYKTIERTMTGIOWPATGNPNYSNETEGMENYSW 526
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 435 -GVNHGYEIEFVGLPLERRNRYTKAEILSRISYVKKRANAKKYGNP--NETQN-NSTSW 490
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 527 DPIKSDDEVYKCLNISDELKMIIDVPEMDIKOMESMFEK 565
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 491 PVFKSTQKYLTLN-TESTRIMTKLRAQOCRFMTSFFPK 528
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-748-739A-4
; Sequence 4, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 574
; TYPE: PRT
```

```
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
; US-09-748-739A-4

Query Match          18.3%; Score 561; DB 10; Length 574;
Best Local Similarity 29.0%; Pred. No. 3,5e-43;
Matches 168; Conservative 94; Mismatches 221; Indels 96; Gaps 23;

OY 31 ETVVAETEGYKVKVRLTVYDSDYSFEGIPYAPVGEIRKAPQRPMPDGV----- 85
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 DDIIATKNGKVRGM-NLTVEGTVTAFLGIPYAPGLRFRKKPQSLTKMSDIMNATK 60
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 86 --RCCNHKDSV-----QVDFITGKCGSEDCILSYTNNLNPETRKRVLY 132
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YANSCCONIDSPFGHSEGMNPNPTDL-----SEDCILNWIWIPAPKPK-NATVLIW 112
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 133 IHGGFTIGENHRDMYGPDPYFIKRD-VVLINIOYRLGALGFLSL--NSEDLVNPGNAGLK 189
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 IYGGFGTGTSSLHYDGKFLARVERIVYVSMNTRVAGLGLALPGNE--AAGNMGFLF 169
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 190 DQVALRMKKNKCNFGNPNITVFGESAGASTHYMTEQTRGLFHRGILMSGNAIC 249
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 DQDALQWQVKNIAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILLOGSFNA 229
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 250 VMFPGPTVEYQYADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFSTILKOMPIV 366
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 PMATVSYEARNRKTLNLAKLKLGCSRE-NETELICLRKRDQDEILNFAFVVPY--GTP 285
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 307 VMFPGPTVEYQYADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFSTILKOMPIV 366
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 LSVNFGPTVDGDFLDM-----PDILLELQGFKKQLIVGNKDEGTAFA--LVYGARPGFS 338
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 367 KELETGVNVPVSELADEART-APETLEMGAKIKKAHYTG--ETPADNPMD----- 414
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 339 KDNNISII--TRKEFOEGKIFFPVSEFGKESILFHYTDWDDORPENYREALGDVVG 396
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 415 --LCSHYF-----WPFMRHLQLRFNHTSGTPVLYLRPDESDLLINPRIRMSGGV 466
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 397 NFICPALEFTKKFSEW-----GNNAFYFEEHRSKSLPWPWM----- 434
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 467 KGVSHADELTFYFNNOLAKRMPKESREYKTIERTMTGIOWPATGNPNYSNETEGMENYSW 526
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 435 -GVNHGYEIEFVGLPLERRNRYTKAEILSRISYVKKRANAKKYGNP--NETQN-NSTSW 490
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 527 DPIKSDDEVYKCLNISDELKMIIDVPEMDIKOMESMFEK 565
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 491 PVFKSTQKYLTLN-TESTRIMTKLRAQOCRFMTSFFPK 528
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-09-748-739A-19
; Sequence 19, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 574
; TYPE: PRT
```

```

; ORGANISM: Homo sapiens
US-09-748-739A-19
      18.2%: Score 558; DB 10; Length 574;
Query Match      29.0%: Pred. No. 6.5e-43;
Best Local Similarity 93; Mismatches 222; Indels 96; Gaps 23;
Matches 168; Conservative

OY 31 ETVAATEYGVKVKRLLTYDDSYSEFEGIPYAPPGVGLRFAKAPQRTPMWGV----- 85
    2 DDIITATKNGKVRGM-NLTVFGGTVAFLGIPYAPPLGRKFRKKQSLTKMSDINWATK 60
    66 --RDCCNHKKDSV-----QVDFITGKVGSEDCLYLSTYNNLNPETRKRVLY 132
    61 YANSCCQNTIDQSPFGFHGSEMNPNTDL-----SEDCLYLWVWIPAKPKR-NATVLIW 112
    133 IHGGGFTIGENHRDMYGPDPYFIKKD-VVLINIOYRIGALGFLSL--NSEDLNPGNAGLK 189
    113 IYGGGQGTGTSLSHYDGFARVERIVVSMNYRVGALGFALGNPE--APGNMGIF 169
    190 DOYVALRWIKNNCANFGNPNITVFGESAGAASHYMWLTQOTGFLPHRGILMSGNATC 249
    170 DQALALWQKNIARFAGNPKSVTLFGESAGASVSLHLSPSGSHSLFTRALLQSGSEFA 229
    OY 250 PMAWT---QOCHRAFTLAKIAGYKKGEDNDKDVLEFLMAKAPDOLIKLEEKVLTLEERTNK 306
    230 PMAVITLYEARNTLMLAKLTGCSRE-NETETIKCLRNKDPQELLNEAFVVPY--GTP 285
    OY 307 VMEPFGEYEPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFTSLIKQMPILV 366
    286 LSNVFGTVDGFLTDM-----PDILLELGQFKKTOILVGNKDEGTAF--LVYGAPGFS 338
    OY 367 KELETGVNPEPSLADAERT-APETLEMGAKIKKAHVVG--ETPRADNPM----- 414
    339 KDNNSTI--TRKEQOGLKIFEPGVSEFGKESLTFHTDWDQORENREALGDVGVGY 396
    OY 415 --LCSHIYF-----WEPHRLQLRENTSGTPVYLYRFDSEDLINPYRIKSGRGVY 466
    397 NFICPALEFTRKSEW-----GNNAFFYYFEHRSSKLPWPEWM----- 434
    OY 467 KGVSHADELYFFWNOAKRMKREKXTIENTGIMIOFATTGNPNEIEGMENVS 526
    435 -GVNHGYEIEFVGLPRLERDNTYKAEELISRSIVKRWANFAKYGNP--NETON-NSTSW 490
    OY 527 DPKKSDVYKCLNISDELKMIIDVPEMDKIKOWESMEK 565
    491 PVKSTVQKYLTLN-TESTRIINTLRAQOCRFWTSFPPK 528
    DB

RESULT 11
US-09-748-739A-21
; Sequence 21, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-748-739A-21
      18.2%: Score 558; DB 10; Length 574;
Query Match      29.2%: Pred. No. 6.5e-43;
Best Local Similarity 100; Mismatches 232; Indels 72; Gaps 21;
Matches 167; Conservative

OY 31 ETVAATEYGVKVKRLLTYDDSYSEFEGIPYAPPGVGLRFAKAPQRTPMWGV----- 85
```

```

    2 EDIIITTKNGKVRGM-NLTVLGGTVAFLGIPYAPPLGRKFRKKQSLTKMSINWATK 60
    OY 86 --RDCCNHKKDSVQVDFITGKVG-----SEDCLYLSTYNNLNPETRKRVLYIHGGGF 138
    61 YANSCCQNTIDQSPF-GFLGSEMNPNTLSEDCLYLWVWIPAKPKR-NATVIMWIYGGGF 118
    OY 139 IIGENHRDMYGPDPYFIKKD-VVLINIOYRIGALGFLSLNSEDLNPGNAGLKDOYVALRW 197
    119 QGTGSSLPYVDGFLARVERIVVSMNYRVGALGFAL--SENDEAGNGLDQDQALW 177
    OY 198 IKNNCANFGNPNITVFGESAGAASHYMWLTQOTGFLPHRGILMSGNATCMAWT--- 254
    178 VOKNIAAFGCGNPSVTLFGESAGASVSLHLSPSRQPLFTRAILQSGSNAPMAWTSLY 237
    OY 255 QOCHRAFTLAKIAGYKKGEDNDKDVLEFLMAKAPDOLIKLEEKVLTLEERTNKVMEPFGE 314
    238 EARRKTLTAKRMCC-SRDNETEMIKLRDKDQELLNEAFVVPY--TLTSLVNGFP 293
    OY 315 VEPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFTSLIKQMPILVKELETCVN 374
    294 VDGEFLTDM-----PDTLLQGLQFKRTQILVGNKDEGTAF--LVYGAPGFSKDNNSIT- 345
    OY 375 FVPSLADAERT-APETLEMGAKIKKAHVVG--ETPRADNPM-----LCSHIY 420
    346 -TRKEFOGLKIFEPGVSEFGRESILFHYMDLDDQRAENREALDQVGVYNNICPALE 404
    OY 421 FWFPHRLQLRFNHTSGTPVYLYRFDSEDLINPYRIKSGRGVSHADELYTFEW 480
    405 FTRKSEL-----GNDAFFYYFEHRSTKLWPEWM-----GVNHGYEIEFVFG 447
    OY 481 NOLAKRMKRESEYKTIERMGTGIMIOFATTGNPNPNEIEGMENVS--WPIKSDVYK 538
    448 IPLERVNTYTRAEELISRSIKRWANFAKYGNP-----NGTQNNSTNPVKESTQKYL 502
    OY 539 INISDELKMIIDVPEMDKIKOWESMEKRD 569
    503 LN-TESPKVYTKLRAQOCRFWTLFPPKYLEL 532
    DB

RESULT 12
US-09-748-739A-18
; Sequence 18, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-18
      18.1%: Score 556; DB 10; Length 574;
Query Match      28.8%: Pred. No. 1e-42;
Best Local Similarity 94; Mismatches 222; Indels 96; Gaps 23;
Matches 167; Conservative

OY 31 ETVAATEYGVKVKRLLTYDDSYSEFEGIPYAPPGVGLRFAKAPQRTPMWGV----- 85
    2 DDIITATKNGKVRGM-NLTVFGGTVAFLGIPYAPPLGRKFRKKQSLTKMSDINWATK 60
    OY 86 --RDCCNHKKDSV-----QVDFITGKVGSEDCLYLSTYNNLNPETRKRVLY 132
    61 YANSCCQNTIDQSPFGFHGSEMNPNTDL-----SEDCLYLWVWIPAKPKR-NATVLIW 112
    OY 133 IHGGGFTIGENHRDMYGPDPYFIKKD-VVLINIOYRIGALGFLSL--NSEDLNPGNAGLK 189
```


Db 113 IYGGFQGTGSSSLHYGKFLARERIVYVMNRVAGALGFLAPGPE---AGNMGFL 169
QY 190 DQVVALFMKNNKNCANFGNDPNITVFGESAGASTHYMMLTEOTRGLFHRGILMSGNAIC 249
Db 170 DQALALWQVOKNIAAFGNSPVTLNFGESAGASVSLHLSFGSHSLFTRAILDQSSSFA 229
QY 250 PMAT---QOCHRAFTLAKLAGYGEDNDKVLEFLMKARQDILKLEKVLTEERTNK 306
Db 230 PMATSYLEARNRNLAKLKGCSRE-NETETIKCLRNDQOELLWEAFVVPY---GTP 285
QY 307 VMFPFGTVEPYQTADCVLPKHPREMYKTAMGNSIPTMNGTSYEGLEFSTILKOMPALV 366
Db 286 LSVAFGPTVDDFLTDM-----PDILLELGFKTKQILVGNKDEGTAFA--LVYGAPGFS 338
QY 367 KELETQVNFVPELADERT-APETLEMGAKIKRAHVGT--ETPTADNEMD----- 414
Db 339 KDNNSII--TRKEFOEGKIFPFGVSEFGKESILFHYTDWVDQRPENYREALGDVYGDY 396
QY 415 --LCSHYE-----WPMHRLLOLRNHTSGTPVLYLRFPDSEDLINPYRIRSGGV 466
Db 397 NFICPALEFKKESW-----GNNAFYFEHRSSKLPWPKM----- 434
QY 467 KGVSHADELTYFFMNOLAKRMPKESREXTIERMTGIMIOFATGPNPYNEIEGEMENYSV 526
Db 435 -GVHGYEIEFVGLPRLERRNNTKAEILSRSTYVKRANPAKYGNP--NETQN-NSTSW 490
QY 527 DPKSKDEYVKCLNISDELKMDVPEMDKIKOMESMEK 565
Db 491 PVFKSTOKYLTLLN-TESTRIMTRLRAQOCRFWTSPFPK 528

RESULT 13

US-09-748-739A-22
; Sequence 22, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748, 739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ. ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Felis catus
US-09-748-739A-22

Query Match 18.0%; Score 554; DB 10; Length 574;
Best Local Similarity 28.1%; Pred. No. 1.5e-42;
Matches 167; Conservative 100; Mismatches 201; Indels 126; Gaps 24;

QY 31 ETVAEPEYGVKVKRLTYVDDSYSPGIPYQAPRGELRFRAPQPTWMDGV----- 85
Db 2 EDIITTKNGKVRGM-NLPVLDGTVAFVAGIPYQAPRGELRFRAPQPTWMDGV----- 60
QY 86 --RDCSNHKDSV-----QVDFITGKVGSEDCILYVYTNLNEPFRKPVLY 132
Db 61 YANSCYQNAODSPFGFPGSEMMNNTDL-----SEDCILYVYTNLNEPFRKPVLY 112
QY 133 IHGGFIIIGENHRDMYGPDYFIKRD-VVLINIOYRLAGLGLSL--NSEDLVNPGNAGLK 189
Db 113 IYGGFQGTGSSSLPYDQKFLARERIVYVMNRVAGALGFLAPGPE---AGNMGFL 169
QY 190 DQVVALFMKNNKNCANFGNDPNITVFGESAGASTHYMMLTEOTRGLFHRGILMSGNAIC 249
Db 170 DQALALWQVOKNIAAFGNSPVTLNFGESAGASVSLHLSFGSHSLFTRAILDQSSSFA 229
QY 250 PMAT---QOCHRAFTLAKLAGYGEDNDKVLEFLMKARQDILKLEKVLTEERTNK 306

Db 230 PMATMSDEAKNRRLTLAKLFGC--SKENDTEIICLRKNDQOELL-LNELLVVSDDTLLS 287
QY 307 VMFPFGTVEPYQTADCVLPKHPREMYKTAMGNSIPTMNGTSYEGLEFSTILKOMPALV 366
Db 288 V--NFGVPVDDFLTDM-----PDTLLQLGFKTKQILVGNKDEGTAFA--LVYGAPGFS 338
QY 367 KELETQVNFVPELADERT-APETLEMGAKIKRAHVGT--ETPTADNEMD----- 400
Db 339 KDNNSII--TRKEFOEGKIFPFGVSEFGKESILFHYTDWVDQRPENYREALGDVYGDY 390
QY 401 HVTE-----PPTAD--NEMDLSHYEPMHRLLOLRNHTSGTPVLYLRFPDSEDL 453
Db 391 DVLGDYNICALLETTKFSGLGNNAPFYFEHRSSQLPW-----PEM----- 434
QY 454 INPYRIRSGRGVGVSHADELTYFFMNOLAKRMPKESREXTIERMTGIMIOFATGPN 513
Db 435 --LCSHYE-----WPMHRLLOLRNHTSGTPVLYLRFPDSEDLINPYRIRSGGV 466
QY 514 YSNEIEGEMENYS--WDPKSKDEYVKCLNISDELKMDVPEMDKIKOMESMEK 565
Db 481 -----NETQNNSTSWPAPRSTOKYLTLLN-AESPKVYTKLRAQOCRFWTSPFPK 528

RESULT 14

US-09-738-626-4754
; Sequence 4754, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ. ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4754
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4754

Query Match 17.8%; Score 548; DB 9; Length 537;
Best Local Similarity 29.2%; Pred. No. 4.9e-42;
Matches 169; Conservative 97; Mismatches 220; Indels 92; Gaps 22;

QY 31 ETVAEPEYGVKVKRLTYVDDSYSPGIPYQAPRGELRFRAPQPTWMDGV----- 85
Db 3 DEMVVPSTGVGVKVK-----GPGKTKWRGILPYGNTGKTYFRAPRAKKWDGVRDCSN 57
QY 91 HKDSVQVDFI-TGKVGSEDCILYVYTNLNEPFRKPVLYIYHGGFIIIG-ENHRDMY 148
Db 58 FGEVASOPTYVWTDKIRSEDCILNDVY--RPDSEKLPVYVYLLHGGFIIIGSSSEKRLR 115
QY 149 GPDYFIKRDVVLINIOYRLAGLGLSLNSEDLVNPGNAGLKDQVVALFMKNNKNCANFGN 208
Db 116 GYNLVNMMNVYVSVNFRGLAGYLDLRSVGEDCVANBALHDQALLQWVSRLNEAFGSD 175

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 2944.03 Seconds

(without alignments)
16933.650 Million cell updates/sec

Title: US-09-776-910-9

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

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6: gb_pat:*
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11: gb_sts:*
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13: gb_un:*
14: gb_vl:*
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19: em_mu:*
20: em_om:*
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27: em_sts:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	100.0	1713	6	ARI53442 Sequence
2	1711.4	99.9	1713	6	ARI53438 Sequence
3	1711.4	99.9	1713	6	ARI53439 Sequence
4	1708.2	99.7	1713	6	ARI53440 Sequence
5	1703.4	99.4	1713	6	ARI53441 Sequence
6	1703.4	99.4	1713	6	ARI53441 Sequence
7	1703.4	99.4	1713	6	ARI53441 Sequence
8	1678.2	98.0	1713	6	ARI53441 Sequence
9	987.2	57.6	2160	3	ARI53341 Musca dom
10	959.4	56.0	2175	3	ARI533082 Haematobi
11	956.6	55.8	1710	6	ARI53445 Sequence
12	678.8	39.6	2017	3	ARI51473 Drosophila
13	378.6	22.1	2660	3	ARI51675 Drosophila
14	375.4	21.9	2820	3	DMU51050 Drosophila
15	370.6	21.6	5735	2	AC015272 Drosophila
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17	370.6	21.6	197597	3	AC011253 Drosophila
18	370.6	21.6	309023	3	AE003671 Drosophila
19	363.8	21.2	1962	3	AY051497 Drosophila
20	323	18.9	2122	3	AY058637 Drosophila
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34	238.2	13.9	309023	3	AE003671 Drosophila
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36	227.6	13.3	2401	3	DMU51054 Drosophila
37	224.2	13.1	933	3	AF216216 Drosophila
38	224.2	13.1	1836	3	COESTRA2EA Drosophila
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41	214	12.5	84252	2	AC009207 Drosophila
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43	207.4	12.1	6028	3	AF177382 Culex pipie
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ALIGNMENTS

RESULT 1
LOCUS ARI53442 1713 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6235515.
ACCESSION ARI53442
VERSION ARI53442.1 GI:15120974
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.,Joyce., Newcomb,R.,David., Campbell,L.,P.Malcolm.,
Robin,G.,Charlesde,Quetleville., Claudianos,C., Smyth,K.,A.,
Boyce,T.,Mark., Oakeshott,J.,Graham. and Brownlie,J.,Colin.
TITLE Malathion carboxylesterase

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: US 6235515-A 9 22-MAY-2001;
FEATURES Location/Qualifiers
Source 1.1713
/organism="unknown"
BASE COUNT 515 a 305 c 370 g 523 t
ORIGIN

Query Match 100.0%; Score 1713; DB 6; Length 1713;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGATTTTCAACGTTAGTTTGTAGAGAAATTAATGAAGATTAAATGATGTAAT 60
OY 61 AAGTTTAACTATCGTTTAACTCAATGAACGTTGTAAGTGAATGAAATATGGC 120
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RESULT 2
ARI53438 1713 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
ORGANISM
SOURCE
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
1.1713
location/Qualifiers

Unclassified.
1 (bases 1 to 1713)
Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Robin, G. Charles, Queteville., Claudianos, C., Smyth, K.-A.,
Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Collin.
Malachon carboxylesterase
Patent: US 6235515-A 1 22-MAY-2001;
location/Qualifiers
1.1713

BASE COUNT 515 a 304 c 370 g 524 t
ORIGIN

Query Match 99.9% Score 1711.4; DB 6; Length 1713;
Best Local Similarity 99.9% Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3
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LOCUS ARI53439
DEFINITION Sequence 3 from patent US 6235515.
ACCESSION ARI53439
VERSION ARI53439.1 GI:15120971
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Robin, G. Charlesde, Quetleville., Claudianos, C., Smyth, K. A.,
Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 3 22-MAY-2001;
FEATURES location/Qualifiers
1..1713
BASE COUNT 515 a 306 c 370 g 522 t
ORIGIN

Query Match	99.9%	Score 1711.4	DB 6	Length 1713	
Best Local Similarity	99.9%	Pred. No. 0			
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					Gaps 0
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DB	1	ATGAAATTCACGTTAGTTGATGGAATAAATAAGGAATTAATGATGAAAT	60		
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OY	541	AAATGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG	600		
DB	541	AAATGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG	600		
OY	601	AAATGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG	660		
DB	601	AAATGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG	660		
OY	661	GCTGCTCTACCCACTGATGATGATGATGATGATGATGATGATGATGATG	720		
DB	661	GCTGCTCTACCCACTGATGATGATGATGATGATGATGATGATGATGATG	720		
OY	721	ATTAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATG	780		
DB	721	ATTAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATG	780		
OY	781	TTACACTTAGCCAAATGTCGCTATAGGATGATGATGATGATGATGATGAT	840		
DB	781	TTACACTTAGCCAAATGTCGCTATAGGATGATGATGATGATGATGATGAT	840		
OY	841	TTTCTTATGAAAGCCACACAGATTAATAAAGTGAAGAAAGTTTAACTCTA	900		
DB	841	TTTCTTATGAAAGCCACACAGATTAATAAAGTGAAGAAAGTTTAACTCTA	900		
OY	901	GAAGACGCTACAAATAGGTCATGTTCTTTTGGTCCACATGTTGACCATAT	960		
DB	901	GAAGACGCTACAAATAGGTCATGTTCTTTTGGTCCACATGTTGACCATAT	960		
OY	961	GCTGATGCTCTTACCAACATCTCGGAAATGTTAAACCTGTTGGGTAATTC	1020		
DB	961	GCTGATGCTCTTACCAACATCTCGGAAATGTTAAACCTGTTGGGTAATTC	1020		

OY	1021	ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1080		
DB	1021	ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1080		
OY	1081	CAATGCTATGCTGTTTAAAGATTTGAACCTGTGTCAATTTTGGCCAGTATG	1140		
DB	1081	CAATGCTATGCTGTTTAAAGATTTGAACCTGTGTCAATTTTGGCCAGTATG	1140		
OY	1141	GCTGATGCTGAACGACCGCCCAAGACCTTGAATAGGCTGCTAAATTAAGGCT	1200		
DB	1141	GCTGATGCTGAACGACCGCCCAAGACCTTGAATAGGCTGCTAAATTAAGGCT	1200		
OY	1201	CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTCATCTAT	1260		
DB	1201	CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTCATCTAT	1260		
OY	1261	TTCTGTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATG	1320		
DB	1261	TTCTGTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATG	1320		
OY	1321	GCTACTTGTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG	1380		
DB	1321	GCTACTTGTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG	1380		
OY	1381	CGTATGAGCGTGTGTTAAGGCTGATGATGATGATGATGATGATGATGATG	1440		
DB	1381	CGTATGAGCGTGTGTTAAGGCTGATGATGATGATGATGATGATGATGATG	1440		
OY	1441	AATCAATGGCCAAACGATGCTTAAGAAATGCGTGATGATGATGATGATGATG	1500		
DB	1441	AATCAATGGCCAAACGATGCTTAAGAAATGCGTGATGATGATGATGATGATG	1500		
OY	1501	ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1560		
DB	1501	ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1560		
OY	1561	ATGGAATATGTTCTGCGATGATGATGATGATGATGATGATGATGATGATG	1620		
DB	1561	ATGGAATATGTTCTGCGATGATGATGATGATGATGATGATGATGATGATG	1620		
OY	1621	ATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1680		
DB	1621	ATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1680		
OY	1681	TCGATGTTGAAAACATAGAGATTAATTTAG	1713		
DB	1681	TCGATGTTGAAAACATAGAGATTAATTTAG	1713		

RESULT 4	AR153440	1713 bp	DNA	Linear	PAT 08-AUG-2001
LOCUS	AR153440				
DEFINITION	Sequence 5 from patent US 6235515.				
ACCESSION	AR153440				
VERSION	AR153440.1	GI:15120972			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1713)				
AUTHORS	Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolm, Robin, G. Charles, Quetleville, Claudianos, C., Smyth, K. A., Boyce, T. Mark, Oakeshott, J. Graham, and Brownlie, J. Collin.				
TITLE	Malathion carboxylesterase				
JOURNAL	Patent: US 6235515-A 5 22-MAY-2001.				
FEATURES	Location/Qualifiers				
source	1..1713				
BASE COUNT	516 a 305 c 369 g 523 t				
ORIGIN					
Query Match	99.7%	Score 1708.2	DB 6	Length 1713	
Best Local Similarity	99.8%	Pred. No. 0			

Matches 1710; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	1	ATGAATTTCAACGTTAGTTTGATGAGAAATTAATGAAGATTAAATGCAATGAAT	60	
Db	1	ATGAATTTCAACGTTAGTTTGATGAGAAATTAATGAAGATTAAATGCAATGAAT	60	
Qy	61	AAAGTTTAACTATCTGTTTAACTACCAATGAAGCGTGTGATGCTGAAGTCAATATGTC	120	
Db	61	AAAGTTTAACTATCTGTTTAACTACCAATGAAGCGTGTGATGCTGAAGTCAATATGTC	120	
Qy	121	AAAGTGAAGCGGTTAAAGCTTAACTGTACGATGATCTTCACTACAGTTTGAAGGT	180	
Db	121	AAAGTGAAGCGGTTAAAGCTTAACTGTACGATGATCTTCACTACAGTTTGAAGGT	180	
Qy	181	ATACCGTACGCGCAACCGCGCTGAGCTGATGATTTAAAGCCCGGAGGACCA	240	
Db	181	ATACCGTACGCGCAACCGCGCTGAGCTGATGATTTAAAGCCCGGAGGACCA	240	
Qy	241	CCCTGGATGCTGCTGATGATTTGCAATCATAAAGATGCTCAAGTTGATTT	300	
Db	241	CCCTGGATGCTGCTGATGATTTGCAATCATAAAGATGCTCAAGTTGATTT	300	
Qy	301	ATACGCGCAAGCTGTGCTCAGAGATGCTTATACCTAAGTGTCTATACGAATAT	360	
Db	301	ATACGCGCAAGCTGTGCTCAGAGATGCTTATACCTAAGTGTCTATACGAATAT	360	
Qy	361	CTAAATCCGGAACATACGCTGCTTATACATACATGCTGCTGCTTATATC	420	
Db	361	CTAAATCCGGAACATACGCTGCTTATACATACATGCTGCTGCTTATATC	420	
Qy	421	GGTGAATATCATCTGATATGATGCTGCTGATTTTCAATTAAGAGATGCTGCTG	480	
Db	421	GGTGAATATCATCTGATATGATGCTGCTGATTTTCAATTAAGAGATGCTGCTG	480	
Qy	481	ATTAACATACATATCTGTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT	540	
Db	481	ATTAACATACATATCTGTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT	540	
Qy	541	AATGCGCGGGAATGCGGCTTAAAGATCAATGATGCTGCTGCTGCTTAAAT	600	
Db	541	AATGCGCGGGAATGCGGCTTAAAGATCAATGATGCTGCTGCTGCTTAAAT	600	
Qy	601	AATGCGCGCACTTGTGCTGATCCGATATATTTACAGTCTTGTGGAAGTCCGCT	660	
Db	601	AATGCGCGCACTTGTGCTGATCCGATATATTTACAGTCTTGTGGAAGTCCGCT	660	
Qy	661	GCTGCTCTACCCACTACATGATGTTAAACGAACAACCTGCGGCTTTTCCATGCTGT	720	
Db	661	GCTGCTCTACCCACTACATGATGTTAAACGAACAACCTGCGGCTTTTCCATGCTGT	720	
Qy	721	ATACATATGCTGGGTAATGCTATTTGCTATGCTATACCAATGTCACATGCTGCT	780	
Db	721	ATACATATGCTGGGTAATGCTATTTGCTATGCTATACCAATGTCACATGCTGCT	780	
Qy	781	TTTCACTTACCAATTTGGCGCTATTAAGGTGAGATTAATGATGAAGATTTTGGAA	840	
Db	781	TTTCACTTACCAATTTGGCGCTATTAAGGTGAGATTAATGATGAAGATTTTGGAA	840	
Qy	841	TTTTCTTATGAAGCCACGACGAGATTTAATAAATCTTGAGAGAAAAGTTTAACTCTA	900	
Db	841	TTTTCTTATGAAGCCACGACGAGATTTAATAAATCTTGAGAGAAAAGTTTAACTCTA	900	
Qy	901	GAAAGCGCTACCAATTAAGGTATGCTTTGCTTGTCCACTGCTGACCAATACAGAC	960	
Db	901	GAAAGCGCTACCAATTAAGGTATGCTTTGCTTGTCCACTGCTGACCAATACAGAC	960	
Qy	961	GCTGATTTGCTTACCAACATCTCGGAAATGTTTAAACGCTTGGGTAATTCG	1020	
Db	961	GCTGATTTGCTTACCAACATCTCGGAAATGTTTAAACGCTTGGGTAATTCG	1020	
Qy	1021	ATACCACTATGATGGGTAACACTTCAATGAGGCTGATTTTTCATCTCAATCTTAAAG	1080	
Db	1021	ATACCACTATGATGGGTAACACTTCAATGAGGCTGATTTTTCATCTCAATCTTAAAG	1080	

Qy	1081	CAATGCTTATCTGTTAAGGATTTGAAACTTGTCATATTTTGCCAGTGAATG	1140	
Db	1081	CAATGCTTATCTGTTAAGGATTTGAAACTTGTCATATTTTGCCAGTGAATG	1140	
Qy	1141	GCTGATGCTGAACGCGACCGCCGAGAGACCTTGAAGTGGTCTAAATTTAAAAAGCT	1200	
Db	1141	GCTGATGCTGAACGCGACCGCCGAGAGACCTTGAAGTGGTCTAAATTTAAAAAGCT	1200	
Qy	1201	CATGTTACAGGAGAAACACCAACAGCTGATTAATTTTATGATCTTTCATCATCTAT	1260	
Db	1201	CATGTTACAGGAGAAACACCAACAGCTGATTAATTTTATGATCTTTCATCATCTAT	1260	
Qy	1261	TTTGGTTCGCCATGCTGTTGTTGAATACCTTCAACACACCTGCGGTACACC	1320	
Db	1261	TTTGGTTCGCCATGCTGTTGTTGAATACCTTCAACACACCTGCGGTACACC	1320	
Qy	1321	GCTACTGTTATGCTGCTGACCTTCAATCGAAGATCTTATCAATCCATGCTATATG	1380	
Db	1321	GCTACTGTTATGCTGCTGACCTTCAATCGAAGATCTTATCAATCCATGCTATATG	1380	
Qy	1381	GCTAGTGAAGCTGCTGTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTG	1440	
Db	1381	GCTAGTGAAGCTGCTGTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTG	1440	
Qy	1441	ATATCAATGCGCAACGATGCTTAAAGATGCGTGAATACAAACATTTGAACGATG	1500	
Db	1441	ATATCAATGCGCAACGATGCTTAAAGATGCGTGAATACAAACATTTGAACGATG	1500	
Qy	1501	ACTGCTATATGATCAATTTTCCACACTGCTATCTTATAGCAATGAATTTAGGT	1560	
Db	1501	ACTGCTATATGATCAATTTTCCACACTGCTATCTTATAGCAATGAATTTAGGT	1560	
Qy	1561	ATGGAATATGTTTCTGCGGATCCAAATTAAGAAATCCGATGAAGTATCAAGTGTGAA	1620	
Db	1561	ATGGAATATGTTTCTGCGGATCCAAATTAAGAAATCCGATGAAGTATCAAGTGTGAA	1620	
Qy	1621	ATTAGTATGATTTGAATGAATGTTGATGCTGCTGAAGTGAATGAATGAAGGAG	1680	
Db	1621	ATTAGTATGATTTGAATGAATGTTGATGCTGCTGAAGTGAATGAATGAAGGAG	1680	
Qy	1681	TGCATGTTTGAAGAAACATAGATTTATTTTAAAG	1713	
Db	1681	TGCATGTTTGAAGAAACATAGATTTATTTTAAAG	1713	

RESULT 5
 LOCUS AR062837 1713 bp DNA Linear PAT 29-SEP-1999
 DEFINITION Sequence 1 from patent US 5843758.
 ACCESSION AR062837
 VERSION AR062837.1 GI:5990528
 KEYWORDS
 SOURCE
 ORGANISM
 UNKNOWN.
 REFERENCES
 1 (bases 1 to 1713)
 Russell, R. Joyce, Newcomb, R. David, Robin, G. Charlesde, Quetleville, Boyce, T. Mark, Campbell, P. Malcolm, Oakeshott, J. Graham, and Smyth, K. A. Enzyme based biomediation
 TITLE JOURNAL Patent: US 5843758-A 1 01-DEC-1998;
 FEATURES
 location/qualifiers
 1..1713
 /organism="unknown"
 BASE COUNT 516 a 305 c 370 g 522 t
 ORIGIN
 Query Match 99.4%; Score 1703.4; DB 6; Length 1713;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 ATGAATTTCAACGTTAGTTTGATGAGAAATTAATGAAGATTAAATGCAATGAAT 60

QY 61 AAGTTTAACTATCGTTTAACCAATGAACGGGTGAGCGAAACGAAATATGCG 120
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 Db 61 AAGTTTAACTATCGTTTAACTACCAATGAACGGGTGAGCGAAACGAAATATGCG 120
 QY 121 AAGTGAAGGCGTTAAACGTTTAAGTGTACGATGATGTTCTACTACGATTTGAGGGT 180
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 Db 1441 AATCAATTTGCGCAACGATGCTTAAGAAATCGCTGAATACAAACAATTAACGATG 1500
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RESULT 7
 LCUS5636
 LOCUS
 DEFINITION
 Lucilia cuprina alpha esterase (lcaet) mRNA, implicated in
 organophosphate resistance, complete cds.
 ACCESSION
 U5636
 VERSION
 U5636.1
 KEYWORDS
 SOURCE
 ORGANISM
 Lucilia cuprina.
 Lucilia cuprina.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Oestroidea; Calliphoridae; Lucilia.
 REFERENCE
 1 (bases 1 to 2240)
 Newcomb,R.D., East,P.D., Russell,R.J. and Oakeshott,J.G.
 Isolation of alpha cluster esterase genes associated with
 organophosphate resistance in *Lucilia cuprina*
 Insect Mol. Biol. 5 (3), 211-216 (1996)
 JOURNAL
 MEDLINE
 PUBMED
 8799740
 96392952
 REFERENCE
 2 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Russell,R.J. and Oakeshott,J.G.
 cDNA cloning, baculovirus expression and kinetic properties of the
 esterase, E3, involved in organophosphorus resistance in *Lucilia*
cuprina
 Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
 JOURNAL
 MEDLINE
 PUBMED
 9061925
 REFERENCE
 3 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Ollis,D.L., Cheah,E., Russell,R.J. and
 Oakeshott,J.G.
 A single amino acid substitution converts a carboxylesterase to an
 organophosphorus hydrolase and confers insecticide resistance on a

blowfly
Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
JOURNAL
MEDLINE
97352821
PUBMED
9207114
4 (bases 1 to 2240)
Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
Two different amino acid substitutions in the all-esterase, E3,
confer alternative types of organophosphorus insecticide resistance
in the sheep blowfly

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Unpublished
5 (bases 1 to 2240)
Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
Direct Submission
Submitted (24-Apr-1996) Richard D. Newcomb, Molecular Genetics,
HortResearch, Private Bag 92 169, Auckland, New Zealand
Location/Qualifiers

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RDLF"

gene
CDS
exon
exon
exon
exon
variation
variation
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exon
BASE COUNT
ORIGIN

exon
exon
exon
exon
variation
variation
exon
exon
exon
BASE COUNT
ORIGIN
Query Match
Best Local Similarity
Matches 1707; Conservative

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Db 478 ATACCGTACGCCAACCGCCAGTGGTGGAGCTGAGATTAAAGCCACGACCAACA 537
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Db 718 GGTGAATAATCATGCTATATGCTATGCTGATTTATTTATTTATTAAGTTAAATCAGAACCTT 777
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Db 778 ATTAACATACATATTCCTTTGGAGCTCTAGTTTCTAAGTTTAAATCAGAACCTT 837
OY 541 AATGTGCGCGTATGCGCGCTTAAAGATCAACATGCTGCTGCTGCTGCTGCTGCT 600
Db 838 AATGTGCGCGTATGCGCGCTTAAAGATCAACATGCTGCTGCTGCTGCTGCTGCT 897
OY 601 AATGTGCGCGTATGCGCGCTTAAAGATCAACATGCTGCTGCTGCTGCTGCTGCT 660
Db 898 AATGTGCGCGTATGCGCGCTTAAAGATCAACATGCTGCTGCTGCTGCTGCTGCT 957
OY 661 GGTGCTTACCACTACATGATGTTTAAACGCAACATGCGGCTCTTTCATCGTGT 720
Db 958 GGTGCTTACCACTACATGATGTTTAAACGCAACATGCGGCTCTTTCATCGTGT 1017
OY 721 ATACTAATGCGGTAATGCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 1018 ATACTAATGCGGTAATGCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077
OY 781 TTCACCTTACCAATTTGCGCGCTTAAAGGATGAGGATATGATAGATGTTTGGA 840
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OY 901 GAAGAGCTACAAATTAAGTGTATGCTTCTTTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 1198 GAAGAGCTACAAATTAAGTGTATGCTTCTTTGCTGCTGCTGCTGCTGCTGCTGCT 1257
OY 961 GGTGATGCTGCTTACCAACATGCTGGAATGCTTAAACGCTGCGGTAATTCG 1020
Db 1258 GGTGATGCTGCTTACCAACATGCTGGAATGCTTAAACGCTGCGGTAATTCG 1317
OY 1021 ATACCACTATGATGCTGCTTACCACTGATGAGGCTGATTTTCACTTCAATTTAAG 1080
Db 1318 ATACCACTATGATGCTGCTTACCACTGATGAGGCTGATTTTCACTTCAATTTAAG 1377
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DB	1378	CANATGGCTATGCTTTGTTAAGGAATGGAACCTTGTCATTTTGTGCGCAAGTAATG	1437
OY	1141	GCTGATGCTGAACGACCGCCGCCAGAGACTTGGAAATGGGTGCTAAATTAATAAAGGCT	1200
Db	1438	GCTGATGCTGAACGACCGCCGCCAGAGACTTGGAAATGGGTGCTAAATTAATAAAGGCT	1497
OY	1201	CATGTTACAGGGAAGAACCAACACCTGATTAATTTATGAGATCTTGGCTGCACATCAT	1260
Db	1498	CATGTTACAGGGAAGAACCAACACCTGATTAATTTATGAGATCTTGGCTGCACATCAT	1557
OY	1261	TTCTGGTTCCCATGATCGTTTGTGTAATTTACCTTCAATCAACACCTCCGGTACACC	1320
Db	1558	TTCTGGTTCCCATGATCGTTTGTGTAATTTACCTTCAATCAACACCTCCGGTACACC	1617
OY	1321	GTCATCTGTATCCGCTTGAGACTTCATTCGGAAGATCTTATCATCTTATCGTATATG	1380
Db	1618	GTCATCTGTATCCGCTTGAGACTTTATTCGGAAGATCTTATTAACCTTATCGTATATG	1677
OY	1381	CGTATGGAACGGTGGTTTAAGGGTTTATGATCAAGTGTGATTAACCTATTTCTCGG	1440
Db	1678	CGTATGGAACGGTGGTGTATTAAGGGTTTATGATCAAGTGTGATTAACCTATTTCTCGG	1737
OY	1441	AATCAATTTGGCCAAACGATGCTTAAGAAATCGCTGAATACAAAACAATTAACGATAG	1500
Db	1738	AATCAATTTGGCCAAACGATGCTTAAGAAATCGCTGAATACAAAACAATTAACGATAG	1797
OY	1501	ACTGATATATGATATCAATTTTGCACACACTGTAATCTTATAGCATGAATTAAGACT	1560
Db	1798	ACTGATATATGATATCAATTTTGCACACACTGTAATCTTATAGCATGAATTAAGACT	1857
OY	1561	ATGGAATAATGTTTCTCGGATCCATTTTAAGAAATCCGATGAAGTATACAGGTTGAAT	1620
Db	1858	ATGGAATAATGTTTCTCGGATCCATTTTAAGAAATCCGATGAAGTATACAGGTTGAAT	1917
OY	1621	ATTAGTGAATGAATTAAGAAATGATGATGTCCTGAATAGATTAACATATGGAG	1680
Db	1918	ATTAGTGAATGAATTAAGAAATGATGATGTCCTGAATAGATTAACATATGGAG	1977
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RESULT 8			
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LOCUS	AR062838		linear
DEFINITION	Sequence 2 from patent US 5843758.		PAT 29-SEP-1999
ACCESSION	AR062838		
VERSION	AR062838.1		GI:5990529
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1713)		
	Russell,R.Joyce., Newcomb,R.David., Robin,G.Charlesde.Quetteville.,		
	Boyce,T.Mark., Campbell,P.Malcolm., Parker,A.Gerard.,		
	Oakesholt,J.Graham. and Smyth,K.-A.		
TITLE	Enzyme based biomedication		
JOURNAL	Patent: US 5843758-A 2 01-DEC-1998;		
FEATURES	Location/Qualifiers		
source	1..1713		
BASE COUNT	506 a 299 c 363 g 515 t		30 others
ORIGIN			
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Best Local Similarity	98.1%;	Pred. No. 0;	
Matches 1680;	Conservative 0;	Mismatches 33;	Indels 0; Gaps 0;
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Db	1	ATGAATTTACAGCTTAGTTGATGAGAAATTAATAATGACAGATTAATTCATTTGAAT	60

QY	61	AAAGTTTAAACTATCGTTTAACTACCAATGAACCGGTGTAGCTGAACATGATATATGGC	120
Db	61	AAAGTTTAAACTATCGTTTAACTACCAATGAACCGGTGTAGCTGAACATGATATATGGC	120
QY	121	AAAGTGAAGAGCGTTTAAACGTTTAACTGATGAGATGATGCTTCTACTACAGTTTAAAGGT	180
Db	121	AAAGTGAAGAGCGTTTAAACGTTTAACTGATGATGAGATGATGCTTCTACTACAGTTTAAAGGT	180
QY	181	ATACCGTACGGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCGACGACCAACA	240
Db	181	ATACCGTACGGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCGACGACCAACA	240
QY	241	CCCTGGGATGCTGTGCTGATTTGTGCATCATAAAGATAAGTCAGTCAGTATTTT	300
Db	241	CCCTGGGATGCTGTGCTGATTTGTGCATCATAAAGATAAGTCAGTCAGTATTTT	300
QY	301	ATAACGGGCAAAAGTGTGGCTCAGAGAGATTTGCTATACCTTAAGTGTCTATCGAATAT	360
Db	301	ATAACGGGCAAAAGTGTGGCTCAGAGAGATTTGCTATACCTTAAGTGTCTATCGAATAT	360
QY	361	CTAAATCCCGAAACTAAACGTCGCCGTTTAAATACATACATGCTGTGGTTTATATATC	420
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QY	421	GCTGAATAATCATGCTGATATGATATGTCCTGATTAATTCATTAAGAAAGATGTGCTGTG	480
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QY	481	ATTAACATACAAATATGCTTTGGGGAGCTGTAGTGTCTTAAGTTTAAATTCAACAACCTT	540
Db	481	ATTAACATACAAATATGCTTTGGGGAGCTGTAGTGTCTTAAGTTTAAATTCAACAACCTT	540
QY	541	AATGTGCCCGGTAAATGCGCGGCTTAAAGATCAACATGTCAGTGGCTTGGCTGATTTAAAT	600
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QY	601	AATGTGCCCAACTTTGGTGGCAATCCCGATAAATTACAGTCTTTGGTGAAGATGCCGT	660
Db	601	AATGTGCCCAACTTTGGTGGCAATCCCGATAAATTACAGTCTTTGGTGAAGATGCCGT	660
QY	661	GCTGCTCTTACCCACTCATGATGATGTTAAACGGAACAACGCGGGTCTTTCCATGCTGTGT	720
Db	661	GCTGCTCTTACCCACTCATGATGATGTTAAACGGAACAACGCGGGTCTTTCCATGCTGTGT	720
QY	721	ATACTAATGTGGGGTAAATGCTATTTGTGCTATTGGCTAATACCAATGTCACATGCTGCC	780
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QY	781	TTACACTTACGCCAAATTTGAGGCTATTAAGGGTGAAGATTAAGATATGATTAAGATCTTTTGGAN	840
Db	781	TTACACTTACGCCAAATTTGAGGCTATTAAGGGTGAAGATTAAGATATGATTAAGATCTTTTGGAN	840
QY	841	TTTCTTATGAAGCCCAAGCCACAGAGATTTAATAACTTGAGGAAAAAGTTTAACTCTGA	900
Db	841	TTTCTTATGAAGCCCAAGCCACAGAGATTTAATAACTTGAGGAAAAAGTTTAACTCTGA	900
QY	901	GAGAGCGCTACAAATTAAGATCATGTTCCCTTTGGTCCCACTGTGAGCATATGAGAC	960
Db	901	GAGAGCGCTACAAATTAAGATCATGTTCCCTTTGGTCCCACTGTGAGCATATGAGAC	960
QY	961	GCTGATTTGTCTTACCCAAACATCTCTCGGGAATGTTAAACCTGCTTGGGGTAATTGG	1020
Db	961	GCTGATTTGTCTTACCCAAACATCTCTCGGGAATGTTAAACCTGCTTGGGGTAATTGG	1020
QY	1021	ATACCCACTATGATGGGTAAACACTTCATATGAGGGTCTATTTTTCACCTTCAATCTTAAAG	1080
Db	1021	ATACCCACTATGATGGGTAAACACTTCATATGAGGGTCTATTTTTCACCTTCAATCTTAAAG	1080
QY	1081	CAAAATGCTATGCTTTGTTAAGGAATTGGAACCTGTGTCAATTTTGTGCGCAAGTAATTG	1140
Db	1081	CAAAATGCTATGCTTTGTTAAGGAATTGGAACCTGTGTCAATTTTGTGCGCAAGTAATTG	1140
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 /EC_number="3.1.1.1"
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 poly_a_signal
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 Query Match 57.6%; Score 987.2; DB 3; Length 2160;
 Best local similarity 73.5%; Pred. No. 1,8e-210;
 Matches 1259; Conservative 0; Mismatches 453; Indels 0; Gaps 0
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 217 ATGATTTTCAAGTTAGTCAAAATGAGAGGCTCTCTGGAAACTCAAAATGCATGTCAAT 276
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 277 AATACACAACTACCGCTGATGACAAATGAAGAACCAATAATCGATGATTAATATGA 336
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OY	181	ATACCGTAGCGCCCAACCGCCAGTGGGTAGCTGAGATTTTAAGCACCCAGGACCAACA	240
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OY	241	CCCTGGGATGGTGTGCGGTGATTTGGTCAATCAATTAAGATTAAGTCAGTGCAGTTGATTTT	300
Db	522	CCCTGGGATGGAGTTAAGATTTGTTCTCATCTGCTCCCGGTTCCGGTTCAACACAGATTTTC	581
OY	301	ATTAACGGGCAAAAGTGTGTGGCTCAGAGAGATTTCTATACCTAAAGTGTCTATACAGTAAT	360
Db	582	ATATCCGGCAACTCAGAGGTTCGAGAGATTTGTTAAATTTGAATGTCTATACAGTAAT	641
OY	361	CTAAATTCGCCGAACATAAACGTCCCGTTTATATACATACATGCTGGGTATTTATATC	420
Db	642	TTTAAATACTGATATCAAAACGTCCGTTTGGTTTCTTCCATCGTGGTGGTTCAATTTGT	701
OY	421	GGGAAATATCATCTGATATGTATGTGCTGATATTTTCAATTAATAAAGATGTGCTTG	480
Db	702	GGCGAAAGCTAATGAAACATATTATGGCGCTGATATTTTCATTAAGAAGAGCTGTCTTC	761
OY	481	ATTACATATCAATATCTGTTTGGGACCTGAGTTTTCATAGTTTAAATTCAGAACTT	540
Db	762	ATTAACGTCAATATCTTTAGGGGTAGTTAGTTTCTTAAGTTAAATTCGGAAATCTC	821
OY	541	AATGTCCCGGTAAATCCCGCTTTAAAGATCAAGTCATGCTTCGCTTGCTTGAATTAAT	600
Db	822	AATGTACTGTGATATCTGGCGCTAAAGATCAAGTATGCGCTTCGATGATTAATAAAC	881
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OY	661	GCTGCGCTTACCCACTACATGATGTTAACCGAACAATCGCGTCTTTCCATGTGT	720
Db	942	CTGCGCTTCAACGCACTATGATGATATACGAAACAGCTGTGTCTATTTCCATCTGTGC	1001
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OY	961	GCTGATGTGTCTTACCBAACATCTCTGGGAATGTATTAACCTGTGGGTAATTCG	1020
Db	1242	CCAGACTGTGTTTCCCAAAACCAAAATCGAAAAATGCTTAACCTGCTGGGTAATCTCA	1301
OY	1021	ATACCCAGATATGATGGTAACTCATATATGAGGTCTATTTTCACTCAATTTCTTAAG	1080
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OY	1081	CAATGCTTATGCTTTGTTAAGGAATGGAACTTGTCTCAATTTTGTGCCAAGTAATTC	1140
Db	1362	CAAAATCTCATCTAATTAAGATTTGGAAACATTTTGAATGTATGTATCTCGTGATGTTG	1421
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Db	1422	GTAGTTGAAGATCGAGTTCTCCAGATCTCTTGAATTTGCATGATCTTAAGAATTTG	1481
OY	1201	CAGTTTACAGAGAAACACCAACAGCTGATAAATTTTATGATCTTTGCTCTCACATCTAT	1260
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QY	1261	TTCTGGTCTCCCATGATCGCTGTTGTGGCAATTACGTTTCAATACACACCTCCGTCACCC	1320
Db	1542	TTTTGTGATCCAAATGATCGCTTTCTGCGCAATTCATCATCATCTGCTGGCTGCC	1601
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QY	1441	AATCAATTTGGCAAAACGATGCTTAAAGAAATCCGCTGAATCAAAACAATTAAGCTATG	1500
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QY	1501	ACTGTATATGATGATCAATTTGCCACACCTGTGTAATCTTATACCATGAATTTGAAGT	1560
Db	1782	ATAGGCAATTTGGACCAATTTGCCCTCGGCAATCATATATGATCCCGAATTAATGGC	1841
QY	1561	ATGGAATAATGTTCCGTGGATCCATTTAAGAAATCCGATGAAGTATCAAGTGTGAT	1620
Db	1842	ATGGAATAATCAACATGATGGATTCATTTGAAAAATCGATGAGGTCTCAATATGATCAAC	1901
QY	1621	ATTAGTATGATTAATGAATTTGATGTCCTGAATATGATTAAGATTAACATGAGGAG	1680
Db	1902	ATAGGCGATGATGATTAAGTTATCGATTTGCCAAGAAATGGAATAATTAAGTATGCGAG	1961
QY	1681	TCGATGTTTGAATAACATGAGATTTATTTTATG	1713
Db	1962	AGTGTTCATATGAAGACGGGAATTTGTTTATG	1994
RESULT 11			
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LOCUS	AR153445	Sequence 14 from patent US 6235515.	
DEFINITION	AR153445		
ACCESSION	AR153445.1	GI:15120977	
VERSION			
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1. (bases 1 to 1710)		
AUTHORS	Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,		
	Robin, G. Charlesde, Queteville., Claudianos, C., Smyth, K. A.,		
	Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Collin.		
TITLE	Malatlon carboxylesterase		
JOURNAL	Patent: US 6235515-A 14 22-MAY-2001;		
FEATURES	location/Qualifiers		
source	1..1710		
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BASE COUNT	498 a 369 c 394 g 449 t		
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Query Match	55.8%; Score 956.6; DB 6; Length 1710;		
Best Local Similarity	73.4%; Pred. NO. 1.3e-203;		
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Db	104	TGATATGCTGATATGAGCAAAATTAAGGCTGTTAAACGATATACCGCTTACGATATCTT	163
QY	164	ACTACAGTTTGAAGGCTATATACGTCACGCCAACCGCACTGGGTAGCTGAGATTAAAG	223
Db	164	ACTACAGTTTGGAGATATATACCTATGCTAAGCCCTCAAGTGGGTGAGTTGAGATTCAAG	223
QY	224	CACCCAGCGACCAACCCCTGGAGTGTGCTCGTGAATTTGCAATATATAAATAGT	283

Db 224 CACCCAGCGCCTGTACCATGGAGGGGTGACGTGATTTGCTGTGGCCACCCAAACAGAT 283
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RESULT 12
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 LOCUS
 DEFINITION
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 AY051473
 ACCESSION
 AY051473.1 GI:15291256
 KEYWORDS
 FLI.CDNA.
 SOURCE
 ORGANISM
 Drosophila melanogaster.
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1017)

REFERENCE
 AUTHORS
 Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
 Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
 Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J.,
 Nuno, J., Pacleb, J., Paragas, V., Park, S., Phouenavong, S., Wan, K.,
 Yu, C., Lewis, S. E., Rubin, G. M. and Celisner, S.
 Direct Submission
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 Sequence submitted by:
 Lawrence Berkeley National Laboratory
 Berkeley Drosophila Genome Project

COMMENT
 This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a polyA tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unspliced precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our Web site
 (<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.
 location/Qualifiers

FEATURES
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	ACCESSION	AY121675
	VERSION	AY121675.1 GI:21464397
	KEYWORDS	FULL-CDNA.
	SOURCE	Fruit fly.
	ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Epiphytoidae; Drosophilidae; Drosophila. 1 (bases 1 to 2650)
	REFERENCE	Stapleton, M., Brokstein, P., Hong, L., Abdayan, A., Carlson, J., Champe, M., Chavez, C., Dorset, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Iiao, G., Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celinker, S. Direct Submission
TITLE		Submitted (13-JUN-2002) Berkeley Drosophila Genome Project,
JOURNAL		Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA
COMMENT		Sequence submitted by: Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Berkeley, CA 94720
		This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to cdna@fruitfly.berkeley.edu.
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BASE COUNT		724 a 632 c 650 g 654 t
ORIGIN		

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Best Local Similarity	53.9%;	Prod. No. 2.6e-74;		
Matches 877;	Conservative 10;	Mismatches 729;	Indels 21;	Gaps 4;
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OY	145	ACTGTGTACGATGATGATTCCTACTACAGTTTGTGAGGTTATACGTTACGCCAACCGCAGTG	204	
Db	606	TCCATCTACAGCAACAACACTACTACAGCTTTCAGAGGCGATCCGCTTGCCACAGCGCGGGTG	665	
OY	205	GCTGAGCTGAGATTTTAAAGCACCCGACCGACACACCCTGGAGTGTGTGCGTATGTT	264	
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OY	265	TGCATTCATPAAAGATTAACGATCGAGTGAATGATTTTATTAAGGCGCAAGGTGTGGCTCA	324	
Db	726	ACACATGTTTCGGCCACACCCCTGCCAGGTCAACATCGTTCTGAACAGGTGAAGGCGACG	785	
OY	325	GAGATTTGTCTATATACCTAAGTGTCTATACGATATCTAAATCCGGAACCTAAAGTCCC	384	
Db	786	GAGAGCTGTCTGTACCTCAATGTCTACACAGAGAGTTTACATCCACAGACACTTTGGCG	845	
OY	385	GTTTATGATATACATACATGGTGTGGTTTATTTATCGGTGAATAATCATCTGATATGAT	444	
Db	846	GTTTGTTGGATCTATAGCGCGTGATTTCCAAATGGGGAAGCATTCGGGGATCTGTAC	905	
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Db	906	ACCCCGGACTACATTATATATGGAATCATCTCGACTGGTGTGTAATTCCTATCGTTAGGA	965	
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OY	565	AAAGATCAAGTCATGSGCTTGCTTGATTTAAAAATTAATGGCCGCACTTTGGTGGCAAT	624	
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OY	625	CCCGATATATATACAGTCTTGTGTGAAGTGGCGGTGCTGCTCTACCCACATCATGATG	684	
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OY	745	TGTGCATGTGGCTAATACCCATGTCA--ACATGTGCTTCCACTGTAGCCAAATTTGGC	801	
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OY	802	GGCTTAAAGGTGAGAGATATATGAAGATGTTTGGAAATTTCTTATGAAGCCAGCCA	861	
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OY	862	CAGGATTTAATAAACTTGAGAAAAGTTTAACTAGAGAGAGCGTCAATAAAGT-	920	
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[illegible]

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 Qy 1463 CTAAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1522
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 Db 2630 CTG 2689

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 Db 2680 CAGTTCCGAAATCCGACAGAGTGCATCAGTCCCTCAACATGATGATGATGATGATGATG 2749
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 Db 2750 TCGATTCCTGCTGAGTGGCCCAATTTGAAGTGTCTGGAGAGGCTGTATGACGACAAAG 2809
 Qy 1703 ATTATTTT 1711
 Db 2810 ATTATTTGT 2818
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 LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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 AC015272
 AC015272
 AC015272.1 GI:6436063
 VERSION HTG: HTGS_PHASE2.
 KEYWORDS Drosophila melanogaster.
 SOURCE Drosophila melanogaster
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 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 57335)
 AUTHORS Adams, M. and Venter, J. C.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
 Rockville, MD, USA
 COMMENT This sequence was identified as CDL-10213452 by the submitter.
 For further information on this sequence e-mail to fly@celera.com.
 * NOTE: This is a working draft sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
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QY 501 GGAAGCTCT----- 509
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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:58:21 ; Search time 246.905 Seconds
(without alignments)
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Title: US-09-776-910-9

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1703.4	99.4	1713	16	AAQ91561
2	1703.4	99.4	1713	18	AAAT68596
3	1682.6	98.2	1713	16	AAQ91566
4	1679.4	98.0	1713	16	AAQ91564
5	1679.4	98.0	1713	16	AAQ91565
6	1677.8	97.9	1713	16	AAQ91563
7	1676.2	97.9	1713	16	AAQ91562
8	956.6	55.8	1710	18	AAAT68597
9	678.8	39.6	2001	23	ABR02067

10	381.8	22.3	1704	23	ABR02081	Drosophila melanog
11	370.6	21.6	6175	23	ABR02066	Drosophila melanog
12	368.2	21.5	1665	23	ABR02099	Drosophila melanog
13	363.8	21.2	1792	23	ABR04689	Drosophila melanog
14	323.6	18.9	1593	23	ABR02103	Drosophila melanog
15	323	18.9	1863	23	ABR01859	Drosophila melanog
16	311.4	18.2	1791	23	ABR10333	Drosophila melanog
17	305.8	17.9	1719	23	ABR102101	Drosophila melanog
18	304.6	17.8	1878	23	ABR01947	Drosophila melanog
19	300.4	17.5	3856	23	ABR10332	Drosophila melanog
20	300.4	17.5	67279	23	ABR07668	Drosophila melanog
21	270	15.8	1809	24	ABA90480	Drosophila cell cy
22	238.2	13.9	4320	23	ABR04688	Drosophila melanog
23	229.6	13.4	1727	23	ABR01943	Drosophila melanog
24	228.6	13.3	4242	23	ABR02102	Drosophila melanog
25	224	13.1	5008	23	ABR02080	Drosophila melanog
26	198.8	11.6	4294	23	ABR02098	Drosophila melanog
27	198.8	11.6	4294	23	ABR02100	Drosophila melanog
28	197.6	11.5	1987	19	AAV40762	C. felis esterace,
29	197.6	11.5	1987	19	AAV40763	C. felis esterace,
30	193.2	11.3	2613	23	ABR19064	Drosophila melanog
31	192.8	11.3	1626	23	ABR01945	Drosophila melanog
32	191.8	11.2	5132	23	ABR01858	Drosophila melanog
33	187.4	10.9	1590	19	AAV40764	C. felis esterace,
34	187.4	10.9	1590	19	AAV40765	C. felis esterace,
35	179.6	10.5	1540	19	AAV40756	C. felis esterace,
36	179.6	10.5	1584	19	AAV40757	C. felis esterace,
37	179.6	10.5	2007	19	AAV40754	C. felis esterace,
38	179.6	10.5	2007	19	AAV40755	C. felis esterace,
39	179.6	10.5	2007	22	AAV21174	Ctenocephalides fe
40	167.6	9.8	4288	23	ABR01942	Drosophila melanog
41	162.6	9.5	1783	23	ABR02029	Drosophila melanog
42	148	8.6	4283	23	ABR01946	Drosophila melanog
43	142.2	8.3	1488	19	AAV40767	C. felis esterace
44	142.2	8.3	1590	19	AAV40743	C. felis esterace
45	142.2	8.3	1590	22	AAV21169	Ctenocephalides fe

ALIGNMENTS

RESULT 1	
ID	AAQ91561 standard; CDNA; 1713 BP.
XX	AAQ91561;
AC	22-DEC-1995 (first entry)
XX	
DT	OP-sensitive esterase E3 LC743 clone.
XX	
DE	
XX	Esterase; E3; bioremediation; organophosphate; carbamate;
KW	Insecticide; pesticide; water decontamination; meat decontamination;
KW	ss.
XX	
OS	Lucilia cuprina.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
XX	1..1713
XX	/*tag= a
PN	W09519440-A1.
XX	
PD	20-JUL-1995.
XX	
PF	13-JAN-1995; 95WO-AU00016.
XX	
PR	13-JAN-1994; 94AU-0003347.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
XX	
PI	Boyce TM, Campbell PM, Newcomb RD, Oakesholt JG; Parker AG, Robin GC, Russell RJ, Smyth K;

XX
DR WPI: 1995-263870/34.
P-PSDB: AAR78142.
XX
PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
eliminate residues of organo-phosphate and carbamate pesticides from
water, meat etc.
XX
PS Claim 5: Page 12-17: 38pp: English.
XX
CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA
library was amplified using cluster-specific esterase primers.
CC Isolated clone Lc743, a probable full-length cDNA, was expressed
CC using a baculovirus vector in insect cells and shown to encode
CC an OP-susceptible E3 esterase, useful in bioremediation.
XX
SQ Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other:

Query Match 99.4%; Score 1703.4; DB 16; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 1321 GTCCTGTTCCCAATGATCTTTGATGATGATGATGATGATGATGATGATGATGATG 1380
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DB 1381 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
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DB 1441 AATCAATTTGCCCAACGATGCTTAAAGATGCTGATGATGATGATGATGATGATGATG 1500
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DB 1501 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
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DB 1681 TCGATGTTGGAATAACATAGAGATTTATTTAG 1713

RESULT 2
AAT68596
ID AAT68596 standard; DNA: 1713 BP.
XX
AC AAT68596;
XX
DT 08-AUG-1997 (first entry)

DE		Lc-alpha-E7 malathion susceptible esterase clone Lc743.
XX		
KW		Malathion carboxylesterase; organophosphate; insecticide;
KM		pesticide; remediation; bioremediation; decontamination; esterase;
XW		ss.
XX		
OS		Lucilia cuprina.
XX		
FH	Key	Location/Qualifiers
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FT	/note= "Lc743 5' primer"	
FT	primer_bind	1686..1713
FT	/tag- b	
FT	/note= "Lc743 3' primer"	
FT	752	
FT	/tag- c	
FT	/note= "base 752 is T in resistant clones (TTP to Leu mutation)"	
FT	mutation	
FT	1344	
FT	/tag- d	
FT	/note= "base 1344 is C in resistant clones (silent mutation)"	
FT	1362	
FT	/tag- e	
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PI	Newcomb RD, Oakesholt JS, Robin GC, Russell RJ, Smyth K;	
DR	WPJ: 1997-298113/27.	
DR	P-PsDB; AAM17765.	
XX		
PT	DNA encoding enzyme that degrades organophosphate pesticides -	
PT	useful for decontamination of soil, water, food etc	
XX		
PS	Claim 4; Fig 1; 52pp; English.	
CC		
CC	DNA molecule Lc743 (AAT65596) codes for an esterase (AAM17765) from	
CC	a malathion susceptible strain of Lucilia cuprina. Comparison	
CC	with a consensus sequence from derived from clones of the	
CC	Lc-alpha-E7 resistant allele (see also AAM17768) indicated only one	
CC	replacement site difference, a TTP to leu substitution at amino	
CC	acid position 251 (nucleotide position 752). This mutation is an	
CC	excellent candidate for the malathion resistance mutation. The	
CC	resistant enzyme acts as a malathion carboxylesterase and can be	
CC	formulated for use in degrading environmental carboxylester or	
CC	dimethyl general-organophosphates.	
XX		
SQ	Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;	
Query Match	99.4%; Score 1703.4; DB 18; Length 1713;	
Best Local Similarity	99.6%; Pred. No. 0;	

		Matches	1707;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
QY	1	ATGAATTTCAACGTTAGTTGATGAGCAAAATTTAAATGGAAGATTAAATGCAATGGAAT	60								
Db	1	ATGAATTTCAACGTTAGTTGATGAGCAAAATTTAAATGGAAGATTAAATGCAATGGAAT	60								
QY	61	AAGTTTAAACCTATCGTTTAACTAACCAATGAACCGGTGAGCTGGAACGGAATATGCG	120								
Db	61	AAGTTTAAACCTATCGTTTAACTAACCAATGAACCGGTGAGCTGGAACGGAATATGCG	120								
QY	121	AAAGTGAAGAGCGTTAAACGTTTAACTGTGACGATGATTTCTACTACAGTTTGAGGGT	180								
Db	121	AAAGTGAAGAGCGTTAAACGTTTAACTGTGACGATGATTTCTACTACAGTTTGAGGGT	180								
QY	181	ATACCGTAGCGCCCAACCGCCACAGTGGGTAGCTGAGATTTTAAAGCACCCGACGACCA	240								
Db	181	ATACCGTAGCGCCCAACCGCCACAGTGGGTAGCTGAGATTTTAAAGCACCCGACGACCA	240								
QY	241	CCCTGAGATGGTGTGCGGTGATTTGTGCATATATAAGTAAAGTCAAGTCAAGTGATTTT	300								
Db	241	CCCTGAGATGGTGTGCGGTGATTTGTGCATATATAAGTAAAGTCAAGTCAAGTGATTTT	300								
QY	301	ATTAACGGGCAAGTGTGCGTCAAGAGATTTGTCATACCAAGTGTATACGAATAT	360								
Db	301	ATTAACGGGCAAGTGTGCGTCAAGAGATTTGTCATACCAAGTGTATACGAATAT	360								
QY	361	CTAATCCCGAAGCAATAAACGTCGCTTTAGTATACATACATGGTGGGTATATATAC	420								
Db	361	CTAATCCCGAAGCAATAAACGTCGCTTTAGTATACATACATGGTGGGTATATATAC	420								
QY	421	GGTGAAGATCATCGTATATGTATGTGTCCTGATTAATTTCAATTAAGAAAGATGGGTG	480								
Db	421	GGTGAAGATCATCGTATATGTATGTGTCCTGATTAATTTCAATTAAGAAAGATGGGTG	480								
QY	481	ATTAACATACATATACGTTTGGAGAGCTAGCTTCTAAGTTTAAATTCAGAAAGCTT	540								
Db	481	ATTAACATACATATACGTTTGGAGAGCTAGCTTCTAAGTTTAAATTCAGAAAGCTT	540								
QY	541	AATGCGCCGGTAAATGCGCGCTTAAAGATGAAGCATAGCGCTTGCGTGGATTAATAAT	600								
Db	541	AATGCGCCGGTAAATGCGCGCTTAAAGATGAAGCATAGCGCTTGCGTGGATTAATAAT	600								
QY	601	AATTGCGCCAACTTGGTGGCAATCCGATTAATATTACAGTCCTTGGTGAAGTGC	660								
Db	601	AATTGCGCCAACTTGGTGGCAATCCGATTAATATTACAGTCCTTGGTGAAGTGC	660								
QY	661	GCTGCTCTACCCACTACATGATGTAAACGCAACAACTCGCGGCTTTCCATCTGTG	720								
Db	661	GCTGCTCTACCCACTACATGATGTAAACGCAACAACTCGCGGCTTTCCATCTGTG	720								
QY	721	ATACTAATGTGGGTAAAGCTATTGTGTCATTGGCTAATACCACATGTCAACATCTGTG	780								
Db	721	ATACTAATGTGGGTAAAGCTATTGTGTCATTGGCTAATACCACATGTCAACATCTGTG	780								
QY	781	TTTACCTTATGCCAAATTTGGCCGGCTATTAAGGTGAGATTAATGATAGAGATGTTTGA	840								
Db	781	TTTACCTTATGCCAAATTTGGCCGGCTATTAAGGTGAGATTAATGATAGAGATGTTTGA	840								
QY	841	TTTTCTATGAAGAACCCACGACGAGATTAAATTAACCTGAGGAAAGGTTTAACTCTA	900								
Db	841	TTTTCTATGAAGAACCCACGACGAGATTAAATTAACCTGAGGAAAGGTTTAACTCTA	900								
QY	901	GAAAGCGCTACAAATAAAGTCAATGTTCTTGTGCTCCACTGTGGACCAATATCAGAC	960								
Db	901	GAAAGCGCTACAAATAAAGTCAATGTTCTTGTGCTCCACTGTGGACCAATATCAGAC	960								
QY	961	GCTGATGTGCTTACCAACCAATCTCTGGGAAATGTTTAAAACTGCTTGGGGTAATTCG	1020								
Db	961	GCTGATGTGCTTACCAACCAATCTCTGGGAAATGTTTAAAACTGCTTGGGGTAATTCG	1020								
QY	1021	ATACCCACTATGATGGGTAAACATTTCAATATAGAGGTCTATTTTCACTTCAATTCCTTA	1080								
Db	1021	ATACCCACTATGATGGGTAAACATTTCAATATAGAGGTCTATTTTCACTTCAATTCCTTA	1080								

QY 721 ATACCAATGTCGGGAATGCTATTGTCATTGGCTAATACCAATGTCACATCGTGC 780
 DB 721 ATACTAATGTCGGTAATGCTATTGTCATTGGCTAATACCAATGTCACATCGTGC 780
 QY 781 TTCACCTTAGCCAAATTTGGCCGGCTAATAGGCTAGAGTAATGATTAAGATGTTTGGAA 840
 DB 781 TTCACCTTAGCCAAATTTGGCTAGATTAAGGCTAGAGTAATGATTAAGATGTTTGGAG 840
 QY 841 TTTCTTATGAAGCCAGCCACAGATTTAATAAAGCTTGAGGAAAAAGTTTAACTCTA 900
 DB 841 TTTCTTATGAAGCCAGCCACAGATTTAATAAAGCTTGAGGAAAAAGTTTAACTCTA 900
 QY 901 GAAGAGGCTACCAATTAAGGCTATGCTTTGCTTCCACTGTTGAGCCATATCAGACC 960
 DB 901 GAAGAGGCTACCAATTAAGGCTATGCTTTGCTTCCACTGTTGAGCCATATCAGACC 960
 QY 961 GCTGATGTCCTTACCACCAATCTCGGGAATGTTAAAGCTTGGGGTAATTCG 1020
 DB 961 GCTGATGTCCTTACCACCAATCTCGGGAATGTTAAAGCTTGGGGTAATTCG 1020
 QY 1021 ATACCCATATGATGGGTAAACACTTATATAGGGTCTATTTTTCACCTTCAATTCCTAAG 1080
 DB 1021 ATACCCATATGATGGGTAAACACTTATATAGGGTCTATTTTTCACCTTCTTCTTAAG 1080
 QY 1081 CAAATGCTATGCTTTGTAAGGAATGGAACCTGTGCATTTTGTGCGCAAGTAATTCG 1140
 DB 1081 CAAATGCTATGCTTTGTAAGGAATGGAACCTGTGTCAATTTTGTGCGCAAGTAATTCG 1140
 QY 1141 GCTGATGTCGTAAGCCACCGCCCGAGAGACTTGGAAATGGTGTCTAAATTAAGAGGCT 1200
 DB 1141 GCTGATGTCGTAAGCCACCGCCCGAGAGACTTGGAAATGGTGTCTCTCAATTAAGAGGCT 1200
 QY 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTTGTCTCACATCTAT 1260
 DB 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTTGTCTCACATCTAT 1260
 QY 1261 TTTCTGTTCCCATGATGCTTTGTCATTTAGCTTTCATTCATCACCCTCGGTACACC 1320
 DB 1261 TTTCTGTTCCCATGATGCTTTGTCATTTAGCTTTCATTCATCACCCTCGGTACACC 1320
 QY 1321 GTTACTACTGTATCGCTTGCCTGACTTGCAGTTCGGAAGATCTTATCAATCCCTATCGATTATG 1380
 DB 1321 GTTACTACTGTATCGCTTGCCTGACTTGCAGTTCGGAAGATCTTATCAATCCCTATCGATTATG 1380
 QY 1381 CGTAGTGCACGTGCTGTTAAGGCTTGTAGTGTATGATGATTAATTAATTTCTTCTG 1440
 DB 1381 CGTAGTGCACGTGCTGTTAAGGCTTGTAGTGTATGATGATTAATTAATTTCTTCTG 1440
 QY 1441 AATCAATTTGGCCAAACGATGCTTAAAGATCGGTGAATCAAAACCAATTAAGAGCTATG 1500
 DB 1441 AATCAATTTGGCCAAACGATGCTTAAAGATCGGTGAATCAAAACCAATTAAGAGCTATG 1500
 QY 1501 ACTGATATATGATTAACAATTTGCCACACTGTAATCTTATAGCAATGAATTAAGAGT 1560
 DB 1501 ACTGATATATGATTAACAATTTGCCACACTGTAATCTTATAGCAATGAATTAAGAGT 1560
 QY 1561 ATGGAATATGTTTCTGCGGATTCCAATTAAGAAATCCGATGAATGAATTAAGAGT 1620
 DB 1561 ATGGAATATGTTTCTGCGGATTCCAATTAAGAAATCCGATGAATGAATTAAGAGT 1620
 QY 1621 ATTAGTATGATTAACAATGATGATGCTGGAATGATTAAGATTAAGATTAAGAGT 1680
 DB 1621 ATTAGTATGATTAACAATGATGATGCTGGAATGATTAAGATTAAGATTAAGAGT 1680
 QY 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713
 DB 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713

RESULT 4
 AA091564
 ID AA091564 standard; cdna: 1713 BP.

XX AC AA091564;
 XX XX 22-DEC-1995 (first entry)
 XX DE OP-resistant esterase Lc7L103C allele.
 XX DE Esterase; E3; bioremediation; organophosphate; carbamate;
 KW insecticide; pesticide; water decontamination; meat decontamination;
 KW ss.
 XX OS Lucilia cuprina.
 XX XX
 FH Key Location/Qualifiers
 FT CDS 1..1713
 FT /*tag= a
 XX
 PN M09519440-A1.
 XX PD 20-JUL-1995.
 XX
 XX 13-JAN-1995; 95WO-AU00016.
 PF 13-JAN-1994; 94AU-0003347.
 PR
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 DR WPI, 1995-263870/34.
 XX
 PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 PS
 XX Example 4; Page 12-17; 38pp; English.
 CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC OP-susceptible esterase E3 of *L. cuprina*) from a diazinon
 CC resistant strain, Llandillo 103. 4 Isolated clones were
 CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used
 CC in bioremediation.
 XX
 SQ Sequence 1713 BP; 512 A; 308 C; 368 G; 525 T; 0 other;
 Query Match 98.0%; Score 1679.4; DB 16; Length 1713;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1692; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
 QY 1 ATGAATTTCAACGTTAGTTTGAATGAGAAATTAATGAGATTAATGATTAAT 60
 DB 1 ATGAATTTCAACGTTAGTTTGAATGAGAAATTAATGAGATTAATGATTAAT 60
 QY 61 AAGTTTAACTATGCTTAACTACCAATGAAGAGGTGCTGAAGCTGAATATGAGC 120
 DB 61 AAGTTTAACTATGCTTAACTACCAATGAAGAGGTGCTGAAGCTGAATATGAGC 120
 QY 121 AAAGTGAAGGCGTTAAAGCTTTAACTGTTAGATGATTTCTTACTACAGTTTGAAGGT 180
 DB 121 AAAGTGAAGGCGTTAAAGCTTTAACTGTTAGATGATTTCTTACTACAGTTTGAAGGT 180
 QY 181 ATACCGTACGCCCAACCGCCAGCTGGGTGAGCTGAATTTAAAGCACCACGACACACA 240
 DB 181 ATACCGTACGCCCAACCGCCAGCTGGGTGAGCTGAATTTAAAGCACCACGACACACA 240
 QY 241 CCTGGATGCTGCTGATTTGTTGCAATCTAATAAGATTAAGTCAAGTCAAGTTATTTT 300
 DB 241 CCTGGATGCTGCTGATTTGTTGCAATCTAATAAGATTAAGTCAAGTCAAGTTATTTT 300
 QY 301 ATACGGGCAAGTGTGCTCAGAGATTTGCTATACCTAAGTGTCTATACGAATAT 360
 DB 301 ATACGGGCAAGTGTGCTCAGAGATTTGCTATACCTAAGTGTCTATACGAATAT 360

Db 301 ATTACAGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGGCTGTATACGATAT 360
 Qy 361 CTAATCCGGAAGTAACGTCCTTTTATATACATACATGCTGTGTTTATATATC 420
 Db 361 CTAATCCGGAAGTAACGTCCTTTTATATACATACATGCTGTGTTTATATATC 420
 Qy 421 GGTGAAATCATCGTATGTATGTATGCTGTATTTTATTTAAAGATGTGTG 480
 Db 421 GGTGAAATCATCGTATGTATGTATGCTGTATTTTATTTTAAAGATGTGTG 480
 Qy 481 ATTAACATACATATGCTTTGGAGCTAGGTTTCTAAGTTTAAATTCAGAGACCTT 540
 Db 481 ATTAACATACATATGCTTTGGAGCTAGGTTTCTAAGTTTAAATTCAGAGACCTT 540
 Qy 541 AATGTCGCCGTAATCCGCGCTTAAAGTCAAGTATGCGCTTGGTGTGATTAAT 600
 Db 541 AATGTCGCCGTAATCCGCGCTTAAAGTCAAGTATGCGCTTGGTGTGATTAAT 600
 Qy 601 AATGTCGCCGTAATCCGCGCTTAAAGTCAAGTATGCGCTTGGTGTGATTAAT 660
 Db 601 AATGTCGCCGTAATCCGCGCTTAAAGTCAAGTATGCGCTTGGTGTGATTAAT 660
 Qy 661 GCTGCTTACCCATCATATGATGTTAACGCAAACTCGCGCTTTTCCATGCTGT 720
 Db 661 GCTGCTTACCCATCATATGATGTTAACGCAAACTCGCGCTTTTCCATGCTGT 720
 Qy 721 ATACTAATGTCGGGTAATGCTATTTTCCATGCTGCTAATACCAATGCTGCTGC 780
 Db 721 ATACTAATGTCGGGTAATGCTATTTTCCATGCTGCTAATACCAATGCTGCTGC 780
 Qy 781 TTGACCTTACCAAAATTTGCGCGCTTAAAGGTAAGGATTAAGATGTTTGGAA 840
 Db 781 TTGACCTTACCAAAATTTGCGCGCTTAAAGGTAAGGATTAAGATGTTTGGAA 840
 Qy 841 TTTCTTATGAAGCCAGCCACAGAGATTTAATAAACTTGAAGAAAAGTTTAACTCTA 900
 Db 841 TTTCTTATGAAGCCAGCCACAGAGATTTAATAAACTTGAAGAAAAGTTTAACTCTA 900
 Qy 901 GAAGAGCGTCAATAGTATGATGTTCTTTTGTGCCACTGTGAGCCATATCAGACC 960
 Db 901 GAAGAGCGTCAATAGTATGATGTTCTTTTGTGCCACTGTGAGCCATATCAGACC 960
 Qy 961 GCTGATTTGTCTTTACCAAAATCTCGGGAATGTTTAAACTGTTGGGTAATTCG 1020
 Db 961 GCTGATTTGTCTTTACCAAAATCTCGGGAATGTTTAAACTGTTGGGTAATTCG 1020
 Qy 1021 ATACCCACTATGATGAGTACACTTCAATGAGGGTCTAATTTTACCTGTTCTTAAG 1080
 Db 1021 ATACCCACTATGATGAGTACACTTCAATGAGGGTCTAATTTTACCTGTTCTTAAG 1080
 Qy 1081 CAATGCTATGCTTTTGAAGAACTTGTCTCAATTTTGTGCCAAGTGAATG 1140
 Db 1081 CAATGCTATGCTTTTGAAGAACTTGTCTCAATTTTGTGCCAAGTGAATG 1140
 Qy 1141 GCTGATGCTGAAGCCAGCCAGAGACCTTGAAGTGGTGTAAATTAAGAAAGCT 1200
 Db 1141 GCTGATGCTGAAGCCAGCCAGAGACCTTGAAGTGGTGTAAATTAAGAAAGCT 1200
 Qy 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTATGATCTTTCTCTACATCTAT 1260
 Db 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTATGATCTTTCTCTACATCTAT 1260
 Qy 1261 TTTCTGTTCCCATGATGCTTTGTGCAATTTACGTTTCAATCAACACTCGGTACACC 1320
 Db 1261 TTTCTGTTCCCATGATGCTTTGTGCAATTTACGTTTCAATCAACACTCGGTACACC 1320
 Qy 1321 GTCTACTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 Db 1321 GTCTACTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 Qy 1381 GGTAGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 Db 1381 GGTAGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440

Qy 1441 AATCAATGGCCAAACGTAATCCCTAAGAAATCGGTAATACAAACAAATTAAGATG 1500
 Db 1441 AATCAATGGCCAAACGTAATCCCTAAGAAATCGGTAATACAAACAAATTAAGATG 1500
 Qy 1501 ACTGTAATGATGATCAATTTTGGCAACCTGCTGTAATCTTTTACCAATGAATGAAGT 1560
 Db 1501 ACTGTAATGATGATCAATTTTGGCAACCTGCTGTAATCTTTTACCAATGAATGAAGT 1560
 Qy 1561 ATGGAATATGTTTCTGCGATCAATTTAGAAATCCAGTAAGTATACAGTGTGTAAT 1620
 Db 1561 ATGGAATATGTTTCTGCGATCAATTTAGAAATCCAGTAAGTATACAGTGTGTAAT 1620
 Qy 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Db 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Qy 1681 TCGATGTTTGAAGAAACATGAGATTTATTTAG 1713
 Db 1681 TCGATGTTTGAAGAAACATGAGATTTATTTAG 1713

RESULT 5
 AAQ91565
 ID AAQ91565 standard; cDNA: 1713 BP.
 XX
 AC AAQ91565;
 XX
 DT 22-DEC-1995 (first entry)
 XX
 DE OP-resistant esterase Lc7L103D allele.
 XX
 KW Esterase; E3; bioremediation; organophosphate; carbamate;
 KW insecticide; pesticide; water decontamination; meat decontamination;
 KW ss.
 XX
 OS Lucilia cuprina.
 XX
 FH
 FT Key Location/Qualifiers
 FT CDS 1..1713
 FT /*tag= a
 XX
 PN W09519440-A1.
 PD 20-JUL-1995.
 XX
 PF 13-JAN-1995; 95WO-AU00016.
 XX
 PR 13-JAN-1994; 94AU-0003347.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 XX
 DR WPI: 1995-263870/34.
 XX
 PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
 PT eliminate residues of organo-phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Example 4; Page 12-17; 38pp; English.
 CC RI-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used
 CC in bioremediation.
 XX
 SQ Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other;
 Query Match 98.0%; Score 1679.4; DB 16; Length 1713;

AA091562	AA091562 standard; cDNA: 1713 BP.
ID	AA091562
XX	AA091562;
AC	
XX	
DT	22-DEC-1995 (first entry)
XX	
DE	OP-resistant esterase Lc7L103A allele.
XX	
KW	Esterase; E3; bioremediation; organophosphate; carbamate;
KW	Insecticide; pesticide; water decontamination; meat decontamination;
KW	ss.
XX	
OS	Lucilia cuprina.
XX	
FT	Key
FT	Location/Qualifiers
CDS	1..1713
FT	/*tag= a
XX	
PN	MO9519440-A1.
PD	20-JUL-1995.
XX	
PE	13-JAN-1995; 95WO-AU00016.
XX	
PR	13-JAN-1994; 94AU-0003347.
XX	
PA	(CSTR) COMMONWEALTH SCT & IND RES ORG.
XX	
PI	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI	Parker AG, Robin GC, Russell RJ, Smyth K;
XX	
DR	WPI: 1995-263870/34.
XX	
PT	Pure E3 esterase from <i>Lucilia cuprina</i> and related DNA - used to
PT	eliminate residues of organo:phosphate and carbamate pesticides from
PT	water, meat etc.
XX	
PS	Example 4; Page 12-17; 38pp: English.
XX	
CC	RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC	OP-susceptible esterase E3 of <i>L. cuprina</i>) from a diazinon
CC	resistant strain, Llandillo 103. 4 isolated clones were
CC	sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
CC	esterases. The esterases, or cells expressing them, are used
CC	in bioremediation.
XX	
SO	Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;
Query Match	97.9%; Score 1676.2; DB 16; Length 1713;
Best Local Similarity	98.7%; Pred. No. 0;
Matches 1690; Conservative	0; Mismatches 23; Indels 0; Gaps
	0;
OY	1 ATGAATTCACAGTTAGTTGATGAGAAATTAATGGAAGATTAAATGCATTGAAAT 60
DB	1 ATGAAATTCACAGTTAGTTGATGAGAAATTAATGGAAGATTAAATGCATTGAAAT 60
OY	61 AAGTTTAAATATACGTTTAACTACACCAATGAACGGTGCTAGCTGAAACTGAATATGCG 120
DB	61 AAGTTTAAATATACGTTTAACTACACCAATGAACGGTGCTAGCTGAAACTGAATATGCG 120
OY	121 AAGAGTAAAGCGCTTAAAGCTTTAACTGTCGATGATGATTCCTACTACAGTTTGAGGGT 180
DB	121 AAGAGTAAAGCGCTTAAAGCTTTAACTGTCGATGATGATTCCTACTACAGTTTGAGGGT 180
OY	181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCACCCGAGGACCAACA 240
DB	181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCACCCGAGGACCAACA 240
OY	241 CCCCTGGATGCGTGCATGATGTTGTCGAAATCAATTAAGATTAACATCAGTCGAAGTTGATTTT 300
DB	241 CCCCTGGATGCGTGCATGATGTTGTCGAAATCAATTAAGATTAACATCAGTCGAAGTTGATTTT 300

QY	301	ATPACGGGCAAAAGTGTGGCTCAGAGAGATGTCTATACCTAAGTGTCTATACGAATAT	360
Db	301	ATTACAGGCAAAAGTGTGGCTCAGAGAGATGTCTATACCTAAGGCTCTATACGAATAT	360
QY	361	CTAATCCCGAAACATAACGTCCCGTTTAAAGTATACATACATGAGTGGTGTATATAC	420
Db	361	CTAATCCCGAAACTAAACGTCCCCGTTTAAAGTATACATACATGAGTGGTGTATATAC	420
QY	421	GGTGAAGATCATGCTGATATGTATGGTCTGATATATTCATTAAAGAGATGTGGTGTG	480
Db	421	GGTGAAGATCATGCTGATATGTATGGTCTGATATATTCATTAAAGAGATGTGGTGTG	480
QY	481	ATTAACTACAAATATCGTTTGGAGAGCTCTAAGTTTTCTAAGTTTAAATTACAGACCTT	540
Db	481	ATTAACTACAAATATCGTTTGGAGAGCTCTAAGTTTTCTAAGTTTAAATTACAGACCTT	540
QY	541	AATGTGCCGGTAAATGCGGCGCTTAAAGATCAAGTCATGCGCTCGTTGGATTTAAAT	600
Db	541	AATGTGCCGGTAAATGCGGCGCTTAAAGATCAAGTCATGCGCTCGTTGGATTTAAAT	600
QY	601	AATTGGCCAACTTTGGTGGCAATCCCGATATATTTACAGTCTTTGGTGAAGTCCGGT	660
Db	601	AATTGGCCAACTTTGGTGGCAATCCCGATATATTTACAGTCTTTGGTGAAGTCCGGT	660
QY	661	GCTGCTCTTACCCACTCATGATGTTTACCAGAAACATCGCGGCTTTTCATGCTGT	720
Db	661	GCTGCTCTTACCCACTCATGATGTTTACCAGAAACATCGCGGCTTTTCATGCTGT	720
QY	721	ATACAAATGTCGGGTATGCTATTTGCCATTTGGCTAAATACCAGATGCATCATGCTGC	780
Db	721	ATACAAATGTCGGGTATGCTATTTGCCATTTGGCTAAATACCAGATGCATCATGCTGC	780
QY	781	TTTCACTTAAAGCAATTGGCCGGCTATAAGGGTGAAGATATAGATGTTTTGGAA	840
Db	781	TTTCACTTAAAGCAATTGGCTGGCTATAAGGGTGAAGATATAGATGTTTTGGAG	840
QY	841	TTTTCTTATGAAGCCAAAGCCACAGATTTATATAAACTTGAGAGAAAAGTTTAACTCTA	900
Db	841	TTTTCTTATGAAGCCAAAGCCACAGATTTATATAAACTTGAGAGAAAAGTTTAACTCTA	900
QY	901	GAAAGGGTACAAATTAAGGTCATGTTCCGTTTGGTCCAGCTTGAGGCATATACAGCC	960
Db	901	GAAAGGGTACAAATTAAGGTCATGTTCCGTTTGGTCCAGCTTGAGGCATATACAGCC	960
QY	961	GCTATTTGTCTTACCCAAACATCCGCGGAATGTTTAAACTGTGGGGTAATTCG	1020
Db	961	GCTATTTGTCTTACCCAAACATCCGCGGAATGTTTAAACTGTGGGGTAATTCG	1020
QY	1021	ATPACCACTATGATGGTAAACCTCATATAGAGGGCTATTTTCACTTCATTTCTTAAG	1080
Db	1021	ATPACCACTATGATGGTAAACCTCATATAGAGGGCTATTTTCACTTCGTTTCTTAAG	1080
QY	1081	CAAAATGCTATGCTTTTAAAGAAATGGAAACCTGTGCTAAATTTGTGCAAGTAATTG	1140
Db	1081	CAAAATGCTATGCTTTTAAAGAAATGGAAACCTGTGCTAAATTTGTGCAAGTAATTG	1140
QY	1141	GCTGATGCTGAAGCACCGGCCCAAGAGACCTTGGAAATGGTCTAAATTTAAAGAGCT	1200
Db	1141	GCTGATGCTGAAGCACCGGCCCAAGAGACCTTGGAAATGGTCTAAATTTAAAGAGCT	1200
QY	1201	CATGTTACAGAGAAACACACAGCTGATATTTTATGAGTCTTGTCTCACATCTAT	1260
Db	1201	CATGTTACAGAGAAACACACAGCTGATATTTTATGAGTCTTGTCTCACATCTAT	1260
QY	1261	TTTGGTGTCCCAATGATGCTTTGTGGCAATTAAGTTTAAACACACCTCGGTCACACC	1320
Db	1261	TTTGGTGTCCCAATGATGCTTTTATGCAATTAAGTTTAAACACACCTCGGTCACACC	1320
QY	1321	GTTCACTTGTATCGCTTCGACTTCGATTTGGAAAGATCTTATCAATCCCTATGATTAAG	1380
Db	1321	GTTCACTTGTATCGCTTCGACTTCGATTTGGAAAGATCTTATTAATCCCATGATTAATG	1380
QY	1381	CGTATGAGACGTGCTTAAAGGCTGTTATGTCATGCTGATGAATTAACCTATTTCTTGG	1440

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Db 1381 CCGTAGGACGCTGGTGTAAAGGCTTGTGTCATGCTGATGATTAACCTATTCTCTGG 1440
OY 1441 AATCAATGGCCAAACGATGCTTAAGATCGCTGATACAAACATATGACGATG 1500
Db 1441 AATCAATGGCCAAACGATGCTTAAGATCGCTGATACAAACATATGACGATG 1500
OY 1501 ACTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Db 1501 ACTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
OY 1561 ATGGAATATGTTCTCGGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 ATGGAATATGTTCTCGGATGATGATGATGATGATGATGATGATGATGATGATG 1620
OY 1621 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Db 1621 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
OY 1681 TCGATGTTGAAAAACATAGATGATGATGATGATGATGATGATGATGATGATG 1713
Db 1681 TCGATGTTGAAAAACATAGATGATGATGATGATGATGATGATGATGATGATG 1713

RESULT 8
AAT68597 standard; DNA; 1710 BP.
XX AAT68597;
AC 08-AUG-1997 (first entry)
DT
DE Md-alpha-E7 gene.
XX Malathion carboxylesterase; organophosphate; insecticide;
KW pesticide; remediation; bioremediation; decontamination; ds.
XX Musca domestica Rutgers strain.
OS
XX Key Location/Qualifiers
FH 752
FT mutation /*tag a "Trp-251 TGG codon is altered to a Ser
FT /note- codon in resistant mutants"
CP

W09719176-A1.
XX
XX 29-MAY-1997.
XX 22-NOV-1996; 96WO-AU00746.
XX 23-NOV-1995; 95AU-0006751.
XX (CSTR ) COMMONWEALTH SCI & IND RES ORG.
PA
XX Boyce T, Brownlie JC, Campbell PM, Claudianos C,
PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
XX MPI: 1997-298113/27.
DR P-PSDB: AAM17767.
XX
XX DNA encoding enzyme that degrades organophosphate pesticides -
XX useful for decontamination of soil, water, food etc
XX
XX Claim 6: Fig 3: 52pp: English.
XX
XX A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7
XX coding sequence of the Musca domestica Rutgers strain. It was
XX isolated by amplification of genomic DNA using alpha-esterase
XX consensus primers (see also AAT68598-99) and use of a 534 bp
XX amplicon to screen a genomic library of M. domestica. A
XX mutation of the gene, resulting in substn. of serine for tryptophan
XX at amino acid position 251 (see also AAM17767), confers malathion

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CC resistance. The resistant enzyme acts as a malathion
CC carboxylesterase and can be formulated for use in degrading
CC environmental carboxylester or dimethyl general organophosphates.
XX
XX
SQ Sequence 1710 BP; 498 A; 369 C; 394 G; 449 T; 0 other:
Query Match 55.8%; Score 956.6; DB 18; Length 1710;
Best Local Similarity 73.4%; Pred. No. 6e-253;
Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;
OY 44 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 103
Db 44 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 103
OY 104 CTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 163
Db 104 CTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 163
OY 164 ACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 223
Db 164 ACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 223
OY 224 CACCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAT 283
Db 224 CACCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAT 283
OY 284 CAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 343
Db 284 CAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 343
OY 344 GTGCTATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 403
Db 344 GTGCTATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 403
OY 404 GTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463
Db 404 GTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463
OY 464 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 523
Db 464 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 523
OY 524 TGAATTCAGAAACCTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 583
Db 524 TGAATTCAGAAACCTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 583
OY 584 TGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 643
Db 584 TGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 643
OY 644 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703
Db 644 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703
OY 704 GTCTTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 763
Db 704 GTCTTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 763
OY 764 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 823
Db 764 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 823
OY 824 ATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
Db 824 ATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
OY 884 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 943
Db 884 CACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 943
OY 944 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1003
Db 944 TAGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1003

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QY 1004 CTGCTGGGGATTTGATACCACTATGATGGTAACTTATGAGGCTATTTT 1063
 DB 1004 GCGCTGGGGAAATTCATACCACTATGATGGTAACTTATGAGGCTATTTT 1063
 QY 1064 TCACCTCAATTTCTTACCAATATGCTTGTGAAGAACTTGTGCAAT 1123
 DB 1064 CCAATCAATTTGCAAAATATGCTTGTGAAGAACTTGTGCAAT 1123
 QY 1124 TTGTGCAAGTATGCTGATCTGACGACCCGAGAGACCTTGAATGGGTG 1183
 DB 1124 ATGTGCTGGGAGCTGACGACGACGACGACGACGACGACGACGACG 1183
 QY 1184 CTAATATTTAAAGGCTATGATACAGAGAAACCAACGATATTTATGATC 1243
 DB 1184 CCAATTTGAAAGGCTATGATACAGAGAAACCAACGATATTTATGATC 1243
 QY 1244 TTGTGCTCAATTTCTTACCAATATGCTTGTGAAGAACTTGTGCAAT 1303
 DB 1244 TTGTGCTCAATTTCTTACCAATATGCTTGTGAAGAACTTGTGCAAT 1303
 QY 1304 ACACCTCCGGTACACCCGCTACTTGTATGCTTGTGAAGAACTTGTGCA 1363
 DB 1304 ACACGCTGGGACCTCCATTTATTTGATGCTTGTGAAGAACTTGTGCA 1363
 QY 1364 ATCCCTATGCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1423
 DB 1364 ACCCTATGCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1423
 QY 1424 TAACCTATTTCTTGTGAATCAATTTGCAACGATATGCTTGTGAAGAACT 1483
 DB 1424 TAACCTATTTCTTGTGAATCAATTTGCAACGATATGCTTGTGAAGAACT 1483
 QY 1484 AAACATTTGAAGCTATGATGCTATGATGATGATGATGATGATGATGAT 1543
 DB 1484 AAACATTTGAAGCTATGATGCTATGATGATGATGATGATGATGATGAT 1543
 QY 1544 GCAATGAAATTTGAAGCTATGATGCTATGATGATGATGATGATGATGAT 1603
 DB 1544 GCAATGAAATTTGAAGCTATGATGCTATGATGATGATGATGATGATGAT 1603
 QY 1604 TATCAAGTGTGTAATATGATGATGATGATGATGATGATGATGATGAT 1663
 DB 1604 TATCAAGTGTGTAATATGATGATGATGATGATGATGATGATGATGAT 1663
 QY 1664 AGATTAACAATGAGTGTGTTGAAAAACATGAGATTTATTT 1710
 DB 1664 AAATTAACAATGAGTGTGTTGAAAAACATGAGATTTATTT 1710
 RESULT 9
 ID ABL02067 standard; cDNA; 2001 BP.
 AC ABL02067;
 XX 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide seq ID NO 683.
 KM Drosophila: developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 XX WO200171042-A2.
 PN 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li FWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR P-PSDB; ABB57964.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Claim 1; SEQ ID NO 683; 21bp + Sequence listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB16175), expressed DNA
 CC sequences (AB161840-AB16175) and the encoded proteins
 CC (ABB57737-ABB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 2001 BP; 502 A; 488 C; 521 G; 490 T; 0 other;
 Query Match 39.6%; Score 678.8; DB 23; Length 2001;
 Best Local Similarity 62.7%; Pred. No. 1.9e-176;
 Matches 1074; Conservative 0; Mismatches 637; Indels 3; Gaps 1;
 QY 1 ATGAATTTCAACGTTAGTGTGAGAGAAATTAATGAAGATTAATGAATGA 60
 DB 95 ATGAATTTCAACGTTAGTGTGAGAGAAATTAATGAAGATTAATGAATGA 154
 QY 61 AAGTTTAACTATGCTTAACTACCAATGAAGGCTGAGTGAAGCAATGATG 120
 DB 155 AAGTTCACGATATGCTTAACTACCAATGAAGGCTGAGTGAAGCAATGATG 214
 QY 121 AAGTGAAGGCTTAACTTAACTGCTACGATGATGATGATGATGATGATG 180
 DB 215 CAAGTGAAGGCTTAACTTAACTGCTACGATGATGATGATGATGATGATG 274
 QY 181 ATACCTGACGCTTAACTTAACTGCTACGATGATGATGATGATGATGATG 240
 DB 275 ATCCGCTGACGCTTAACTTAACTGCTACGATGATGATGATGATGATGATG 334
 QY 241 CCTGCGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 300
 DB 335 CCTGCGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 394
 QY 301 ATAAAGGCAAGTGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 360
 DB 395 GTCTTCATTAAGTGAAGGCTGATGCTGATGCTGATGCTGATGCTGATGCT 454
 QY 361 CTAAATCCGAACTAAAGCTGCTTAACTTAACTGCTGATGCTGATGCTG 420
 DB 455 GTGAAGCCGCAAGGCTGCTTAACTTAACTGCTGATGCTGATGCTGATGCT 514
 QY 421 GGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 515 GGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
 QY 481 ATTAACATCAATATGCTTGAAGCTTAACTTAACTGCTGATGCTGATGCTG 540
 DB 575 GTCAAGATATCAATGCTTGAAGCTTAACTTAACTGCTGATGCTGATGCTG 634
 QY 541 AATGTCCTGATGCTGCTTAACTTAACTGCTGATGCTGATGCTGATGCTG 600
 DB 635 AATGTCCTGATGCTGCTTAACTTAACTGCTGATGCTGATGCTGATGCTG 694
 QY 601 AATGTCCTGATGCTGCTTAACTTAACTGCTGATGCTGATGCTGATGCTG 660

Db	695	AATTGCGCTACTGTTTCGGGGGAGATCCCAACTGCATCTACTGTTTTTTTGGAGAGAGTGGTGA	754
Qy	661	GCTGCGCTTACCCACTACATGATGTTTAAACGACAAACATCGCGGTCCTTTTCATCTGTTG	720
Db	755	GCGCGCTTCACTCACTACATGATGCTAAACGATCAGAACCCAAAGGGCTCTTTCACTCGCGGC	814
Qy	721	ATACTAATGTCGGGTAATGCTATTGTTCTCATTTGGC---TAATACCCAATGTCACATCGT	777
Db	815	ATCTTGACAGTGGCGGACAGTCCATTGTTGCTTGGGCGTACCAAGCGCGACATTACCATTAT	874
Qy	778	GCGTTCACCTTAGCCAAATTTGGCGGGCTATTAAGGGTGAAGATTAATGATMAAGATGTTTG	837
Db	875	CCCTACAGGATGCCAACGTGTTGGCTTCAACAGGGCCGAGAACACGACAAAGATGTGCTG	934
Qy	838	GAATTTCTTATGAAAGCCAAAGCCACACGATTTTAATAACTTGAAGAAAAGTTTAACT	897
Db	935	GAGTCTTGACAGACGTAAAGGCCAAGATCTTATTCCGCTGGAGAAATGTCCTGACA	994
Qy	898	CTAAGAAAGCGTACAAATTAAGTGCATGTTTCTTTTGGGCCACAGTGTAGACCATATCAG	957
Db	995	CTGGAGGAAGCATGAACAAATGATGTTTGGCTTTGGGCCATCCCTGGAACCATTTGCC	1054
Qy	958	ACCGCTGATTTGTCTTACCCAACATCTCTGGGAATGTTTAAACTGCTTGGGGTAT	1017
Db	1055	ACCGCCGAATGTGTGATTTCCAAAGCCTCCAAAGAGATGATMAAAGCCCTGGAGTAAC	1114
Qy	1018	TGCATACCCACTATGATGGGTAACTGTATATGAGAGGCTATTTTTCACCTCAATCTT	1077
Db	1115	TTCATCCCCATGTTTATAGAAACACTTGTAAGAGGGCTCTGCGGTTCCAGAGTA	1174
Qy	1078	AACCAATGCCCTATGCTGTTTAAAGAAATTTGGAACCTGTGTCATTTTGTCCAACTGA	1137
Db	1175	AAGCTTATGCGGACAGGTGCTGACGACGTGATGCTGGCACACCTTTCATTCOCNAAGAA	1234
Qy	1138	TTGGCTGATGCTGAAGCACCAGCCGCCAGAGACCTTGGAAATGGGTCCTAAATTTAAAG	1197
Db	1235	TTTGCTGGCCACAGGAGCCCAATAAGAAAATCTGGATTTCTGGAGTGCACAGATTCGAGAT	1294
Qy	1198	GCTCATGTTTCAGAGAAACACCAACAGCTGATTAATTTTATGAGATTTTGTGCTCAATTC	1257
Db	1295	GTTTATGCACTGCGCTCAGAAAGCACCCAGATTAATTAATGATGATCTCTGTTGATTTAC	1354
Qy	1258	TATTTCTGTTCCCATGATCGTTTGTTCATTTACGTTTCAATCACAACCTCGGGTACA	1317
Db	1355	TACTTCGATGTTTCGGGCGCTGAGGGTGTGTCATTCGCCAGACGCTAGCGTGGGCTGACT	1414
Qy	1318	CCCGTCTACTGTTATGCGCTTGCATTTGCGATTTGCGAATCTTTATCAATCCCTATGTAAT	1377
Db	1415	CCAGTATATTTCTATCGATTAATGACTTGTGACTCGAGAGCTCANTTTTCGTTACCGCAT	1474
Qy	1378	ATGCTATGAGACGTGTTAAAGGATTAAGTATGCTGATGATTAACCTATTTCCTC	1437
Db	1475	ATGCGGTTGGGACGGGGGTGTCAGAGGGGTACAGCTGCCGACGATTTGAGTGCATCAATTC	1534
Qy	1438	TGGAATCAATTGGCCAAACGATATGCTTAATAAATCGGCTGAAATCAAAACAAATTTGAAGT	1497
Db	1535	AGCACCTCTGCTGGCTCGCGGCTTGGCGGAGAAAGTGCAGATCAGAGACATTTGAAAGA	1594
Qy	1498	ATGACCTGATATGATGATCAATTTGCCACCACTGGTAAATCCCTTATAGCAATGAATTTGAA	1557
Db	1595	ACCGTGGGATCTGACCAACGATTTGCTGCCACGGGTATCCCTACAGGAGAAATGATCAAC	1654
Qy	1558	GGTATGAAATGTTTCTGGGATCCATTTAAGAAATCCGATGAAAGTATACAGTGTG	1617
Db	1655	GGATGAGACACTCTACCTGATTCAGATTTGCAATATCCGAGAGTATATAAGTGCCTC	1714
Qy	1618	AATATTAGATGAATTTGAAATGATTAATGATGCTGAAATGATTAAGATTTAAACATGG	1677
Db	1715	AACATCAGTGAATGACTGAAGTTTCAATGATCTGCTTGATGGGCCCAATTTGAAGGTCTGG	1774
Qy	1678	GAGTCATGTTGAAAAACATAGAGATTTATTTT	1711

Db	1775 GAGACCTTATGACGCACCACAAGAATTATTGTCT	1808
	RESULT 10	
Xx	ABL02081	
XX	ABL02081 standard; cDNA: 1704 BP.	
XX	ABL02081;	
Ac		
Df	26-MAR-2002 (first entry)	
xx	Drosophila melanogaster expressed polynucleotide SEQ ID NO 725.	
DE		
xx	Drosophilina: developmental biology; cell signalling; insecticide;	
KW	pharmaceutical; gene; ss.	
KM	Drosophilla melanogaster.	
OS		
XX	WO200171042-A2.	
Pn		
PD	27-SEP-2001.	
XX	23-MAR-2001; 2001MO-US09231.	
PF		
XX	23-MAR-2000; 2000US-191637P.	
PR	11-JUL-2000; 2000US-061415O.	
XX	(PEKE) PE CORP NY.	
PA		
XX	Venter JC, Adams M, Li PWD, Myers EW;	
PI		
XX	WFI; 2001-656860/75.	
DR	P-PDSB; ABB57978.	
XX	New isolated nucleic acid detection reagent for detecting 1000 or more	
PT	genes from Drosophila and for elucidating cell signalling and cell-cell	
PT	interactions -	
Claim 1:	SEQ ID NO 725; 21pp + Sequence Listing; English.	
PS	The invention relates to an isolated nucleic acid detection reagent	
CC	cable of detecting 1000 or more genes from drosophila. The invention is	
CC	useful in developmental biology and in elucidating cell signalling and	
CC	cell-cell interactions in higher eukaryotes for the development of	
CC	insecticides, therapeutics and pharmaceutical drugs. The invention	
CC	discloses genomic DNA sequences (ABLI16176-ABIJ30511), expressed DNA	
CC	sequences (ABLI0840-ABLI6175) and the encoded proteins	
CC	(ABB57737-ABB72072).	
CC	The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
at ftp.wipo.int/pub/published_pct.sequences.		
Sequence 1704 BP; 417 A; 445 C; 460 G; 382 T; 0 other;		
SQ		
Query Match	22.3%; Score 381.8; DB 23; Length 1704;	
Best Local Similarity	54.0%; Pred. No. 1.le-94;	
Matches 879; Conservative	0; Mismatches 727; Indels 21; Gaps	
Oy	85 ACCAATGAACGGTGTAAGCGTTAAACTCAATATGCGAACACTGAAAGCCTTAAAGCTTAA 144	
Bd	64 AGCATATGCAAGATTCATGCCGACACGCTTACGGAAGGTGAAGGGGTGAAGTGGCAG 123	
Oy	145 ACTGTGTAOGATGATTCTCTACTACAGTTTTGAGGGTTFACGTCAGCCCCAACCCGCAAGTG 204	
Bd	124 TTCATCTCAGGCAACAACTACTACAGCTTCGAGGGCATCCCCTGGCGCAAGCCGCCGGTG 183	
Oy	205 GGATGAGCTGAGATTATAAGCACCCAGCCAGCAAACACCTTGGGTGTGTCGTGATTGT 264	
Bd	184 GCGGACCTCCGTTCAAGCGCCGCTGAGCCAGGCACTGGTAGATGTCACAGCGGTGC 243	
Oy	265 TGCAATCATTAAGATTAAGTCAAGTCAAGTGAATTTTAAAGGGCCAAGAGTGTGGCTCA 324	
Bd	244 ACACATGTTGGCGCCAAAGCCCTGCGAGGTCAACATCGTTCTGAAGCAGAGTCAAGGCGAGC 303	

QY 325 GAGATGTTGCTATACCTAAGTGTCTATACGAATAATCTAATCCGGAACATAACGTCC 384
 DB 304 GAGAGCTGTCTGTAACCTCAATGCTACACGAGGATTCACACAGACCTTTGGCG 363
 QY 385 GTTTAGTATACATACATGAGTGTGTTTATATCGGTGAATAATCATCGATATGAT 444
 DB 364 GTTGTGTTGATCTATGAGGGGTGATTCGAATGGAGAGAGATCGGGGATCTGTAC 423
 QY 445 GGTCTGATTAATTTCAATTAAGAGATGTGTTGATTAACATACATATCGTTGGGA 504
 DB 424 AGCCCGGACTATATGATGATGACATGTCTACTGTGCTAATATCTTATCGTTAGA 483
 QY 505 GCTAGATTTTCAAGTTTAAATTCAGAAACCTTATGTGCCCCGTAATCCGGCTT 564
 DB 484 GCGCTGGATTCCTTAGCTTGACAGACGAAACGTGATGTTCTGTGAACGCGGACTA 543
 QY 565 AAGATCAAGTCAATGAGCTTGGTGTGATTAATAATATTCGCGCAACTTGTGGCAAT 624
 DB 544 AAGATCAAGTATATGAGCTTGGTGTGATTAATAATATTCGCGCAACTTGTGGCAAT 603
 QY 625 CCCGATTAATATACAGTCTTGTGAAAGTCCGCTGCTTACCCACTACATGATG 684
 DB 604 CCCGATTAATATACAGTCTTGTGAAAGTCCGCTGCTTACCCACTACATGATG 663
 QY 685 TTAACCGAACAACGTCGCTTGTTCATGCTGTGATACATATGTTGGAATGCTATT 744
 DB 664 CTGACGATTCAGGCGCAAGGCTTATTTACAAAGCTATTAATGTTGGATCCGACTG 723
 QY 745 TGTCCATTGGCTAATACCAATGTCA--ACATGTCGCTTACCTTACCCAAATTGGCC 801
 DB 724 GCACCTTGGCGGACAGCCCAACCAACCAATTAATGGCCCTTATGCGCTGGACAGCCACT 783
 QY 802 GGCCTAAGGTTGAGATGATGATAGAGATTTTGGAAATTTCTTATAAAGCCAGCCA 861
 DB 784 GGCCTAAGGTTGAGATGATGATAGAGATTTTGGAAATTTCTTATAAAGCCAGCCA 843
 QY 862 CAGATTTAATTAATACTGAGAAAGTTTAACTAGAGAAAGCCGTAATAAGT- 920
 DB 844 AGTAGCATGCTGAAGGTGCGGAGATATCATCAGCATGAGAGAGACACACGAGTTG 903
 QY 921 --CATGTTCTTGTGTCACAGTGTGAGCCATATCAGACCGCTGATTTGTCTTACC 978
 DB 904 ACCATGTTCACTTGTGAGCCATCAGCCCTATTTGATTCCTCATTTGTGTATCC 963
 QY 979 AAACATCTCGGGAATGTTAAACTGCTGGGTAAATTTGATACCCACTATGAGGT 1038
 DB 964 AAGTCGACAGTGAATATGATCGGAGCTGTTGGGCAACACATTCCTGTCATCGA 1023
 QY 1039 AACATTCATTTGAGGCTCTATTTTCTCAATTTCTTAAGCAAAATGCTATGCTT 1098
 DB 1024 GGAACCTCTTCGAAGGCTCTCTCATGTTTCCCAAGTGAACAGTGCCGGAATGCTT 1083
 QY 1099 AAGGAATTTGAACCTTGTCAATTTTGTGCAAGTGAATTTGGCTGATGTCAGACACC 1158
 DB 1084 TGCCAGCTGGGTGACGGAACCTGCGCCCTCAAGATGCCCAGTGATGAGAGCAA 1143
 QY 1159 GCCCAGAGACTTGGAAATGAGTGTCTAAATTAATAAGGCTCATGTTACAGAGAAACA 1218
 DB 1144 AGAAAGGTTTGAAGAAAGATGAGAGCTATATTTCGGCGATGAGACTCTCGGAGG 1203
 QY 1219 CCAACAGCTGATTAATTTATGATCTTGTCTCATATTTTGTGTTCCCTCCATGAT 1278
 DB 1204 AAGACATATTTGAGTACAGGATCTTCTTCGTAACAATATTTTGGCANTGACATTTAT 1263
 QY 1279 CGTTTGTGCAATTAAGTTCAATCACACTCCGCTACACCCGCTTACTGTATGCTTC 1338
 DB 1264 AGGACTTTGCTGCTGCTGCTACACAGCCCATTTGGCCCAACATTCCTGTACCGATTC 1323
 QY 1339 GACTTCGATTTGGAGATCTTATCATCCCTATGCTATTAATGCGTAGTGAGCGTGTTC 1398
 DB 1324 GATTCGACTCG--AACCTTCAATATCATGCAATTAATACACTTGTGGCGCAAGGTG 1380

QY 1399 AAGGCTTAGCATGCTGATGAATTAACCTATTCTTCTGGAATCATTTGGCAACGT 1458
 DB 1381 CGCGGACCTGTACGCGGATGATCTGTCTATTGTTCTACAAAGCGGCTCCAAAG 1440
 QY 1459 ATGCTTAAGAATCGCTGAATACAAACAATTTGAACCTATGACTGATATGATACAA 1518
 DB 1441 CTGAAGCCGACACAGCGGAGTCAAGACATTAAGCCTTTTGTGATGCTGCTTAC 1500
 QY 1519 TTTGGCCACTGTTGATCTTATTA-----GCATGAATAAGATATGAA 1566
 DB 1501 TTTGCAATTTCCGGGATCCCAACATACGATGCTGCTCCAGATGAGAAAGCAAGCCG 1560
 QY 1567 AATGTTCTCGGATCCATTAAGAATCCCATGAAGTATCAATGCTTTGAATTTACT 1626
 DB 1561 CGTGCGGCTGCTGCCATTTTCGAAGSAGATTAAGTGTTCACAGTCCCTGAATATTCG 1620
 QY 1627 GATGAATTAAGAATATGATGATGCTGCTGAATGATTAAGATTAACAATGAGATCAGT 1686
 DB 1621 CACGATGTCATGATGATGATTTTGGCCGAGCGCAAGCGCAAAAGCTGACACTTGGACTGCATC 1680
 QY 1687 TTTGAAA 1693
 DB 1681 TACGACA 1687
 RESULT 11
 ABL02066
 ID ABL02066 standard; cDNA; 6175 BP.
 XX
 AC ABL02066;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 680.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 XX
 DR P-PSDB; ABB57963.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 680; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB5737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

xx Sequence 6175 BP: 1732 A; 1242 C; 1350 G; 1851 T; 0 other:
SO Query Match 21.6%; Score 370.6; DB 23; Length 6175;
Best Local Similarity 54.5%; Pred. No. 2,2e-91;
Matches 1052; Conservative 0; Mismatches 614; Indels 263; Gaps 5;

QY 46 AATTCATTGAAATTAAGTTTAACTATGCTTAACTACTAACAATGAAGCTGTAGCT 105
DB 3054 AGAACCATGAGCATTAAGCTCCAGCATATCCAGCATGAACCAATGAACATGTGCCC 3113
QY 106 GAATCGAATATGGCAAGGAAAGGCGTTAAAGCTTTAACTGTGTACGATGATTCCTAC 165
DB 3114 GACACGGAGTACGGCCAAAGTGAAGGGGTATCAAGCGCTATCTCTACGATGTGCCAC 3173
QY 166 TACAGTTTGGAGGTATACCTACGCCCAACGCCAGTGGGTGAGTGGATTTAAAGCA 225
DB 3174 TTGAGCTTCGAGGGTATCCCTGACGCCAGCCCTCGGTGGGGAGTGGGTTTAAAGCC 3233
QY 226 CCCCAGGACCAACACCCTGGAGTGGTGGCTGATTTGCAATCAATGAAGTGA 285
DB 3234 CCTGAGAGGCCCATTCCTGAGAGCCAGTTCGCGACTGCAAGCCGGAAGATTAAGCC 3293
QY 286 GTGCAAGTTGATTTATTAAGGGGCAAGGTGTGGCTCAGAGATTTGTCTATACCTAAGT 345
DB 3294 GTCCAGGTGCACTTCCTGATTAAGGTAGAGGGCTCCGAGAGCTGCTTATCTCAAT 3353
QY 346 GTCTATACGAATTAAT----- 360
DB 3354 GTGTACACCAACAAATGAGTAATTTCTATTAATCTGTATCAATGAACATCGTTAAAC 3413
QY 361 -----CTAATCCCAACAAACG 380
DB 3414 GTAATTAACCTTAAACATTTTATTTGTGTACATTTTAAAGTGAAGCCGAGGCTCG 3473
QY 381 TCCCGTTTATGATATCATATCATATGCTGTATTTATTTATTCGTAATAATCATCTGATAT 440
DB 3474 CCGGGTATGATTTGATTCACGAGAGGCTTCAATTTACGGCGGCAATCCGGAGATG 3533
QY 441 GTATGGTCTGATTTATTTCAATTAAGAGATGTGTGTGATTAACATCAATCAATTCGTT 500
DB 3534 GTATGGCCCGGATTAATTTATGAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3533
QY 501 GGAAGCTCT----- 509
DB 3594 TGGGGCTTGGGTAATCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3553
QY 510 -----AGTTTTTCTAAGTTTAAATTCAGAAAGCTTATGTGCCGGTATGCGCGCC 562
DB 3654 CCTTACACAGGATTTATGAGTCTTAAGTCCCGAGCTAATATGACAGGAATTCCTGTGCC 3713
QY 563 TTAAAGTCAAGTCAAGTCCCTGCGTTGATTAATAATTTGCGCAACTTTGTGTGCA 622
DB 3714 TCAAGGATCAGT 3773
QY 623 ATCCCGAATATATACAGTCTTTGGTGAAGTCCCGGTGTGTGTGTGTGTGTGTGTGTGT 682
DB 3774 ATCCCACTGATCACTGTTTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3833
QY 683 TGTTAACCGAACAACCTGCGGTCTTTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 742
DB 3834 TGTCAACCGATCAAGCCCAAGGCTCTTTCATGCGCGCATCTTGTGTGTGTGTGTGT 3893
QY 743 TTTTGTTCATTTGAC--TAAATACCAATGTCAACATGCTGCTTACCTTATGCAATTTG 799
DB 3894 TTTTGTCTTTGGGCTTACAAAGCGCATTTACCAATATCCCTACAGGATGACCAAGCTGG 3953
QY 800 CCGGCTATTAAGGTGAGATATGATTAAGATGTTTGAATTTCTATGAAGCCAAAGC 859
DB 3954 TTGGCTACAAAGGCGAGCAACAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4013
QY 860 CACAGGATTTAATAAAGCTTGAAGAAAAGTTTAACTCTAGAAGAGCTTCAATATAGG 919

DB 4014 CCAAGATCTTATTCGCGTGGAGAAAATGTCTGACACTGTGAGGAACGATGAACAGA 4073
QY 920 TCATGTTTCTTTTGT 979
DB 4074 TAAATGTTTCTTTGCGCATTCCTGTGAACATTTCTCCAGCCCGGATGTGTATCA 4133
QY 980 AACATCTCGGGAATATGTTTAAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1039
DB 4134 AGCTTCAAGAGATGATGAAGACCGCTGTGATCAATCCATCCATGTTTAAAGAA 4193
QY 1040 ACATCTCATATGAGGTCT----- 1058
DB 4194 ACATCTGTACAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4253
QY 1059 -----ATTTTCACTCAATTTCTTAAGCAATGCTTATGCTGT 1097
DB 4254 TTCTTTCAATTAAGTAATTTAATTTATTTATTTCAAGAGTAAGCTTATGCGCAG 4313
QY 1098 TAAAGATTTGAAACCTGTGTCAATTTTGTGCAAGTGAATGTGTGTGTGTGTGTGT 1157
DB 4314 GCACGACTTGATGT 4373
QY 1158 CGCCCAAGACCTTGTGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1217
DB 4374 TAAAGAAAACCTGT 4433
QY 1218 ACCAAGACCTGATTAATTTATGAT----- 1242
DB 4434 AAGCAACCCAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 4493
QY 1243 -----CTTGTCTCACTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1282
DB 4494 AAGCTGTAATTTATTTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4553
QY 1283 TGTTCATTTACCTTTCAATCAACCTCCGCTACACCGCTCTCTGTGTGTGTGTGTGT 1342
DB 4554 TGTTCATTTCCGACACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4613
QY 1343 TCGATTCGGAATCTTATCAATCCCTATGATTTATGATGTGTGTGTGTGTGTGTGT 1402
DB 4614 TCGACTCGAGAGGCTCATTTTCCGTACCCATATGCTGTGTGTGTGTGTGTGTGT 1463
QY 1403 GTGTATGATGCTGT 1462
DB 4674 GGGTACAGCATCCGACGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4733
QY 1463 CTAAAGATCGGCTGAATCAAAACATTTGAAGATGATGATGATGATGATGATGATG 1522
DB 4734 CGAAGGAAGTCCGAGTACAGAAACATGAGAACGAGTGTGTGTGTGTGTGTGTGT 4793
QY 1523 CCACACCTGTATTCCTTATAGCAATGAATGAAGTGTGTGTGTGTGTGTGTGTGTGT 1582
DB 4794 CTGCGACGGGTAAATCCCTACAGGAGAGATCAACGATGTGTGTGTGTGTGTGTGT 4853
QY 1583 CAATTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1642
DB 4854 CAGTTGCCAATTCGAGAGAGTCAATCAAGTCAATCAATCAATCAATCAATCAATCA 4913
QY 1643 TTGATGTGCTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1702
DB 4914 TCGATTCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4973
QY 1703 ATTTATTTT 1711
DB 4974 ATTTATTTG 4982

RESULT 12
AB102099
ID AB102099 standard; cdna; 1665 bp.
xx
AC
xx AB102099;
xx

DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 779.
 DE
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PD 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 XX MPI; 2001-656860/75.
 DR P-PSDB; ABB57996.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 779; 21np + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB16175), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX Sequence 1665 BP; 397 A; 446 C; 468 G; 354 T; 0 other;
 SX

Query Match 21.5%; Score 368.2; DB 23; Length 1665;
 Best Local Similarity 52.4%; Pred. No. 5.8e-91;
 Matches 861; Conservative 0; Mismatches 773; Indels 9; Gaps 2;

QY 53 TTGAAATTAAGTTTAACTATGTTTAACTACCAATGAACGGGTAGCTGAACCTG 112
 DB 5 TCGACTTTAAGTCCAAACAGACGATACAGACGAGAAAGACGTCTCAGCACCA 64
 QY 113 AATATGCAAGTGAAGGCGTTAAACGTTTAACTGTAGATGATTCCTACTACAGTT 172
 DB 65 CCGTACGACCACTCAAGGGGTGTAAGGAGGATCCATCTACGGCAGCTTCTCACT 124
 QY 173 TTGAGGATTAACCTAGCCCAACCGCAGTGGTGAAGTTTAAGACCCAGC 232
 DB 125 TCGAGGATTCCTCTGCGCAACACCGGCGGAGCTACGCTAACAGGCTCCAGC 184
 QY 233 GACCAACACCTCGGATGTTGCGTGTGCTGATGCTCAATCAATGAAGTACGTCGAG 292
 DB 185 CCGCGGAGGCTTGACGAGAGGTCAAGAGCTGACCTCCAGGGTCCCAAGCCACTGCA 244
 QY 293 TTGATTTTAAACGGCAAGTGTGTGCTCAGAGATTTGCTATACCTAAGTCTATA 352
 DB 245 AGCACTTCGTGTGATGACATGACGATGCTCCAGGACTGCTTACTCTCATTTCTACA 304
 QY 353 CGAATTAATCTAATCCGGAATCAACGTCCTGTTAGTATACATACATGCTGCTGTT 412
 DB 305 CAAGAATTTGTATCCACCAACCAATGCCGTGATGCTGTGATCTATGAGCGGTGCT 364

QY 413 TTATTATCGTGAATAATCATGCTATATGATGCTGATTTATTTATTAAGAGATG 472
 DB 365 TCCAGTTTGGGAGAGCCTCAGCGGAATGTTACAGTCCGAGTTATTTGCTGCTGAGATG 424
 QY 473 TGTGTTGATTAAACATCAATATGCTTTGGAGCTAGATTTTCTAAGTTTAAATTCAG 532
 DB 425 TGTGTCATTTCTATCAACTACAGATGTTGGAGACCACTGGATTTCTGTCCTGGAGCATC 484
 QY 533 AAGACCTTAATATGTCGGGATATGCGGCTTAAAGATCAAGTCATGCGCTTGGTGA 592
 DB 485 CCGAATCTGATGTCCCGGCAATGCGGATCAAGAGATCAAGTGTGCGCTGGCTGGG 544
 QY 593 TTAATAATTAATTTGGCCCACTTTGTGCAATCCCGATATATTACATCTTTGGTGA 652
 DB 545 TCAAGGCCAATGTTCCGCTTTGCGAGGCGATTTCCGCAATATTAACAATTTTGGGACA 604
 QY 653 GTGCGGCTGCTGCTCTACACCATACATATGATTAACCAACAACTGCGCTCTTTCC 712
 DB 605 GTGCGGAGAGTCTCGGTTCACTACATGATGATCAGACAGACGATGAGACTTTTCC 664
 QY 713 ATCGTGTATCTATATGTCGGGTAAATGCTATTTGTCATTTGCTAATACCAATGTCAAC 772
 DB 665 ACAAGGCCATCTGATGCTGGGTATATAGCTTTCCCTGGGCGAGTCTCTCAGAGAA 724
 QY 773 ATCGTGCCTTCACCTTACCCAAATTTGGCGGCTTAAAGGTGAGATATATAGATG 832
 DB 725 ACTGCGCATATCGGTGTGCTGTCCAGGCGGGTTACGAGGTGAAACACACCGCGATG 784
 QY 833 TTTTGAATTTCTTATGAAAGCCAAAGCCACAGATTTAATTAACCTTGAGAAAAAGTTT 892
 DB 785 TCTGGAGATCTCGAAGAACCCCAAGGATCCGAATATCATCAAGCCAAATGAGAACTCT 844
 QY 893 TAACCTAGAGACAGCTACAAATTAAGTCAATGTTTCTTTTGGTCCCACTGTAGCCAT 952
 DB 845 GCATTGACGAGAAAGAAAGAGCGGATGATGCTCTTTTGGCGCTTAATTCGAAACGCT 904
 QY 953 ATCAGACCGCTGATGTTGCTTACCAACATCTCGGGAATGATTAACCTGCTGGG 1012
 DB 905 ATGTAACGACGACCTGTGTGTTGCGGAAAGAACCATTCGAATATATGAAACCGCTGGA 964
 QY 1013 GTAAATGATACCCACATATGATGAGTAACTTCAATATGAGGCTATATTTTCACTTCAA 1072
 DB 965 GCAATTAATATCCCACTTATCATTCGAGCGCTTCCCAAGAGGCGCTCTCTGTACTCAG 1024
 QY 1073 TTCTTAAGCAATGCTATATGCTTGTAGGAATTTGGAACCTGTCTCAATTTTGGCCAA 1132
 DB 1025 AGACCAAGACGAATCCGAAGTGTCTAAACGATGTGAGACGACTGCGGTTTGTGTCCTA 1084
 QY 1133 GTGAATTTGCTGATGCTGAACGCAACCGC-----CCGAGAGACCTTGGAATGGGTGCTA 1186
 DB 1085 TCGAATTAATATGACAGGGAAGAGTGCCCTGTGCGGGAGATTACGGCATCAGTGAAGC 1144
 QY 1187 AAATTAAGAGCTCATGTTACAGAGAAACACACACAGCTGATTAATTTATGATCTTT 1246
 DB 1145 AGTCTACTAGCGGATTAAGACGCCAGTCTGACACCCCTCATGTAATACCTTCAGATGG 1204
 QY 1247 GCTCTCATATATTTCTGCTTCCCATGATGCTGTTTGTGCAATTTAGCTTTCAATCA 1306
 DB 1205 TTTCCCAAGATCTCTGTTGTTTCCCAATATATACCGACATATTTGCTCCGCTGCAATG 1264
 QY 1307 CCTCGGATACACCGCTTACTTGTATGCTCTGATGCTGATTTGGAATCTTATCAATC 1366
 DB 1265 CTGCGACGTGCGCCGACGATTTTGTATCCCTTCCGACTTGCAGCTC---CAAGCACTTCAACC 1321
 QY 1367 CCTATCGTATTATGCTGATGAGAGTGTGTTAAGGGTGTATAGTCATCTGATGAATTA 1426
 DB 1322 ACCTGCGCATCTCTGATGTTGCGCAAAAAGGTGAGGGGACACGTCCACGCGCAGATCTGT 1381
 QY 1427 CCTATTTCTTGTGAATCAATTTGGCAACCTATGCTTAAGAGATCGCGTGAATCAAAA 1486
 DB 1382 CCTACTGTTTGTACAACTCGCTGAGAGAACTCAAAAGACACACGCGGAGATGAACAAGT 1441
 QY 1487 CAATTAAGATGATGCTGATATGATGAACAATTTGCCACACACGTGATATCTTATACCA 1546

QY	1190	TTAAAAGGCTATGTTATCAGGGAACCAACACACCTGATTAATTTATGGATCTTCCCT	1249
Db	1281	TCCTACTCCAAACAGAGATCAGAGAAATTCATGAGATGTTGACGCCCTGAAATATATTTT	1340
QY	1250	CTCACATCTATTTCTGGTTCCCATCATCGTTTGTGGCAATTACGTTTCAATCACACCT	1309
Db	1341	CGCATCCCCAGATTTTGGCAGATACCAATCGCTTTATCTCCGCCGTCMAATCTTATGCC	1400
QY	1310	CCGGTACACCGCTACTTTGATCGGTGACCTGGATTCGGAAGATCTTATCATCCCT	1369
Db	1401	CCAAACGCCCACCCTATCTATATCGTTTGGACTTTGGACTC---CCCGCATTCATATCAT	1457
QY	1370	ATCGTATTTATGCGTAGTGAAGCGTGTAAAGGGTTTATGTCATGCTGATGAATTAACCT	1429
Db	1458	TTCCGCACGTGTTGGCGGGATTCGGATTCCGGATAGCCATCGGATGAATCATATCAT	1517
QY	1430	ATTCTCTCTGGAATCAATTTGGCCAAACGTAATGCTTAAGAATTCGCTGAATTCAAACAA	1489
Db	1518	ACCGTTCTCCAAACATCATATGCCCTCCAAACATGGATAGTCATGATGAATCAAAACCA	1577
QY	1490	TTGACCTATGACTGCTATATATGATACAAATTTGCCACACTGTAATCCTTATACATG	1549
Db	1578	TTGAGAGAAATGTGGCATATGGACGTCTTTGCCCTCCAGTGGGAATCCAAATTTGCCAG	1637
QY	1550	AAATTTGAAGCTATGCAAAATGTTTCTCGGATCCAAATTAAGAATTCGATGAAGTATACA	1609
Db	1638	AACGTGATCTGCCAAATGGGAAGCCGTCCAG-----TTAAACAAATGCCGTGGAGA	1691
QY	1610	AGCTTTGAATATATATGATGAATTTGAATATGATATGCTCTGAATATGAT	1662
Db	1692	AGCTCTTCAACATTAGCCACAGACTCTTGAGTGTGGAGATTTTGGCGGAGTCCGAT	1744

CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
XX	
PS	Claim 1; SEQ ID NO 791; 21pp + Sequence Listing; English.
PT	
PR	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
XX	
DR	P-PSDB: ABB58000.
PI	WPI: 2001-656860/75.
XX	
PA	Venter JC, Adams M, Li PWD, Myers EW;
XX	
PE	(PEKE) PE CORP NY.
XX	
PD	23-MAR-2001; 2001WO-US09231.
PN	23-MAR-2000; 2000US-191637P.
XX	
OS	11-JUL-2000; 2000US-0614150.
XX	
DE	Drosophila melanogaster.
KW	Drosophila melanogaster.
XX	
AC	WO200171042-A2.
XX	
AB	27-SEP-2001.
DT	
XX	
AB	26-MAR-2002 (first entry)
XX	
AB	Drosophila melanogaster expressed polynucleotide SEQ ID NO 791.
XX	
AB	Drosophila developmental biology; cell signalling; insecticide;
XX	
AB	pharmaceutical; gene; ss.
XX	
ID	ABL02103 standard; CDNA; 1593 BP.
XX	
AB	ABL02103;
XX	
RESULT	14

CC useful developmental biology in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceuticals. The invention
CC discloses genomic DNA sequences (AB161716-AB130511), expressed DNA
CC sequences (AB101840-AB161617) and the encoded proteins
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPAC
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SQ Sequence 1593 BP; 417 A; 394 C; 405 G; 377 T; 0 other;

Query match	18.9%;	Score 323.6;	DB 23;	Length 1593;
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Matches 831; Conservative 0; Mismatches 709; Indels 32; Gaps 5;

OY	111	TGATATGGCGAAGTGAAGAGCGCTTAAAGCTTTAACTGTGATCAAGTATGTTCTCTACG	170
Db	6	TGACTGGGGCTCTGTGGGGGAGTGAAGAGAAACACATCTGGGGAGAACACTTCTTACG	65
OY	171	TTTTGAGGGTATACCGTACCGCCCAACCGCCAGTGGGTGAGCTGAGATTTTAAAGCACCCA	230
Db	66	TTTGGAAATATACCTTCTCGCAAGAGCTCCGGTGGGAGATCTGCCTTCAGAGCCCGGA	125
OY	231	GGGACCAACCCCTGGGATGCTGGCTATTTGCTTCATCTCTAAAGTAAAGTCAATGCA	290
Db	126	AGCAGTGGACCCATGGGATAGGAATTTGATTTGCATCTTCGCGGGAGCAAGCCCTTCA	185
OY	291	AGTTGATTTTATTAACGGGCAAGTGTGTGGCTCAGAGATTTGTCTATCTATAGTCTTA	350
Db	186	GACACACATGTTTTCAGAAAATACCGGGGCTCAGAGAGCTCCCTCTCTTAATATGTGA	245
OY	351	TACGATATATCTAAATCCGCAACTAAGCTCCCTTTTAACTATACATACATGCTGTGG	410
Db	246	TGTCAAAGATCTGACGGCGGATTAACGTGGCTCCGCTGATGTTTGATCTACGGAGAGG	305
OY	411	TTTTATATGGGGAAGATCATGATATGATATGATGCTGCTGATTTTTCATTAATAAGGA	470
Db	306	CTATCAGTTGGGCAACCTTCTGGGATATGACATGCTCCGCTTTTTCATATGTGGAAGA	365
OY	471	TGTGTGTTTATTAACATACATACATATGTTTGGAGCTATAGTTTTCTAACTTTAAATTC	530
Db	366	TGTGTGATATGTCACCGTGTCTTATGACGTGGGTGCTTGGGCTTCCTACGCTGATGA	425
OY	531	AGAAAGCCTTAATATGTGCCGGTATATCCCGGCTTAAAGTCAAGTCATGCGCTTGCTTG	590
Db	426	TCCCAACTAAAGCTTCCCGGAATACAGATCTCAAGATCTAAATCATAGGCGCTTCATG	485
OY	591	GATTAAATAATATGCGCCCAACTTGTGTGCAATCCGATATATTAAGTCTTTGGGA	650
Db	486	GGTGCACAAACATGCAAGCATTTGGCGGTGATTTCCAAACATATTAACACTTTTGGCGA	545
OY	651	AAGTGGCGGTGCTGCTTACCACATCATGATGTTAACGCAACAACTCGCGGCTCTTTT	710
Db	546	AAGTGGCGGGAGCGCTGACCCACTTCTTGACATAGTCTCCCAACTGAAGGCTTAT	605
OY	711	CCATGCTGTATACTAATGTGCGGGTATGCTATTTGTCTATTGGCTAATACCAATGTCA	770
Db	606	CCACAAAGCATGTTATTTGTCGGGAGTGTTTTGTGCCCTGTGAGCAGCAACCGAGAAA	665
OY	771	ACATGCTGCCCTTACCTTACCACAAATTGGCGGGCTATAAGGTTGAGATTAATGAATAAGA	830
Db	666	TAAATTTGGCTTATAGCTTGCCCAAAAATTTGGGATACACGGTGTGCAATTAAGCAAGCC	725
OY	831	TGTTTGAATTTCTTATGAAGCCCAAGCCACAGATTTTAATAAACTTGAAGAAAAGT	890
Db	726	GATCTTTGATTTCTGCGATCAATGATGTGGCGGGAGATTTCAAGGCGCACCGCAACAGT	785
OY	891	TTTAACCTTGAAGAGGCTCAAAATTAAGTCATGTTTCTTTGGTCCACTGTGAGCC	950
Db	786	TCTGACGACGATGAAGAGCATCATGAGATCTTTTTCGCTTCGAGACCTGTGCTGAGAAC	845
OY	951	ATATCAACCGCTGATTTGTCTTTACCACAACATCTCTGGGAAATGTTAAACCTGCTTG	1010

DB 846 ATATCTACCGGACACACTGTGTGCTTAACACCGCATGATGACGAAATAGCTG 905
1011 GGGTAATTCGATACCCACATATGATGGTAACACTTCATATAGGGTCTATTTTCACTTC 1070
DB 906 GAGTCTCAGAGATACCCATGATCTTTGAGAGCCAGAGCTTCGAGGGATGATCTTATCC 965
OY 1071 AATTTTAAAGCAAAATGCCATATGCTTTTAAAGAACTTGTGCAATTTTGTGCC 1130
DB 966 AGAGGTTTCAAGCGCGGACCAACCCCTCGATGAGGTGGTMACTGCAAGAAATCTCTACC 1025
OY 1131 AAGTGAATGGCTGATGATGCAACGCGCCCGAGAGACCTTGAATGGGTGCTAAAT 1190
DB 1026 GAGCGATCTCGT---CTTAACCTAGATCCAAACTGCGTAGAACTAGGCGCTTGACAC 1081
OY 1191 TAAAGGCTCATGTTACAGAGAAACACCAACAGCTGTAAT-----TTTATGG 1240
DB 1082 TGAAGAAAGCGGTATTTTCGGGAGCAACCCGTACACGCAACATGATGAAGTTTCTCG 1141
OY 1241 ATCTTTGCTTCACATCTATTTCTGGTCCCATGCGATGCTTGTGCAATTAACGTTCA 1300
DB 1142 AGCTATCTCATATCGAGATTTCTGGACCCCTATATACAGGCGAGCTTTGAACCGGTGCC 1201
OY 1301 ATACACCTCCGCTACACCCGCTACTTGTATGCTTGCACCTTCGATGGAAATCTTA 1360
DB 1202 GCGAATCCAGCG---CACCCACGATCTGTATGATGATTCGATCGAATCCAA---CTGT 1255
OY 1361 TCATTCCTATCGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1420
DB 1256 GCAACGCCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1315
OY 1421 AATTAACCTATTTCTTGTGATATATTTGGCAACGTAAGCTTAAGAAATGCGGTGAAT 1480
DB 1316 ATCTGTCTATATTTTCCACAGCATGTTGTGCAATCCGCTCCGATTTCCGGAAC 1375
OY 1481 ACAAAACATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1540
DB 1376 ACAAGCTTATTAACCGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1435
OY 1541 ATAGCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1600
DB 1436 ACTGCGAAAGTAAATACACTCAAGTTTGCACCCATGCAAAACGTAACCACTTT---- 1491
OY 1601 AAGTATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1660
DB 1492 -----AAGTGTCTCATATTTGGGATGATGATGATGATGATGATGATGATGATGATG 1543
OY 1661 ATAGATTTAAAC 1672
DB 1544 AGAAATTCGAC 1555

RESULT 15
ABL01859
ID ABL01859 standard; cDNA: 1863 BP.
XX
XX ABL01859;
AC
XX 26-MAR-2002 (first entry)
DT
XX
DE Drosophila melanogaster expressed polynucleotide SHQ ID NO 59.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
OS
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX

PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX P-PDB; ABB57756.
PT
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
PS Claim 1; SEQ ID NO 59; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 1863 BP; 425 A; 493 C; 523 G; 422 T; 0 other;

Query Match 18.9%; Score 323; DB 23; Length 1863;
Best Local Similarity 51.5%; Pred. No. 1,7e-78;
Matches 796; Conservative 0; Mismatches 745; Indels 6; Gaps 2;

OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGAAATGATGATGATGATGATGATG 60
DB 166 ATGAGATCCGAGTGGAGTGGGCGATGCTGGAATGAGCAACCAAGCTATTTGGCCAC 225
OY 61 AAGTTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
DB 111 ATGATGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 285
OY 121 AAGTGAAGGCGTTAAACGTTAACTGTGT---ACGATGATGCTTACTATGATGATGATG 177
DB 286 CAGTCCGCGGACATCGCGGAGGACACTCTACGAGGAGATGATGATGATGATGATGATG 345
OY 178 GGTATACCGTACCGCCACCGGAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 237
DB 346 GGAATCCCTTTGACACGCGCGGCGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 405
OY 238 ACACCTGGAGTGTGTGCTGATGTTGTCATTAAGATTAAGTGAAGTGAAGTGAAGTGA 297
DB 406 CATCCCTGTTGGGGGCGGATGACCTATCCCGGGCCAGCGGATGGAAGAC 465
OY 298 TTTATTAACGGGCAAGTGTGTGCTGAGAGATGTTCTATTAAGTGAAGTGAAGTGAAGT 357
DB 466 TTTGCTGCTCAGCATGCTGCAAGGACGAGAGATGCTGCTGATGATGATGATGATGATG 525
OY 358 AATCTAAATCCGAACTAAACGTTCCGTTTATGATTAATACATGATGATGATGATGATG 417
DB 526 CGCTGAGATCGCAACGCGCTGCGTGTGATGATGATGATGATGATGATGATGATGATG 585
OY 418 ATCGGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
DB 586 TTCGCGAGCGTGTGAGATTTCTAAGTCAAGACTACTTATGACAGCAAGACGATGAG 645
OY 478 TTGATTAACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 537
DB 646 GTTGACATTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 705
OY 538 CTTAATGTCCCGGATATGCGGCGCTTAAGATCAATGATGATGATGATGATGATGATGATG 597
DB 706 TTGATGTGCGCGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 765

QY 598 AATAATGCGCAACTTGGTGGCAATCCGATATATTAACGTTTGTGTAAGTCC 657
 Db 766 CAGAAACATAGGCCAATTCATGAGATGCCAAATATTAACGTTGATGGGAGAGTCC 825
 QY 658 GGTGCTGCTCTACCCACTACATGATGTTAACGACAAACCTCGGCTTTTCCATCGT 717
 Db 826 GGACACAGCTCCGTTACGCGTGTATGACCCAGCAAAACCCAGGCGCTTCCACAAG 885
 QY 718 GGTATCTAATGTGGGTAATGCTATTGTTCATTTGGCTAATACCAATGTCACATCGT 777
 Db 886 GCCATCATGCAATGGATGCCATGTCGAGTGGCCATGAGCCAAATGGCAGGTGG 945
 QY 778 GCCCTCACTTACCAATTTGGCGGCTATTAAGGTGAGTAAATGATAGGATTTTG 837
 Db 946 GCATACCGACTGGCTGCAATTTGGATACTGGGCACTGGAACGAGAAAGTGTTC 1005
 QY 838 GAATTTCTTATGAAGCCCAAGCCACAGGATTTAATAAACTTGAGAAAGTTTAACT 897
 Db 1006 CGATACCTTCAGAAAGCACCGGCTCCGAATGGCCGACAGGATTTACTTGTCTCC 1065
 QY 898 CTAGAAGAGCTACAAATAGCTATGTTTCTTTGGTCCACTGTTGAGCAATATCAG 957
 Db 1066 CAAAGAGAACGCGCGAGTACGTCCTGTTCCCTTACTCCGTTGTGGAACCAATATTC 1125
 QY 958 ACCGCTGATTTGTTCTTACCCAAACATCCCTCGGAAATGTTAAACGCTTGGGTAAT 1017
 Db 1126 ACCAGGATTTGCTTTTGGCCCGCTTGCACAGGAGATGTCGCGAAGCTTGGGGTAT 1185
 QY 1018 TCGATACCCACTATGATGAGGTATGACATTCATATGAGGTCATTTTCTCAATTCYT 1077
 Db 1186 GACCTGCGGCTGATCTCGGGGCGACACTCCTTGAAGTCTTCTCTACCAGAGTACC 1245
 QY 1078 AAGCAATGCTTATGCTTTTGAAGAAATGGAACCTGTGCAATTTTGTGCCAAGTGA 1137
 Db 1246 CTGCACGACGAGAACACATGCTGATGCTTTTGAAGTCTTAATTCCTCGGAGATCAG 1305
 QY 1138 TTGCTGATGCTGAACGACCGCCCGACAGACTTGGAAATGGGCTTAATAAATGAAG 1197
 Db 1306 GAGAAAGATACCCAGTGGCATCTTAAGGATCTGCTACGTCATTTAAGTGATTAATCTC 1365
 QY 1198 GCTCATGTTACAGAGAAACACACAGCTGATATTTATGATCTTGTCTCACATC 1257
 Db 1366 GATGATGAGACTCGAGGGCGAATGAGTTCAATGATGCCATATCTGTCGGTTAA 1425
 QY 1258 TATTTCTGTTCCCATGATGCTTTGTGCAATTTAGCTTCAATTCACACCTCCGTTACA 1317
 Db 1426 CACTTTTGGCATGGCATTCAGCACTGTATTTGGCCCGGCTCAGCCACGCCCGCAAG 1485
 QY 1318 CCCGTTACTGTATGCTTGCATGCTGATCGGAAAGATCTTATCAATCCCTATCGTAT 1377
 Db 1486 CCCACCTTACCTGTACCGCTTGAATGTGACTCG--CCCAATTCATACCTTCCGGCAG 1542
 QY 1378 ATGCGTAGTGACGTGTGTAAAGGCTGTAGTATGCTGATGATTAACCTATTTCTTC 1437
 Db 1543 GTGATGCGCGGAAACAGGTTCCGGGAGTATGATGCCGACGATCTCTCTACCTTTC 1602
 QY 1438 TGAATCAATTTGGCCAAACGATGCTTAAGAAATCGCGTGAATACAAACATTTGAACGT 1497
 Db 1603 TATCACATTTTGGCCAAACGATGATTAAGTCTGATGAGTACCAAAACCATACAGAGA 1662
 QY 1498 ATGACGTGATATGATACATTTGGCAACCCAGTGTATCCTTATAG 1544
 Db 1663 CTGGTGGCATGTGGGTGCTTCCCGGAAACACATCCCAATGTG 1709

Search completed: April 11, 2003, 01:06:53
 Job time : 263.905 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1663.49 Seconds
(without alignments)
16677.553 Million cell updates/sec

Title: US-09-776-910-9
Perfect score: 1713

Sequence: 1 atgaattcaccgttagttt.....aacatagagattattttag 1713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	313.6	18.3	778	9	AI062034 GH01076.5
2	282.4	16.5	649	9	AI388926 GH19977.5
3	265.2	15.5	688	9	AI403569 GH23036.5
4	256.6	15.0	671	9	AI517692 GH28740.5
5	254.4	14.9	569	13	BI609541 RH14337.5
6	250	14.6	674	13	BI628316 RH56682.5

7	249.4	14.6	676	13	BI635372 SD16705.5
8	248.6	14.5	660	13	BI639486 SD22067.5
9	248.4	14.5	673	13	BI614181 RH43493.5
10	246.8	14.4	672	13	BI614443 RH43812.5
11	246.4	14.4	670	13	BI233202 RE29491.5
12	245	14.3	648	9	AI113763 GH10213.5
13	245	14.3	648	9	AI403098 GH2464.5
14	243.4	14.2	646	9	AI109901 GH09292.5
15	243.4	14.2	646	9	AI293416 LH06524.5
16	241	14.1	526	9	AI108080 GH06811.5
17	239.8	14.0	516	9	AI108156 GH06911.5
18	239.2	14.0	658	13	BI564586 RH61888.5
19	238.4	13.9	656	13	BI619037 RH49995.5
20	236.8	13.8	656	13	BI614821 RH44296.5
21	236.6	13.8	669	13	BI588370 RH29561.5
22	236.2	13.8	656	13	BI621302 RH52624.5
23	233.2	13.6	628	9	AI109573 GH080808.5
24	232.2	13.6	630	9	AI403830 GH23353.5
25	231.4	13.5	619	9	AI516869 GH27454.5
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27	230.8	13.5	628	13	AI513346 GH26524.5
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32	229.2	13.4	622	9	AI134524 GH12012.5
33	228	13.3	633	13	BI370683 RE57396.5
34	222.6	13.0	670	9	AI389766 GH21022.5
35	219.8	12.8	614	13	BI617897 RH48369.5
36	219.2	12.8	615	13	BI588504 RH29849.5
37	218.6	12.8	587	9	AI517539 GH28541.5
38	218.6	12.8	588	13	BI638519 SD20822.5
39	218.6	12.8	607	13	BI624437 RH63994.5
40	218.6	12.8	609	13	BI567399 RH37771.5
41	218.6	12.8	609	13	BI607309 RH74350.5
42	218.6	12.8	609	13	BI622392 RH54254.5
43	218.6	12.8	609	13	BI630054 RH59016.5
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45	217.8	12.7	612	13	BI631806 RH61455.5

ALIGNMENTS

RESULT 1
LOCUS AI062034 778 bp mRNA
DEFINITION GH01076.5prime GH Drosophila melanogaster head POT2 Drosophila melanogaster cDNA clone GH01076 5prime similar to U51050:
Drosophila melanogaster alpha esterase (ae7) gene, partial cds,
mRNA sequence.

ACCESSION AI062034
VERSION AI062034.1 GI:3337873
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 778)

REFERENCE Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.
BDGP/HMMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP

TITLE JOURNAL
COMMENT Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
Plate: 10 row: G column: 4
High quality sequence stop: 363.
Location/Qualifiers

FEATURES

QY 908 GTACAAATAGGTCATGTTCTTTGGTCCACGTGTGACCATATACAGCCGTCATT 967
 Db 484 GCATGAACCAAGATATGTTTGGCTTTGGCCCATCCCTGGAACATTCTCCAGCCCGAAT 543
 QY 968 GTGTCTTACCCCAACATCTCGGGAATGGTTAAACCTGCTGGGTAATTCGATACCCA 1027
 Db 544 GTGTGATATCCAGGCTCCCAAGAGATGATGAAGACCGGCTGAGTAACCTCATCCCA 603
 QY 1028 CTATGATGGTACACTTATATGAGGCTCTATT 1063
 Db 604 TGTATTAGGAACACTGCTGACGAGGCTGCTGT 639
 RESULT 3
 A1403569 688 bp mRNA linear EST 19-APR-2001
 LOCUS GH23036.5prtime GH Drosophila melanogaster head POT2 Drosophila
 DEFINITION melanogaster cDNA clone GH23036 5prtime similar to U51050:
 Drosophila melanogaster alpha esterase (ae7) gene, partial cds,
 mRNA sequence.
 ACCESSION A1403569
 VERSION A1403569.1 GI:4246556
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 688)
 AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S. and Rubin, G. M.
 TITLE BDGP/HM1 Drosophila EST project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 Plate: 230 row: C column: 12
 High quality sequence stop: 648.
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 /dev_stage="adult"
 /lab_host="DH5 - alpha"
 /note="Organ: head; Vector: POT2; Site_1: EcoRI; Site_2:
 XhoI; Sized fractionated cDNAs were directly ligated into
 POT2. Plasmid cDNA library."
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 Best local Similarity 65.2%; Pred. No. 1.7e-61;
 Matches 390; Conservative 0; Mismatches 208; Indels 0; Gaps 0;
 QY 1 ATGAATTTCACGTTAGTTGATGAGAAATTAATGCAAGTAAATGCATTGAAAT 60
 Db 91 ATAAATTAAGAACCTCGCTTGTGAGCGCTTGGCGGCTCAAAACACATCGACAT 150
 QY 61 AAGTTTTTAACTATCGTTTAACTACCAATGAACGCTGCTAGCTGAATGAATAGC 120
 Db 151 AAGTCCAGAGATATCGCCAGTGCACCAATGAACAGTTTGTCCGACACGAGTAGCGC 210
 QY 121 AAGTGAAGCGCTTAAGCTTAACTGTGTACGATGATTCCTACTACAGCTTTGAGGT 180
 Db 211 CAAGTGAAGGGTATCAAGGCTCTATCTCTACTAGTGGCTTACTTACCTTCGAGGGT 270
 QY 181 ATACGCTAGCCCAACGCCAGTGGGTGAGCTGAGATTTAAACACCCCAACCAACA 240

Db 271 ATCCCGTAGCCCAACGCTCCGGGTGGGAGTGTGCGTTTAAAGCCCTCGAGGCCAT 330
 QY 241 CCCTGGAGTGTGTGGCTGATTTGTCATCAATCAATGAATGAATGATGCAAGTTGATTT 300
 Db 331 CCTGGAGGAGCATGTGCGGCTGCTGACGACCCAGAGATGAAGCCGCTGAGTGCAGTTC 390
 QY 301 ATACGCGCAACTGTGTGCTCAGAGATTTGTCTATACCTAAGTGTCTATAGCAATAT 360
 Db 391 GTCTTCATTAAGGTATAGAGGCTCCGAGACTGCTCTATCTCATGTGTACCAACAAAT 450
 QY 361 CTAATATCCGAACATAACGCTCCGTTTGTATATACATACATGTGTGTTTATATATC 420
 Db 451 GTGAAGCCGACCAAGGCTGCCCGGTTATGTTGATTCACGAGAGAGGCTTCATTATC 510
 QY 421 GTGAAAATCATCTGTATATGATGTCCTGATTTATTTCAATAAAGATGTGTGTTG 480
 Db 511 GCGAGGCCAATGCGGATGTATGGCCGAGATTACTTATGAAGAAGATGTTGTTCTC 570
 QY 481 ATTAACATACATATGCTTTGGAGCTCTAGTCTTCTAGTTTAATTCAGAAAGACCTT 540
 Db 571 GTACGATACAGTACGACACTTGGGCTTGGATTATGAGTCTTAAGTCCCGGAGCTA 630
 QY 541 AATGCCCCGTAATGCGCGCTTAAAGATCAATCATGCTGCTTGCATTGATTA 598
 Db 631 AATGTACAGGAATATGCTGCGCTCAAGATCAGTGTGCGCTCAAGTGTGATCAGA 688
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 LOCUS GH28740.5prtime GH Drosophila melanogaster head POT2 Drosophila
 DEFINITION melanogaster cDNA clone GH28740 5prtime similar to U51050:
 Drosophila melanogaster alpha esterase (ae7) gene, partial cds,
 mRNA sequence.
 ACCESSION A1517692
 VERSION A1517692.1 GI:4420792
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 671)
 AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S. and Rubin, G. M.
 TITLE BDGP/HM1 Drosophila EST project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 Plate: 287 row: D column: 4
 High quality sequence stop: 538.
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 Best local Similarity 65.4%; Pred. No. 3.9e-59;

KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 674)

AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Mungall, C.J., Nuno, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.

TITLE BDGP/HMI RH Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST/estfruitfly.berkeley.edu>
Plate: RH.566 row: G column: 10
High quality sequence stop: 558.
Location/Qualifiers
1. 674

FEATURES
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/dev_stage="Adult"
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/note="Organ: head; Vector: pfic1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
BASE COUNT 153 a 170 c 195 g 155 t 1 others

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Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 111 ATGAATTAAGAACTCGGCTTTGTGAGCGCTTGGCGGCTCAAAACCATGAGCAT 170
61 AAGTTTAAACTATGTTAACTACCAATGAACGGTGGTGAAGTGAATATGCG 120
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
121 AAGTGAAGGCGTTAAAGCTTTAACTGTAGACGATTTCTACAGTTTGAAGGT 180
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 231 CAAGTAGGGGTATCAAGCGCTATCTCTACAGATGTGCCCTACTTACAGTTGAGGT 290
181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCACCACGACCAACA 240
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361 CTAAATCCCAAACTAAAGCTCCGTTTGTATACATACATGTTGGTTTATTATC 420
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Db 471 GTAAAGCCCAACAAGCTCCCGGTTATGTTGATTCACGAGAGAGCTTCATTATC 530
421 GTGAATAATCATGCTGATATGATGTCGATATTATTCAATAAAGATGTGTTG 480

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LOCUS
DEFINITION SD16705.5 prime SD Drosophila melanogaster Schneider L2 cell culture
POT2 Drosophila melanogaster cDNA clone SD16705 5 similar to
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carboxyesterase (GO:0004091)] located on: 3R 84D5:: 05/18/2001
, mRNA sequence.
BI635372
BI635372.1 GI:15537582
VERSION
KEYWORDS
SOURCE
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 676)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST/estfruitfly.berkeley.edu>
Plate: SD.167 row: A column: 5
High quality sequence stop: 641.
Location/Qualifiers
1. 676

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Best Local Similarity 65.2%; Pred. No. 3.7e-57;
Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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Db 114 ATGAATTAAGAACTCGGCTTTGTGAGCGCTTGGCGGCTCAAAACCATGAGCAT 173
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Db 174 AAGTCCAGCAGTATCCGACGATGACCAATGAACAGTTGTCGCCGACAGAGTACGGC 233
121 AAGTGAAGGCGTTAAAGCTTTAACTGTAGACGATTTCTACTACAGTTTGAAGGT 180
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Dd	489	AGTAACCTCCATCCCCATGTTTATAGAACAACCTTCGTACGAGGGCTCTGCTGGSTTCCA	548
Qy	1072	ATTCTTAGCAAAATGCCATGCTGTTTAAAGAAATTTGGAACCTGTGTCAATTTTGTGCCA	1131
Dd	549	GAGGTAAAGCTTTATGCCCGCAGGTGCTGACAGACACTTGATGCTGGACACACTTTCATTC	608
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Dd	609	AAAGATT	615

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	Drosophila melanogaster cDNA clone RH43493.5 similar to alpha-Est7				
	PBAN001112 GO: [carboxylesterase (GO:0004091); carboxylesterase				
	(GO:0004091)] located on: 3R 84D5-84D5; : 08/18/2001, mRNA sequence				
ACCESSION	Bt614181				
VERSION	Bt614181.1				GI:15509706
KEYWORDS	EST.				
SOURCE	fruit fly,				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
	Dicostera; Diptera; Brachycera; Muscomorpha;				

REFERENCE	TITLE
AUTHORS	JOURNAL
	COMMENT
1 (bases 1 to 673)	
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson	
J., Champe, M., Chavez, C., Dorsett, V., Fartan, D., Frise, E., George	
R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miera, S.,	
Mungall, C. J., Nunoo, J., Paclob, J., Paragas, V., Park, S.,	
Phonuananong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin	
, G. M.	
BDGP/HMMI RH Drosophila EST Project	
Unpublished (2001)	
Contact: Stapleton, M.	
BDGP	
Lawrence Berkeley National Lab	

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu

Plate: RH.434 row: H column: 9

High quality sequence stop: 553.

FEATURES

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BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
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BASE COUNT 153 a 169 c 195 g 155 t 1 others

ORIGIN

Query Match 14.5%; Score 248.4; DB 13; Length 673;
Best Local Similarity 65.0%; Pred. No. 6.9e-57;
Matches 366; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

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QY 1 ATGAATTTCAACGTTAGTTGATGAGCAATTAATAATGCAAGTTAATGATTGAAT 60
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Db 111 ATGAATTAAGAACCTCGGCTTTGTGAGCGCTTGGGGGCCCTCAAAACATGACAT 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AAGTTTTAACTATCTGTTAACTACCAATGAAACGGTGTAGCTGAATGATATGCG 120
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 AAGTTCAGAGATATCGCCAGTGCACCAATGAACATTTGCGCCGACAGGATACGCC 230
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QY 121 AAGTGAAGGCGTTAAGCTTTAACTGTGTAGAGATTTCTACTACAGTTTGAAGGT 180
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 231 CAAGTGGGGTATCAAGCTCTATCTCTAGAGTGTCCCTACTCAGCTTGCAGGCT 290
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QY 181 ATACCGTACGCCCAACGCCAGTGGGAGCTGAGTTTAAAGCCCGCCAGCCACACA 240
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Db 291 ATCCCGTACGCCCAACGCCAGTGGGAGTGGGTTAAGGCCCTCAGAGGCCATT 350
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QY 241 CCTGGGATGTGCTGATGTTGTCATCAATCAATGAATGAATGATGATTTT 300
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Db 351 CCTGGGAGGAGTGTGCGCTGCTGACAGCCAGCAAGATGAAGCCGTCAGGTCATTC 410
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QY 301 ATAAAGGCAAGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACCAATAT 360
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QY 361 CTAAATCCGAACCTAAGCCGTTTGTATACATACATGATGTTGTTTATATC 420
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 471 GTGAAGCCCAACAGCTGCCCGGTTATGTTGATTTACGAGAGAGGCTTATTATC 530
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QY 421 GGTGAATATCATGCTGATATGATGCTGATATTATTTCAAAAAGATGTGCTTG 480
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Db 531 GCGAGGCCAATCGGGAATGATGATGCGCGGATTAATTGAAGAAGATGTGCTC 590
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QY 481 ATTAACATTAATATGCTTTGGAGCTCTAGAGTTTCTAAGTTTAAATTGAGAAGCTT 540
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Db 591 GTACAGTAAATAGTACACACTTGGGCTTTGGGATTTAGTCTTAAGTCCCGGACCTA 650
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QY 541 AATGTCGCGGTATGCGGCT 563
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Db 651 AATGTACAGGAATGCTGGCT 673
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```

RESULT 10

BI614443 672 bp mRNA linear EST 07-SEP-2001
LOCUS RH43812.5 Sprime RH Drosophila melanogaster normalized Head p1C-1
DEFINITION Drosophila melanogaster cDNA clone RH43812.5 similar to alpha-Est7;
Fban0001112 GO: [carboxyesterase (GO:0004091); carboxyesterase

ACCESSION

BI614443

VERSION GI:15509968

KEYWORDS EST.

SOURCE fruit fly.

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

1 (bases 1 to 672)

Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson

J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George

R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,

Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,

Pouanenhavong, S., Wan, K., Yu, C., Lewis, S.E., Celnik, S. and Rubin

G.M.

BDGP/HHMI RH Drosophila EST Project

Unpublished (2001)

COMMENT Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu

Plate: RH.438 row: A column: 12

High quality sequence stop: 554.

FEATURES

source

```
1. 672
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1lb="RH43812"
/clone_1lb="RH Drosophila melanogaster normalized Head
p1C-1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: p1C1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
```

BASE COUNT 154 a 169 c 194 g 155 t

ORIGIN

Query Match 14.4%; Score 246.8; DB 13; Length 672;
Best Local Similarity 64.9%; Pred. No. 1.9e-56;
Matches 365; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

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QY 1 ATGAATTTCAACGTTAGTTGATGAGCAATTAATAATGCAAGTTAATGATTGAAT 60
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Db 111 ATGAATTAAGAACCTCGGCTTTGTGAGCGCTTGGGGGCCCTCAAAACATGACAT 170
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QY 61 AAGTTTTAACTATCTGTTAACTACCAATGAAACGGTGTAGCTGAATGATATGCG 120
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Db 171 AAGTTCAGAGATATCGCCAGTGCACCAATGAACATTTGCGCCGACAGGATACGCC 230
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QY 121 AAGTGAAGGCGTTAAGCTTTAACTGTGTAGAGATTTCTACTACAGTTTGAAGGT 180
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Db 231 CAAGTGGGGTATCAAGCTCTATCTCTAGAGTGTGCCCTACTTACGCTTGAGGGT 290
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QY 421 GGTGAATATCATGCTGATATGATGCTGATATTATTTCAAAAAGATGTGCTTG 480
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Db 531 GCGAGGCCAATCGGGAATGATGATGCGCGGATTAATTGAAGAAGATGTGCTC 590
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QY 481 ATTAACATTAATATGCTTTGGAGCTCTAGAGTTTCTAAGTTTAAATTGAGAAGCTT 540
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Db 591 GTACAGTAAATAGTACACACTTGGGCTTTGGGATTTAGTCTTAAGTCCCGGACCTA 650
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QY 541 AATGTCGCGGTATGCGGCT 563
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 651 AATGTACAGGAATGCTGGCT 672
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Db 471 GTGAAGCCGCAAGGCTCCCGGTTATGTTGATTCACGAGGAGGCTTATTATC 530

Qy 421 GGTGAAATCATCGTATATGATGTCCTGATATTATTCATTAAGAGATGCTGTTG 480

Db 531 GCGGAGGCGCATCGGAAATGATGATGCGCGGATTCATTATGAAGAGATGTTCTC 590

Qy 481 ATTAACATACATATGCTTTGGAGCCTAGTCTTCTTAAGTTAAATTCAGAACCTT 540

Db 591 GTCAGATACATACGCTGCGGCTTGGGATTTAGATCTTAAGTCCCCGAGCTA 650

Qy 541 AATGCGCGGATATGCGGCG 562

Db 651 AATGTACCAAGAAATGCTGCG 672

RESULT 11

BI233202 670 bp mRNA linear EST 11-JUL-2001

LOCUS RE29491.5prtime RE Drosophila melanogaster normalized Embryo pfic-1

DEFINITION Drosophila melanogaster cDNA clone RE29491 5 similar to alpha-EST7: FBan0001112 located on: 3R 84D5-84D5; 04/12/2001, mRNA sequence.

ACCESSION BI233202

VERSION BI233202.1 GI:14700784

KEYWORDS EST.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila;

AUTHORS 1 (bases 1 to 670)

Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Wungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phoumenavong, S., Wan, K., Yu, C., Lewis, S.E., Celinker, S. and Rubin, G.M.

TITLE BDGP/HMMT RE Drosophila EST Project

JOURNAL Unpublished (2001)

COMMENT Contact: Stapleton, M.

BDGP

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Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Plate: RE:294 row: H column: 7

High quality sequence stop: 534.

Location/Qualifiers

1. 670

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone_lib="RE Drosophila melanogaster normalized Embryo pfic-1"

/sex="male and female"

/dev_stage="0-24 hours mixed stage embryonic"

/lab_host="DHS-alpha Tona"

/note="Organ: embryo; Vector: pfic1; Site:1: XhoI; Site:2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

BASE COUNT 152 a 168 c 194 g 155 t 1 others

ORIGIN

Query Match 14.4% Score 246.4; DB 13; Length 670;

Best Local Similarity 64.9% Pred. No. 2.4e-56;

Matches 364; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

Qy 1 ATGAATTCACGCTTAGTATGAGAAATTAATGACATTAATGATGAAAT 60

Db 110 ATGAATTAAGACCTCGGCTTGGAGCGCTTCCGCTCAAAACCATCGAGCAT 169

Qy 61 AAGTTTAACTATGCTTAACTACCAATGAAGCGTGATGCTGAACCTAATATGCG 120

Db 170 AAAGTCACAGATATGCGAGTCGACCAATGAACAGTTGTGCCGACGAGATACGCC 229

Qy 121 AAAGTGAAGCGCTTAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTGAAGGT 180

Db 230 CAAGTGAAGGCTATACAGGCTATCTCTACGATGTGCGCTTACTTACAGTTGAGAGGT 289

Qy 181 ATACGTCAGCCCAACCGGACGAGTGTGAGCTAGATTTTAAAGCACCCGACGACCA 240

Db 290 ATCCCTAGCCGACGCTCCGGGGAGTTCGCGTTAAGGCCCCCAAGGCCCATTT 349

Qy 241 CCCTGGAGTGTGTGCTGCTATTTGTCATTCATTAAGATAGTCAAGTTCATTTT 300

Db 350 CCCTGGAGGAGTGTGCGACCTGACGACCGACGAGATAGAGCCGCTCAGAGTGA 409

Qy 301 ATAAAGGCGAAAGTGTGTGCTGACGACGAGATGTCTATACCTAAGTCTATACGAAT 360

Db 410 GTCTTGATATAGTATAGAGGCTCCGAGGACTGCTTATCTCAATGTGACCAACAT 469

Qy 361 CTAAATCCGAAACCTAAAGCTCCGTTTATATATACATACATGAGTGTGTTTATATC 420

Db 470 GTGAAGCCGCAAGGCTCCCGGTTATGCTTGGATTCACGAGAGGCTTCAATTATC 529

Qy 421 GGTGAATCATGCTGTATGATGTCCTGATTTATTTCAAAAAGATGTGTGTTG 480

Db 530 GCGAGGCGCAATCGGAGATGATGCGCGGATTTACTTATGANAAGATGTTGTTCTC 589

Qy 481 ATTAACATACAAATATCGTTTGGAGCTTAGGTTTCTAAGTTTAAATTCAGAACCTT 540

Db 590 GTCAGATACGATCCGACTTGCGGCTTGGATTTATGATGCTTAAAGTCCCCGAGCTA 649

Qy 541 AATGCGCGGATATGCGGCG 561

Db 650 AATGTACCAAGAAATGCTGCG 670

RESULT 12

A1113763 648 bp mRNA linear EST 19-APR-2001

LOCUS GH10213.5prtime GH Drosophila melanogaster head pot2 Drosophila

DEFINITION melanogaster cDNA clone GH10213 5prtime similar to U51050: Drosophila melanogaster alpha esterase (aet7) gene, partial cds, mRNA sequence.

ACCESSION A1113763

VERSION A1113763.1 GI:3514566

KEYWORDS EST.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila;

AUTHORS 1 (bases 1 to 648)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.

TITLE BDGP/HMMT Drosophila EST Project

JOURNAL Unpublished (2001)

COMMENT Contact: Stapleton, M.

BDGP

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One Cyclotron Rd. Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Plate: 102 row: B column: 1

High quality sequence stop: 435.

Location/Qualifiers

1. 648

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="GH10213"

/clone_lib="GH Drosophila melanogaster head pot2"

/sex="male and female"

/dev_stage="adult"

/lab_host="DHS - alpha"

/note="Organ: head; Vector: pot2; Site:1: EcoRI; Site:2: